



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 112348

To: Karen A Lacourciere

Location: REM-2D15

Art Unit: 1635

Wednesday, January 21, 2004

Case Serial Number: 09/423035

From: Beverly Shears

Location: Remsen Bldg.

RM 1A54

Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes

THIS PAGE BLANK (USPTO)

STIC-Biotech/ChemLib

112348

From: Lacourciere, Karen
Sent: Friday, January 16, 2004 2:13 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search 09/423,035

Please search SEQ ID NO:122 and 121 for 09/423,035 in the commercial databases. Please length limit the search to hits less than 100 nucleotides in length.

Thanks-
Karen

Karen A. Lacourciere Ph.D.

Remsen 2D15 GAU 1635
(571) 272-0759

CRF

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

THIS PAGE BLANK (USPTO)

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 01-21-04
Searcher: Beverly C. 2528
Terminal time: 33
Elapsed time: _____
CPU time: _____
Total time: 38
Number of Searches: _____
Number of Databases: 2

Search Site

☐ STIC
☐ CM-1
☐ Pre-S
Type of Search
☐ N.A. Sequence
☐ A.A. Sequence
☐ Structure
☐ Bibliographic

Vendors

☐ IG
☒ STN
☐ Dialog
☐ APS
☐ Geninfo
☐ SDC
☒ DARC/Questel
☒ Other CGN

THIS PAGE BLANK (USPTO)

09/423035

L1 FILE 'REGISTRY' ENTERED AT 12:29:20 ON 21 JAN 2004
37479 S RGGCTAGC[HT]ACAACGA/SQSN

L7 37 S L1 AND SQL=<20

L8 FILE 'HCAPLUS' ENTERED AT 12:39:58 ON 21 JAN 2004
26 S L7

L8 ANSWER 1 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:1007150 HCAPLUS
TITLE: Antisense oligonucleotides against the PIM1 gene
for use in analgesia
INVENTOR(S): Altan, Oezlem; Kurreck, Jens; Gruenweller,
Arnold; Erdmann, Volker
PATENT ASSIGNEE(S): Gruenenthal G.m.b.H., Germany
SOURCE: PCT Int. Appl., 37 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: German
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003106681	A2	20031224	WO 2003-EP6158	20030612
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			

PRIORITY APPLN. INFO.: DE 2002-10226702 A 20020614
AB Antisense DNA for use in inhibiting expression of the PIM1 gene are described for use in the diagnosis and control of PIM1 kinase-mediated pain perception. Use of PIM1 antisense oligonucleotides injected into the spinal cord to increase the threshold of pain perception is demonstrated in rat.
IT 638223-95-7
RL: PRP (Properties)
(unclaimed nucleotide sequence; antisense oligonucleotides against the PIM1 gene for use in analgesia)

L8 ANSWER 2 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:971390 HCAPLUS
DOCUMENT NUMBER: 140:26917
TITLE: Antibodies having specificity for
2'-deoxy-2'-C-allyl uridine-containing nucleic acids, and their use in detecting and monitoring therapeutic nucleic acid molecules in mammalian biological samples
INVENTOR(S): Radka, Susan; Beigelman, Leonid; Peter, Haeberli
PATENT ASSIGNEE(S): USA

THIS PAGE BLANK (USPTO)

09/423035

SOURCE: U.S. Pat. Appl. Publ., 38 pp.
 CODEN: USXXCO
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003228590	A1	20031211	US 2003-366191	20030212
PRIORITY APPLN. INFO.:			US 2002-356298P	P 20020213

AB The present invention relates to antibodies, antibody conjugates, and compns. thereof, methods of antibody synthesis, and applications of antibodies useful for the in vivo-detection of nucleic acid mols. containing 2'-deoxy-2'-C-allyl Uridine, such as in a clin. setting. The antibodies of the invention are also useful as screening agents which allow the selection of candidate therapeutic mols. for optimum bioavailability and/or activity, and as agents for cell and tissue specific-delivery of nucleic acid mols. The example discloses the development of a monoclonal antibody, CAIUSR, and its use for detection of the ANGIOZYME® ribozyme therapeutic in vivo. This antibody was developed for use in monitoring clin. trials of ANGIOZYME.

IT 633370-08-8

RL: PRP (Properties)
 (unclaimed nucleotide sequence; antibodies having specificity for 2'-deoxy-2'-C-allyl uridine-containing nucleic acids, and their use in detecting and monitoring therapeutic nucleic acid mols. in mammalian biol. samples)

L8 ANSWER 3 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2003:855650 HCAPLUS
 DOCUMENT NUMBER: 139:317479
 TITLE: Nucleic acid-based modulation of NOGO and NOGO receptor interactions and genes for treatment and/or diagnosis of associated diseases
 INVENTOR(S): Blatt, Lawrence; McSwiggen, James; Chowrira, Bharat M.; Haeberli, Peter
 PATENT ASSIGNEE(S): Ribozyme Pharmaceuticals, Inc., USA
 SOURCE: U.S. Pat. Appl. Publ., 77 pp., Cont.-in-part of Appl. No. PCT/US02/10512.
 CODEN: USXXCO

DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 12
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003203870	A1	20031030	US 2003-430882	20030506
WO 2001059103	A2	20010816	WO 2001-US4273	20010209
WO 2001059103	A3	20020613		
WO 2001059103	C2	20021024		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ,

THIS PAGE BLANK (USPTO)

09/423035

UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU,
TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH,
CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE,
TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD,
TG
US 2003060611 A1 20030327 US 2001-780533 20010209
US 2003113891 A1 20030619 US 2001-827395 20010405
WO 2002081628 A2 20021017 WO 2002-US10512 20020403
WO 2002081628 A3 20030220
WO 2002081628 C1 20030828
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH,
CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD,
GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ,
LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,
NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ,
TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM,
AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE,
CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT,
SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE,
SN, TD, TG

PRIORITY APPLN. INFO.:

US 2000-181797P P 20000211
US 2001-780533 B2 20010209
WO 2001-US4273 A2 20010209
US 2001-827395 B1 20010405
WO 2002-US10512 A2 20020403
US 2000-185516P P 20000228
US 2000-187128P P 20000306
US 2001-294412P P 20010529
US 2001-315315P P 20010828

AB The present invention relates to nucleic acid mols., including aptamers and antisense and enzymic nucleic acid mols., such as hammerhead ribozymes, DNazymes, and antisense oligonucleotides, which modulate the expression of NOGO and NOGO receptor genes. In particular, novel nucleic acid-based techniques are provided to inhibit the expression of NOGO-A, NOGO-B, and/or NOGO-C, NOGO-66 receptor, and/or NI-250, myelin-associated glycoprotein, tenascin-R, and NG-2. The sequence of human NOGO and NOGO receptor genes are screened for accessible sites using a computer-folding algorithm; regions of the RNA that do not form secondary folding structures and contain potential enzymic nucleic acid mol and/or antisense binding/cleaving sites are identified. The nucleic acids of the present invention can be used to treat a patient having a condition associated with the level of NOGO or NOGO receptor.

IT 613321-58-7

RL: PRP (Properties)

(unclaimed nucleotide sequence; nucleic acid-based modulation of NOGO and NOGO receptor interactions and genes for treatment and/or diagnosis of associated diseases)

L8 ANSWER 4 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2003:731500 HCAPLUS

DOCUMENT NUMBER: 139:224402

TITLE: Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection

INVENTOR(S): Blatt, Lawrence; McSwiggen, James; Roberts,

Searcher : Shears 571-272-2528

THIS PAGE BLANK (USPTO)

09/423035

PATENT ASSIGNEE(S): Elisabeth; Pavco, Pamela A.; MacJack, Dennis
SOURCE: USA
U.S. Pat. Appl. Publ., 172 pp., Cont.-in-part of
U.S. Ser. No. 740,332.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 104
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003171311	A1	20030911	US 2001-817879	20010326
AU 9851819	A1	19980611	AU 1998-51819	19980112
AU 729657	B2	20010208		
US 2002082225	A1	20020627	US 1999-274553	19990323
AU 9939188	A1	19990916	AU 1999-39188	19990713
US 2002013458	A1	20020131	US 2000-504231	20000215
US 2003125270	A1	20030703	US 2000-740332	20001218
PRIORITY APPLN. INFO.:			US 1998-83217P	P 19980427
			US 1998-100842P	P 19980918
			US 1999-257608	B2 19990225
			US 1999-274553	A2 19990323
			US 2000-504231	A2 20000215
			US 2000-611931	A2 20000707
			US 2000-740332	A2 20001218
			AU 1995-26422	A3 19950518
			US 1996-623891	A 19960325

AB This invention relates to enzymic nucleic acid mols. (e.g., ribozymes and DNazymes) directed to cleave RNA species of hepatitis C virus (HCV) and/or encoded by the HCV. Specifically, the present invention describes enzymic nucleic acid mols. that would cleave in the conserved regions of the HCV genome. In a preferred embodiment, the invention features the use of an enzymic nucleic acid mol., preferably in the hammerhead, Inozyme (NCH), G-cleaver, Amberzyme, Zinzyme and/or DNazyme motif, to inhibit the expression and/or replication of HCV. Chemical modifications in the sugar, base, and/or phosphate backbones of these enzymic nucleic acids is carried out to improve their stability. Such enzymic nucleic acid mols. may be used to treat diseases associated with HCV infection. Ribozymes in combination with interferons and polyethylene glycol interferons which have the potential to improve the effectiveness of treatment of HCV are also described. [This abstract record is one of two records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT 591261-44-8

RL: PRP (Properties)

(unclaimed nucleotide sequence; enzymic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection)

L8 ANSWER 5 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2003:568525 HCAPLUS

DOCUMENT NUMBER: 139:358722

TITLE: Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection

INVENTOR(S): Blatt, Lawrence; McSwiggen, James; Roberts,

Searcher : Shears 571-272-2528

THIS PAGE BLANK (USPTO)

09/423035

PATENT ASSIGNEE(S): Elisabeth; Pavco, Pamela A.; Macejack, Dennis
SOURCE: USA
U.S. Pat. Appl. Publ., 198 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 104
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003125270	A1	20030703	US 2000-740332	20001218
AU 9851819	A1	19980611	AU 1998-51819	19980112
AU 729657	B2	20010208		
AU 9939188	A1	19990916	AU 1999-39188	19990713
US 2003125270	A1	20030703	US 2000-740332	20001218
PRIORITY APPLN. INFO.:			US 2000-740332	A 20001218
			AU 1995-26422	A3 19950518
			US 1996-623891	A 19960325

AB This invention relates to enzymic nucleic acid mols. (e.g., ribozymes and DNazymes) directed to cleave RNA species of hepatitis C virus (HCV) and/or encoded by the HCV. Specifically, the present invention describes enzymic nucleic acid mols. that would cleave in the conserved regions of the HCV genome. In a preferred embodiment, the invention features the use of an enzymic nucleic acid mol., preferably in the hammerhead, Inozyme (NCH), G-cleaver, amberzyme, zinzyme and/or DNazyme motif, to inhibit the expression and/or replication of HCV. Chemical modifications in the sugar, base, and/or phosphate backbones of these enzymic nucleic acids is carried out to improve their stability. Such enzymic nucleic acid mols. may be used to treat diseases associated with HCV infection. Ribozymes in combination with interferons and polyethylene glycol interferons which have the potential to improve the effectiveness of treatment of HCV are also described. [This abstract record is one of two records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT 557143-59-6
RL: PRP (Properties)
(unclaimed nucleotide sequence; enzymic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection)

L8 ANSWER 6 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:309404 HCAPLUS
DOCUMENT NUMBER: 139:143909
TITLE: Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors
INVENTOR(S): Akhtar, Saghir; McSwiggen, James
PATENT ASSIGNEE(S): Kuwait
SOURCE: U.S. Pat. Appl. Publ., 199 pp., Cont.-in-part of U.S. Ser. No. 401,063.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 104
PATENT INFORMATION:

THIS PAGE BLANK (USPTO)

09/423035

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003073207	A1	20030417	US 2001-848754	20010503
US 6057156	A	20000502	US 1997-985162	19971204
AU 9851819	A1	19980611	AU 1998-51819	19980112
AU 729657	B2	20010208		
AU 9939188	A1	19990916	AU 1999-39188	19990713
US 6623962	B1	20030923	US 1999-401063	19990922
PRIORITY APPLN. INFO.:			US 1997-36476P P	19970131
			US 1997-985162 A1	19971204
			US 1999-401063 A2	19990922
			AU 1995-26422 A3	19950518
			US 1996-623891 A	19960325

AB The present invention relates to nucleic acid mols., including antisense and enzymic nucleic acid mols., such as hammerhead ribozymes, DNazymes, allozymes and antisense, which modulate the expression of epidermal growth factor receptor genes. The sequence of human epidermal growth factor receptor (EGFR) gene is screened for accessible sites using a computer-folding algorithm. Regions of the RNA that do not form secondary folding structures and contain potential enzymic nucleic acid mol. and/or antisense binding/cleavage sites are identified and used to design the complementary regions of the antisense and enzymic nucleic acid mols. Two human cell lines, A549 lung carcinoma cells and SKOV3 ovarian carcinoma cells known to express medium to high levels of EGFR protein, are used in anti-proliferation assays for nucleic acid screening. The invention designs, synthesizes and tests nucleic acid mols. that target both EGFR and HER2 RNA in cell proliferation and RNA reduction assays for potential use in treating cancer. [This abstract record is one of two records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT 506617-43-2

RL: PRP (Properties)

(unclaimed nucleotide sequence; enzymic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors)

L8 ANSWER 7 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2003:261042 HCAPLUS

DOCUMENT NUMBER: 138:282290

TITLE: Methods and kits containing nucleic acid-based enzymes for detection of single nucleotide polymorphisms in diagnosis of diseases

INVENTOR(S): Usman, Nassim; McSwiggen, James A.; Zinnen, Shawn; Seiwert, Scott; Haeberli, Peter; Chowrira, Bharat; Blatt, Lawrence; Vaish, Narendra K.

PATENT ASSIGNEE(S): USA

SOURCE: U.S. Pat. Appl. Publ., 116 pp., Cont.-in-part of U.S. Ser. No. 992,160.

CODEN: USXXCO

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 12

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
------------	------	------	-----------------	------

Searcher : Shears 571-272-2528

THIS PAGE BLANK (USPTO)

09/423035

```
-----
US 2003065155      A1    20030403      US 2002-56761      20020123
WO 2001066721      A2    20010913      WO 2001-US7163     20010306
WO 2001066721      A3    20020725
  W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH,
      CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE,
      GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,
      LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO,
      NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT,
      TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD,
      RU, TJ, TM
  RW:  GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH,
      CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE,
      TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD,
      TG
US 2002102568      A1    20020801      US 2001-877526     20010608
US 2003008295      A1    20030109      US 2001-992160     20011105
WO 2003089650      A2    20031030      WO 2002-US35529    20021105
  W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH,
      CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD,
      GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ,
      LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,
      NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ,
      TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW,
      AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
  RW:  GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE,
      BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU,
      MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ,
      GW, ML, MR, NE, SN, TD, TG
US 2004009510      A1    20040115      US 2003-422050     20030423
PRIORITY APPLN. INFO.:      US 2000-187128P    P 20000306
                                US 2001-800594      A2 20010306
                                WO 2001-US7163      W 20010306
                                US 2001-877526      A2 20010608
                                US 2001-992160      A2 20011105
                                US 2002-56761       A 20020123
                                US 2002-283858      A 20021030
                                US 2002-286492      A 20021101
                                WO 2002-US35529     A2 20021105
AB  Nucleic acid sensor mols. and methods are provided for the detection
    and amplification of signaling agents using enzymic nucleic acid
    constructs, including hammerhead enzymic nucleic acid mols.,
    inozymes, G-cleaver enzymic nucleic acid mols., zinzymes, amberzymes
    and DNazymes. Also provided are kits for detection and
    amplification. The nucleic acid sensor mols., methods and kits
    provided herein can be used in diagnostics, nucleic acid circuits,
    nucleic acid computers, therapeutics, target validation, target
    discovery, drug optimization, single nucleotide polymorphism (SNP)
    detection, single nucleotide polymorphism (SNP) scoring, and
    proteome scoring as well as other uses described herein.
IT  504513-55-7
    RL: PRP (Properties)
        (unclaimed nucleotide sequence; methods and kits containing nucleic
        acid-based enzymes for detection of single nucleotide
        polymorphisms in diagnosis of diseases)
L8  ANSWER 8 OF 26  HCAPLUS  COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER:      2003:261013  HCAPLUS
```

Searcher : Shears 571-272-2528

THIS PAGE BLANK (USPTO)

09/423035

DOCUMENT NUMBER: 138:292713
TITLE: Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors
INVENTOR(S): Akhtar, Saghir; McSwiggen, James
PATENT ASSIGNEE(S): Kuwait
SOURCE: U.S. Pat. Appl. Publ., 113 pp., Cont.-in-part of U.S. Ser. No. 848,754.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 104
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003064945	A1	20030403	US 2001-916466	20010725
US 6057156	A	20000502	US 1997-985162	19971204
AU 9851819	A1	19980611	AU 1998-51819	19980112
AU 729657	B2	20010208		
AU 9939188	A1	19990916	AU 1999-39188	19990713
US 6623962	B1	20030923	US 1999-401063	19990922
US 2003073207	A1	20030417	US 2001-848754	20010503
US 2003170891	A1	20030911	US 2002-251117	20020919
US 2003186909	A1	20031002	US 2002-277494	20021021
WO 2003070912	A2	20030828	WO 2003-US5045	20030220
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
PRIORITY APPLN. INFO.:	US 1997-36476P P 19970131 US 1997-985162 A1 19971204 US 1999-401063 A2 19990922 US 2001-848754 A2 20010503 AU 1995-26422 A3 19950518 US 1996-623891 A 19960325 US 1997-36749P P 19970127 US 2001-296249P P 20010606 US 2001-916466 A2 20010725 US 2002-358580P P 20020220 US 2002-363124P P 20020311 WO 2002-US16840 A1 20020529 US 2002-163552 A2 20020606 US 2002-386782P P 20020606 US 2002-393924P P 20020703 US 2002-406784P P 20020829 US 2002-408378P P 20020905 US 2002-409293P P 20020909 US 2002-251117 A1 20020919 US 2002-277494 A1 20021021 US 2003-440129P P 20030115			

THIS PAGE BLANK (USPTO)

09/423035

AB The present invention relates to nucleic acid mols., including antisense and enzymic nucleic acid mols., such as hammerhead ribozymes, DNazymes, allozymes and antisense, which modulate the expression of epidermal growth factor receptor genes.

IT 503875-66-9
RL: PAC (Pharmacological activity); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(enzymic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors)

L8 ANSWER 9 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:76966 HCAPLUS
DOCUMENT NUMBER: 138:142441
TITLE: Enzymatic nucleic acid peptide conjugates
INVENTOR(S): Beigelman, Leonid; Azhayev, Alex; Azhayeva, Elena
PATENT ASSIGNEE(S): Ribozyme Pharmaceuticals, Inc., USA; Antopolsky, Maxim
SOURCE: PCT Int. Appl., 88 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003008628	A2	20030130	WO 2002-US23324	20020722
WO 2003008628	A3	20031030		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			

US 2003148928 A1 20030807 US 2002-201389 20020722
PRIORITY APPLN. INFO.: US 2001-306995P P 20010720
OTHER SOURCE(S): MARPAT 138:142441

AB This invention features conjugates, compns., methods of synthesis, and applications thereof, including galactose, galactosamine, N-acetyl galactosamine, PEG, phospholipid, and human serum albumin (HSA) derived conjugates of nucleosides, nucleotides, non-nucleosides, and nucleic acids including enzymic nucleic acids, DNazymes, allozymes, antisense, dsRNA, siRNA, triplex oligonucleotides, 2,5-A chimeras, decoys and aptamers.

IT 493068-33-0
RL: PRP (Properties)
(unclaimed nucleotide sequence; enzymic nucleic acid peptide conjugates)

L8 ANSWER 10 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:23421 HCAPLUS
DOCUMENT NUMBER: 138:84437

THIS PAGE BLANK (USPTO)

09/423035

TITLE: Methods and kits containing nucleic acid-based enzymes for detection of single nucleotide polymorphisms in diagnosis of diseases

INVENTOR(S): Usman, Nassim; McSwiggen, James A.; Zinnen, Shawn; Seiwert, Scott; Haeberli, Peter; Chowrira, Bharat; Blatt, Lawrence; Vaish, Narendra

PATENT ASSIGNEE(S): USA

SOURCE: U.S. Pat. Appl. Publ., 100 pp., Cont.-in-part of U.S. Pat. Appl. 2002 102,568.
CODEN: USXXCO

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 12

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003008295	A1	20030109	US 2001-992160	20011105
WO 2001066721	A2	20010913	WO 2001-US7163	20010306
WO 2001066721	A3	20020725		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
US 2002102568	A1	20020801	US 2001-877526	20010608
US 2003065155	A1	20030403	US 2002-56761	20020123
WO 2003089650	A2	20031030	WO 2002-US35529	20021105
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
US 2004009510	A1	20040115	US 2003-422050	20030423
PRIORITY APPLN. INFO.:			US 2000-187128P	P 20000306
			US 2001-800594	A2 20010306
			WO 2001-US7163	W 20010306
			US 2001-877526	A2 20010608
			US 2001-992160	A2 20011105
			US 2002-56761	A 20020123
			US 2002-283858	A 20021030
			US 2002-286492	A 20021101
			WO 2002-US35529	A2 20021105

AB The present invention provides nucleic acid sensor mols. and methods for the detection and amplification of signaling agents using

THIS PAGE BLANK (USPTO)

enzymic nucleic acid constructs. These include hammerhead enzymic nucleic acid mols., inozymes, G-cleaver enzymic nucleic acid mols., zinzymes, amberzymes and DNAzymes. Kits for detection and amplification and uses of the invention in diagnostics, nucleic acid circuits, nucleic acid computers, therapeutics, target validation, target discovery, drug optimization, SNP detection, SNP scoring, proteome scoring and other uses are disclosed.

IT 483392-16-1

RL: PRP (Properties)

(unclaimed nucleotide sequence; methods and kits containing nucleic acid-based enzymes for detection of single nucleotide polymorphisms in diagnosis of diseases)

L8 ANSWER 11 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:974509 HCAPLUS

DOCUMENT NUMBER: 139:46323

TITLE: Cellular uptake, distribution, and stability of 10 - 23 deoxyribozymes

AUTHOR(S): Dass, Crispin R.; Saravolac, Edward G.; Li, Yang; Sun, Lun-Quan

CORPORATE SOURCE: Johnson and Johnson Research Laboratories, Eveleigh, 1430, Australia

SOURCE: Antisense & Nucleic Acid Drug Development (2002), 12(5), 289-299
CODEN: ANADF5; ISSN: 1087-2906

PUBLISHER: Mary Ann Liebert, Inc.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The cellular uptake, intracellular distribution, and stability of 33-mer deoxyribozyme oligonucleotides (DNAzymes) were examined in several cell lines. PAGE anal. revealed that there was a weak association between the DNAzyme and DOTAP or Superfect transfection reagents at charge ratios that were minimally toxic to cultured cells. Cellular uptake was analyzed by cell fractionation of radiolabeled DNAzyme, by FACS, and by fluorescent microscopic anal. of FITC-labeled and TAMRA-labeled DNAzyme. Altering DNAzyme size and chemical did not significantly affect uptake into cells. Inspection of paraformaldehyde-fixed cells by fluorescence microscopy revealed that DNAzyme was distributed primarily in punctate structures surrounding the nucleus and that substantial delivery to the nucleus was not observed up to 24 h after initiation of transfection. Incubation in human serum or plasma demonstrated that a 3'-inversion modification greatly increased DNAzyme stability ($t_{1/2} \approx 22$ h) in comparison to the unmodified form ($t_{1/2} \approx 70$ min). The 3'-inversion-modified DNAzymes remained stable during cellular uptake, and catalytically active oligonucleotide could be extracted from the cells 24 h posttransfection. In smooth muscle cell proliferation assay, the modified DNAzyme targeting the c-myc gene showed a much stronger inhibitory effect than did the unmodified version. The present study demonstrates that DNAzymes with a 3'-inversion are readily delivered into cultured cells and are functionally stable for several hours in serum and within cells.

IT 543745-67-1D, 5'-FITC labeled

RL: PAC (Pharmacological activity); PKT (Pharmacokinetics); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(cellular uptake, distribution, and stability of 10-23 deoxyribozymes)

THIS PAGE BLANK (USPTO)

09/423035

REFERENCE COUNT: 34 THERE ARE 34 CITED REFERENCES AVAILABLE
FOR THIS RECORD. ALL CITATIONS AVAILABLE
IN THE RE FORMAT

L8 ANSWER 12 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:927617 HCAPLUS
DOCUMENT NUMBER: 138:19530
TITLE: Nucleic acid treatment of diseases or conditions
related to levels of Ras, HER2 and HIV
INVENTOR(S): McSwiggen, James
PATENT ASSIGNEE(S): Ribozyme Pharmaceuticals, Incorporated, USA
SOURCE: PCT Int. Appl., 185 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 104
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002097114	A2	20021205	WO 2002-US16840	20020529
WO 2002097114	A3	20030508		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
AU 9851819	A1	19980611	AU 1998-51819	19980112
AU 729657	B2	20010208		
AU 9939188	A1	19990916	AU 1999-39188	19990713
WO 2002097114	A2	20021205	WO 2002-XA16840	20020529
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
US 2003153521	A1	20030814	US 2002-238700	20020910
WO 2003070912	A2	20030828	WO 2003-US5045	20030220
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE,			

THIS PAGE BLANK (USPTO)

09/423035

BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT,
LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA,
GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.:

US 2001-294140P P 20010529
US 2001-296249P P 20010606
US 2001-318471P P 20010910
AU 1995-26422 A3 19950518
US 1996-623891 A 19960325
US 2001-916466 A 20010725
US 2002-358580P P 20020220
US 2002-363124P P 20020311
WO 2002-US16840 A 20020529
US 2002-163552 A1 20020606
US 2002-386782P P 20020606
US 2002-393924P P 20020703
US 2002-406784P P 20020829
US 2002-408378P P 20020905
US 2002-409293P P 20020909
US 2002-251117 A1 20020919
US 2002-277494 A1 20021021
US 2003-440129P P 20030115

AB The present invention relates to nucleic acid mols., including enzymic nucleic acid mols., such as DNazymes (e.g. DNA enzymes, catalytic DNA), siRNA, aptamers, and antisense that modulate the expression of Ras genes such as K-Ras, H-Ras, and/or N-Ras, HIV genes such as HIV-1, and HER2 (c-erbB2) gene. The sequence of human HER2 or Ras genes were screened for accessible sites using a computer-folding algorithm. Regions of the RNA that do not form secondary folding structure and contain potential enzymic nucleic acid mol. and/or antisense binding/cleavage sites are identified. The sequences of c-Ki-ras, c-Ha-ras, HER2, and HIV RNA binding/cleavage sites are provided, as are the sequences of designed enzymic nucleic acid mols., e.g., hammerhead ribozymes, DNazymes, inozymes, zinzymes, and Amberzymes. [This abstract record is one of two records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.]

IT 478129-01-0

RL: PRP (Properties)

(unclaimed nucleotide sequence; nucleic acid treatment of diseases or conditions related to levels of Ras, HER2 and HIV)

L8 ANSWER 13 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:828621 HCAPLUS

DOCUMENT NUMBER: 138:314544

TITLE: Oligonucleotide-mediated inhibition of hepatitis B virus and hepatitis C virus replication

INVENTOR(S): Blatt, Lawrence; Macejak, Dennis; McSwiggen, James; Morrissey, David; Pavco, Pamela; Lee, Patrice; Draper, Kenneth; Roberts, Elisabeth

PATENT ASSIGNEE(S): Ribozyme Pharmaceuticals, Inc., USA

SOURCE: PCT Int. Appl., 387 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 104

PATENT INFORMATION:

THIS PAGE BLANK (USPTO)

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
-----	---	-----	-----	-----
WO 2002081494	A1	20021017	WO 2002-XD9187	20020326
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, ML, MR, NE, SN, TD, TG			
AU 9851819	A1	19980611	AU 1998-51819	19980112
AU 729657	B2	20010208		
AU 9939188	A1	19990916	AU 1999-39188	19990713
US 2003171311	A1	20030911	US 2001-817879	20010326
US 2003068301	A1	20030410	US 2001-877478	20010608
US 2003148985	A1	20030807	US 2002-310294	20021205
PRIORITY APPLN. INFO.:			US 2001-817879	A 20010326
			US 2001-296876P	P 20010608
			US 2001-877478	A 20010608
			US 2001-335059P	P 20011024
			US 2001-337055P	P 20011205
			US 1992-882712	B1 19920514
			US 1994-193627	A1 19940207
			AU 1995-26422	A3 19950518
			US 1996-623891	A 19960325
			US 1998-83217P	P 19980427
			US 1998-100842P	P 19980918
			US 1999-257608	B2 19990225
			US 1999-274553	A2 19990323
			US 1999-436430	A2 19991108
			US 2000-504231	A2 20000215
			US 2000-531025	A2 20000320
			US 2000-611931	A2 20000707
			US 2000-636385	A2 20000809
			US 2000-696347	A2 20001024
			US 2000-740332	A2 20001218
AB	<p>The present invention relates to nucleic acid mols., including antisense and enzymic nucleic acid mols., such as hammerhead ribozymes, DNAzymes, Inozymes, Zinzymes, Amberzymes, and G-cleaver ribozymes, which modulate the synthesis, expression and/or stability of a hepatitis C virus (HCV) or hepatitis B virus (HBV) RNA and methods for their use alone or in combination with other therapies. In addition, nucleic acid decoy mols. and aptamers that bind to HBV reverse transcriptase and/or HBV reverse transcriptase primer sequences and methods for their use alone or in combination with other therapies, are disclosed. Oligonucleotides that specifically bind the Enhancer I region of HBV DNA are further disclosed. The present invention further relates to the use of nucleic acids, such as decoy and aptamer mols. of the invention, to modulate the expression of HBV genes and HBV viral replication. Furthermore, HBV animal models and methods of use are disclosed, including methods of screening for compds. and/or potential therapies directed against HBV. The present invention also relates to compds., including enzymic nucleic acid mols., ribozymes, DNAzymes, nuclease-activating</p>			

THIS PAGE BLANK (USPTO)

compds. and chimeras such as 2',5'-adenylates, that modulate the expression and/or replication of HCV. [This abstract record is one of five records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT 491672-93-6

RL: PRP (Properties)

(unclaimed nucleotide sequence; oligonucleotide-mediated inhibition of hepatitis B virus and hepatitis C virus replication)

L8 ANSWER 14 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:822462 HCAPLUS

DOCUMENT NUMBER: 138:265678

TITLE: Modulation of gene expression associated with inflammation, proliferation and neurite outgrowth using antisense and enzymic nucleic acid-based technologies

INVENTOR(S): Blatt, Lawrence; Chowrira, Bharat; Haeberli, Peter; McSwiggen, James; Fosnaugh, Kathy

PATENT ASSIGNEE(S): Ribozyne Pharmaceuticals, Incorporated, USA

SOURCE: PCT Int. Appl., 317 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 12

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002081628	A2	20021017	WO 2002-XC10512	20020403
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
US 2003113891	A1	20030619	US 2001-827395	20010405
US 2003119017	A1	20030626	US 2002-156306	20020528
US 2003143732	A1	20030731	US 2002-224005	20020820
US 2003148507	A1	20030807	US 2002-226992	20020823
US 2003191077	A1	20031009	US 2002-230006	20020828
PRIORITY APPLN. INFO.:			US 2001-827395	A 20010405
			US 2001-294412P	P 20010529
			US 2001-315315P	P 20010828
			US 2000-181797P	P 20000211
			US 2001-780533	A2 20010209

AB The present invention relates to nucleic acid mols., including antisense, enzymic nucleic acid mols., and RNA interference mols., which modulate the expression of genes encoding prostaglandin D2 receptor, adenosine receptor A1, NOGO receptor, IκB protein kinase, and protein kinase PKR. Thus, nucleic acids encoding these products are scanned to identify targets for cleavage by designed

THIS PAGE BLANK (USPTO)

enzymic nucleic acids, such as hammerhead ribozymes, Inozymes, Zinzymes, DNAzymes, and Amberzymes. Chemical modifications in the sugar, base, and/or phosphate backbones of these enzymic nucleic acids is carried out to improve their stability. Inhibition of gene product expression may be used for treatment of diseases associated with said expression. [This abstract record is one of four records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **484802-52-0**

RL: PRP (Properties)

(unclaimed nucleotide sequence; modulation of gene expression associated with inflammation, proliferation and neurite outgrowth using antisense and enzymic nucleic acid-based technologies)

L8 ANSWER 15 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:698624 HCAPLUS

DOCUMENT NUMBER: 138:66656

TITLE: Nucleic acid-based treatment of diseases or conditions related to West Nile virus infection

INVENTOR(S): Blatt, Lawrence; McSwiggen, James A.

PATENT ASSIGNEE(S): Ribozyme Pharmaceuticals, Inc., USA

SOURCE: PCT Int. Appl., 495 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 9

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002068637	A2	20020906	WO 2001-XH48350	20011019
W:				
AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW:				
GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
WO 2002068637	A2	20020906	WO 2001-US48350	20011019
WO 2002068637	C1	20030515		
W:				
AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW:				
GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				

PRIORITY APPLN. INFO.:

US 2000-242411P P 20001020

WO 2001-US48350 A 20011019

THIS PAGE BLANK (USPTO)

AB The present invention relates to nucleic acid mols. (e.g., ribozymes, DNAzymes, antisense oligonucleotides, triplex-forming oligonucleotides, 2-5A oligonucleotides, decoys) that modulate the expression and/or replication of West Nile Virus (WNV). Such enzymic and antisense nucleic acids can be used to diagnose and treat diseases associated with WNV infection, such as pancreatitis, encephalitis, myocarditis, meningitis, neurol. infection, hepatitis, liver failure, hepatocellular carcinoma, and cirrhosis. Thus, the sequence of human WNV was screened for accessible sites using a computer-folding algorithm; regions of the RNA that do not form secondary folding structures and contain potential enzymic nucleic acid and/or antisense binding/cleavage sites were identified. Enzymic nucleic acids mols. are designed that could bind each target and are individually analyzed by computer folding. Varying binding arm lengths can be chosen to optimize activity. Five different enzymic nucleic acid mols. of different motifs (hammerhead, inozyme, DNAzyme, Amberzyme, and zinzyme) show cleavage data with full-length or partially full-length, internally-labeled target RNA. The enzymic nucleic acid mols. are effective against WNV RNA in vivo (HeLa cells) and in animal models (mice infected with WNV). [This abstract record is one of nine records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT 479786-61-3

RL: PRP (Properties)

(unclaimed nucleotide sequence; nucleic acid-based treatment of diseases or conditions related to West Nile virus infection)

L8 ANSWER 16 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:414955 HCAPLUS

DOCUMENT NUMBER: 137:121425

TITLE: A general strategy for effector-mediated control of RNA-cleaving ribozymes and DNA enzymes

AUTHOR(S): Wang, Dennis Y.; Lai, Beatrice H. Y.; Sen, Dipankar

CORPORATE SOURCE: Department of Molecular Biology & Biochemistry, Simon Fraser University, Burnaby, BC, V5A 1S6, Can.

SOURCE: Journal of Molecular Biology (2002), 318(1), 33-43

CODEN: JMOBAK; ISSN: 0022-2836

PUBLISHER: Elsevier Science Ltd.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A novel and general approach is described for generating versions of RNA-cleaving ribozymes (RNA enzymes) and DNAzymes (DNA enzymes), whose catalytic activity can be controlled by the binding of activator mols. Variants of the RNA-cleaving 10-23 DNAzyme and 8-17 DNAzyme were created, whose catalysis was activated by up to .apprx.35-fold by the binding of the effector adenosine. The design of such variants was possible even though the tertiary folding of the two DNAzymes is not known. Variants of the hammerhead ribozyme were constructed, to respond to the effectors ATP and FMN. Whereas in conventional allosteric ribozymes, effector-binding modulates the chemical step of catalysis, here, effectors exercise their effect upon the substrate-binding step, by stabilizing the enzyme-substrate complex. Because such an approach for controlling the activity of DNAzymes/ribozymes requires no prior knowledge of the enzyme's

THIS PAGE BLANK (USPTO)

09/423035

secondary or tertiary folding, this regulatory strategy should be generally applicable to any RNA-cleaving ribozyme or DNzyme, natural or in vitro selected, provided substrate-recognition is achieved by Watson-Crick base-pairing.

IT 444035-98-7

RL: BSU (Biological study, unclassified); CAT (Catalyst use); PRP (Properties); BIOL (Biological study); USES (Uses)

(DNzyme; design and properties of effector-mediated aptamer-containing DNzymes)

REFERENCE COUNT: 51 THERE ARE 51 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 17 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:171921 HCAPLUS

DOCUMENT NUMBER: 136:241681

TITLE: Antisense oligonucleotides against vanilloid receptor 1 (VR1), therapeutic and diagnostic uses, and screening method

INVENTOR(S): Kurreck, Jens; Erdmann, Volker A.

PATENT ASSIGNEE(S): Grunenthal GmbH, Germany

SOURCE: PCT Int. Appl., 76 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: German

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002018407	A2	20020307	WO 2001-EP10081	20010831
WO 2002018407	A3	20021003		
WO 2002018407	C2	20030515		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
DE 10043674	A1	20020321	DE 2000-10043674	20000902
DE 10043702	A1	20020314	DE 2000-10043702	20000904
AU 2001095531	A5	20020313	AU 2001-95531	20010831
EP 1313768	A2	20030528	EP 2001-976176	20010831
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR			
US 2004002473	A1	20040101	US 2003-376341	20030303
PRIORITY APPLN. INFO.:			DE 2000-10043674 A	20000902
			DE 2000-10043702 A	20000904
			WO 2001-EP10081 W	20010831

AB The invention provides antisense oligodeoxynucleotides against VR1, corresponding nucleotide constructs, cells containing the nucleotide constructs, pharmaceuticals and diagnostic substances, the use thereof in pain therapy, and methods for diagnosing symptoms related

THIS PAGE BLANK (USPTO)

09/423035

to VR1 and identifying pain-modulating substances.

IT 403777-66-2
RL: PRP (Properties)
(Unclaimed; antisense oligonucleotides against vanilloid receptor 1 (VR1), therapeutic and diagnostic uses, and screening method)

L8 ANSWER 18 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:122738 HCAPLUS
DOCUMENT NUMBER: 136:194272
TITLE: Ribozymes and antisense oligonucleotides for the inhibition of gene expression by calcium-activated chloride channel-1 gene CLCA-1
INVENTOR(S): Thompson, James; McSwiggen, James; McKenzie, Timothy; Ayers, David; Szymkowski, David E.; Grupe, Andrew
PATENT ASSIGNEE(S): Ribozyme Pharmaceuticals, Incorporated, USA; Syntex (U.S.A.) LLC
SOURCE: PCT Int. Appl., 152 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002011674	A2	20020214	WO 2001-US24970	20010809
WO 2002011674	A3	20030925		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
US 2003064946	A1	20030403	US 2001-927046	20010809
PRIORITY APPLN. INFO.:			US 2000-224383P	P 20000809
AB	Nucleic acid mols., including antisense and enzymic nucleic acid mols., such as hammerhead ribozymes, DNazymes, and GeneBlocs, which modulate the expression of calcium-activated chloride channels (CLCA1, CLCA2, CLCA3, and CLCA4) are provided. A target discovery target validation approach was used for finding genes that are involved in chronic mucous hypersecretion. The reporter system consists of a plasmid construct, termed pMUC5AC-EGFP, bearing a gene coding for green fluorescent protein (GFP). The promoter region of the GFP gene is replaced by a portion of the mucin 5AC promoter sufficient to direct efficient transcription of the GFP gene; the plasmid also contains the neomycin drug resistance gene. The cell line selected as host for these studies, NCI-H292 (ATCC CRL-1848), is derived from a human lung mucoepidermoid carcinoma. A ribozyme library with two randomized regions comprising six-nucleotide binding "arms" is used to enrich cells for non-responders to mucin induction and a bioinformatics approach used to identify human CLCA1 as a regulator of MUC5AC expression. Antisense, hammerhead,			

THIS PAGE BLANK (USPTO)

09/423035

DNAzyme, NCH, amberzyme, zinzyme, and G-Cleaver ribosome binding/cleavage sites in CLCA1 were identified. The nucleic acid mols. are individually analyzed by computer folding to assess whether the sequences fold into the appropriate secondary structure and to anneal to various sites in the RNA target. Those nucleic acid mols. with unfavorable intramol. interactions such as between the binding arms and the catalytic core are eliminated from consideration. Varying binding arm lengths can be chosen to optimize activity.

IT 400185-65-1

RL: PRP (Properties)

(unclaimed nucleotide sequence; ribozymes and antisense oligonucleotides for the inhibition of gene expression by calcium-activated chloride channel-1 gene CLCA-1)

L8 ANSWER 19 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2001:582042 HCAPLUS

DOCUMENT NUMBER: 135:175355

TITLE: Nucleic acid reagents for inhibition of checkpoint kinase-1 gene expression for therapeutic use

INVENTOR(S): Fattaey, Ali R.; Jarvis, Thale; McSwiggen, James; Booher, Robert N.; Holman, Patricia S.

PATENT ASSIGNEE(S): Ribozyme Pharmaceuticals, Inc., USA

SOURCE: PCT Int. Appl., 115 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001057206	A2	20010809	WO 2001-US3504	20010202
WO 2001057206	A3	20020829		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			

US 2003087847 A1 20030508 US 2001-776474 20010202

PRIORITY APPLN. INFO.: US 2000-179983P P 20000203

AB The present invention relates to nucleic acid mols., including antisense and enzymic nucleic acid mols., such as hammerhead ribozymes, DNAzymes, and antisense, which modulate the expression of the Chk-1 gene. Inhibition of the enzyme may be useful in the treatment of a number of cancers including lung, breast, prostate and colorectal cancer.

IT 190795-31-4

RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(nucleotide sequence, antisense DNA inhibiting checkpoint kinase

THIS PAGE BLANK (USPTO)

09/423035

gene expression; nucleic acid reagents for inhibition of
checkpoint kinase-1 gene expression for therapeutic use)

L8 ANSWER 20 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2001:186701 HCAPLUS

DOCUMENT NUMBER: 135:57661

TITLE: Characterization in terms of the NUX rule of
G-inserted mutant hammerhead ribozymes with high
level of catalytic power

AUTHOR(S): Kuwabara, Tomoko; Warashina, Masaki; Kato,
Yoshio; Kawasaki, Hiroaki; Taira, Kazunari

CORPORATE SOURCE: Gene Discovery Research Center, National
Institute of Advanced Industrial Science and
Technology (AIST), Tsukuba Science City,
305-8562, Japan

SOURCE: Journal of Biochemistry and Molecular Biology
(2001), 34(1), 51-58

CODEN: JBMBE5; ISSN: 1225-8687

PUBLISHER: Springer-Verlag Singapore Pte. Ltd.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Attempts using in vitro and in vivo selection procedures have been
made to search for hammerhead ribozymes that have higher activities
than the wild-type ribozyme and also to determine whether other sequences
might be possible in the catalytic core of the hammerhead ribozyme.
Active sequences selected in the past conformed broadly to the
consensus core sequence except at A9, and no sequences were associated
with higher activity than that of the hammerhead with the consensus
core, an indication that the consensus sequence derived from viruses
and virusoids is probably the optimal sequence. Recently, during
construction of ribozyme expression vectors, we isolated a mutant
hammerhead ribozyme, with an insertion of G between A9 and G10.1,
that appeared to show significant activity. We, therefore,
characterized kinetic properties of the G-inserted mutant ribozymes
in terms of the NUX rule. We demonstrate that the NUX rule is
basically applicable to the G-inserted ribozymes and, more
importantly, one type of G-inserted ribozyme was very active with
kcat value of 6.4 min⁻¹ in 50 mM Tris-HCl (pH 8.0) and 10 mM MgCl₂
at 37°C.

IT 345373-30-0 345373-31-1

RL: BAC (Biological activity or effector, except adverse); BSU
(Biological study, unclassified); PRP (Properties); BIOL (Biological
study)

(characterization in terms of the NUX rule of G-inserted mutant
hammerhead ribozymes with high level of catalytic power)

REFERENCE COUNT: 91 THERE ARE 91 CITED REFERENCES AVAILABLE
FOR THIS RECORD. ALL CITATIONS AVAILABLE
IN THE RE FORMAT

L8 ANSWER 21 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2001:48059 HCAPLUS

DOCUMENT NUMBER: 134:291623

TITLE: In vitro-selected RNA cleaving DNA enzymes from
a combinatorial library are potent inhibitors of
HIV-1 gene expression

AUTHOR(S): Sriram, Bandi; Banerjee, Akhil C.

CORPORATE SOURCE: Laboratory of Virology, National Institute of
Immunology, New Delhi, 110067, India

Searcher : Shears 571-272-2528

THIS PAGE BLANK (USPTO)

09/423035

SOURCE: Biochemical Journal (2000), 352(3), 667-673
CODEN: BIJOAK; ISSN: 0264-6021
PUBLISHER: Portland Press Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Selective inactivation of a target gene by antisense mechanisms is an important biol. tool to delineate specific functions of the gene product. Approaches mediated by ribozymes and RNA-cleaving DNA enzymes (DNA enzymes) are more attractive because of their ability to catalytically cleave the target RNA. DNA enzymes have recently gained a lot of importance because they are short DNA mols. with simple structures that are expected to be stable to the nucleases present inside a mammalian cell. The authors have designed a strategy to identify accessible cleavage sites in HIV-1 gag RNA from a pool of random DNA enzymes, and for isolation of DNA enzymes. A pool of random sequences (all 29 nucleotides long) that contained the earlier-identified 10-23 catalytic motif were tested for their ability to cleave the target RNA. When the pool of random DNA enzymes was targeted to cleave between any A and U nucleotides, DNA enzyme 1836 was identified. Although several DNA enzymes were identified using a pool of DNA enzymes that was completely randomized with respect to its substrate-binding properties, DNA enzyme-1810 was selected for further characterization. Both DNA enzymes showed target-specific cleavage activities in the presence of Mg²⁺ only. When introduced into a mammalian cell, they showed interference with HIV-1-specific gene expression. This strategy could be applied for the selection of desired target sites in any target RNA.

IT 334544-13-7 334544-14-8

RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(RNA-cleaving DNazymes from combinatorial library are potent inhibitors of HIV-1 gene expression)

REFERENCE COUNT: 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 22 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2000:725799 HCAPLUS

DOCUMENT NUMBER: 133:291920

TITLE: Method for identifying antisense DNA-, ribozyme-, or DNazyme-accessible binding sites on RNA

INVENTOR(S): Rossi, John; Riggs, Arthur; Scherr, Michaela

PATENT ASSIGNEE(S): City of Hope, USA

SOURCE: PCT Int. Appl., 38 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000060115	A2	20001012	WO 2000-US7920	20000327
WO 2000060115	A3	20010426		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN,

Searcher : Shears 571-272-2528

THIS PAGE BLANK (USPTO)

09/423035

CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM,
HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT,
RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG,
UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF,
BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

US 6562570 B1 20030513 US 2000-536393 20000328
US 2003228615 A1 20031211 US 2003-435044 20030512
PRIORITY APPLN. INFO.: US 1999-127529P P 19990402
US 2000-536393 A1 20000328

AB A method for identifying sites on a target RNA which are accessible to pairing by antisense DNA, ribozymes or DNazymes. Native or in vitro -synthesized target RNA is incubated with defined ODNs and RNase H, or with a random or semi-random ODN library and RNase H, or with defined ribozymes or DNazymes, or with a semi-random ribozyme or DNazyme library, in a cell extract containing endogenous RNA binding proteins, or in a medium which mimics a cell extract due to presence of one or more RNA-binding proteins. Any antisense ODN, ribozyme or DNazyme which is complementary to an accessible site in the target RNA hybridizes to that site and the RNA is cleaved at that site. Reverse transcription can be used to generate a first strand DNA from the RNA cleavage product, and terminal deoxynucleotidyl transferase-dependent polymerase chain reaction (TDPCR) can be used to identify sites on target RNA to which antisense ODNs, ribozymes or DNazymes have bound and cleavage has occurred. The method was applied to identification of hammerhead ribozyme cleavage sites on human gene AIB1 mRNA as well as murine DNA methyltransferase mRNA.

IT 300756-64-3 300756-65-4

RL: PRP (Properties)

(unclaimed nucleotide sequence; method for identifying antisense DNA-, ribozyme-, or DNazyme-accessible binding sites on RNA)

L8 ANSWER 23 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2000:413290 HCAPLUS

DOCUMENT NUMBER: 133:234043

TITLE: Alternative Conformations of a Nucleic Acid
Four-way Junction

AUTHOR(S): Nowakowski, Jacek; Shim, Peter J.; Stout, C.
David; Joyce, Gerald F.

CORPORATE SOURCE: Department of Chemistry, Skaggs Institute for
Chemical Biology, Scripps Research Institute, La
Jolla, CA, 92037, USA

SOURCE: Journal of Molecular Biology (2000), 300(1),
93-102

CODEN: JMOBAK; ISSN: 0022-2836

PUBLISHER: Academic Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A crystal structure of a 108 nucleotide RNA-DNA complex containing a four-way junction was solved at 3.1 Å resolution. The structure of the junction differs substantially from the "stacked-X" conformation observed previously, due to a 135° rotation of the branches. Comparison of the two conformers provides insight into the factors contributing to the flexibility of four-way junctions. The stacked-X conformation maximizes base-stacking but causes unfavorable repulsion between phosphate groups, whereas the 135

THIS PAGE BLANK (USPTO)

°-rotated "crossed" conformation minimizes electrostatic clashes at the expense of reduced base-stacking. Despite the large rotation of the branches, both junction structures exhibit an antiparallel arrangement of the continuous strands and opposite polarity of the crossover strands. (c) 2000 Academic Press.

IT 292890-11-0

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(four-chain RNA-DNA complex; alternative conformations of a nucleic acid four-way junction)

REFERENCE COUNT: 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 24 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1999:124703 HCAPLUS

DOCUMENT NUMBER: 130:321986

TITLE: Crystal structure of an 82-nucleotide RNA-DNA complex formed by the 10-23 DNA enzyme

AUTHOR(S): Nowakowski, Jacek; Shim, Peter J.; Prasad, G. Sridhar; Stout, C. David; Joyce, Gerald F.

CORPORATE SOURCE: Department of Chemistry and The Skaggs Institute for Chemical Biology, The Scripps Research Institute, La Jolla, CA, 92037, USA

SOURCE: Nature Structural Biology (1999), 6(2), 151-156
CODEN: NSBIEW; ISSN: 1072-8368

PUBLISHER: Nature America

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The structure of a large nucleic acid complex formed by the 10-23 DNA enzyme bound to an RNA substrate was determined by x-ray diffraction at 3.0 Å resolution. The 82-nucleotide complex contains two strands of DNA and two strands of RNA that form five double-helical domains. The spatial arrangement of these helices is maintained by two four-way junctions that exhibit extensive base-stacking interactions and sharp turns of the phosphodiester backbone stabilized by metal ions coordinated to nucleotides at these junctions. Although it is unlikely that the structure corresponds to the catalytically active conformation of the enzyme, it represents a novel nucleic acid fold with implications for the Holliday junction structure.

IT 223694-53-9

RL: PRP (Properties)

(crystal structure of 82-nucleotide RNA-DNA complex formed by 10-23 DNA enzyme)

REFERENCE COUNT: 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 25 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1998:728600 HCAPLUS

DOCUMENT NUMBER: 130:1776

TITLE: Design and catalytic activity of enzymic DNA molecules

INVENTOR(S): Joyce, Gerald F.; Breaker, Ronald R.

PATENT ASSIGNEE(S): The Scripps Research Institute, USA

SOURCE: PCT Int. Appl., 161 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

THIS PAGE BLANK (USPTO)

09/423035

LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9849346	A1	19981105	WO 1998-US8677	19980429
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9872675	A1	19981124	AU 1998-72675	19980429
AU 735522	B2	20010712		
EP 981646	A1	20000301	EP 1998-920015	19980429
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
BR 9809433	A	20000613	BR 1998-9433	19980429
JP 2002514080	T2	20020514	JP 1998-547359	19980429
AU 743767	B2	20020207	AU 1999-65509	19991224
AU 9965509	A1	20000309		
PRIORITY APPLN. INFO.:			US 1997-45228P	P 19970429
			WO 1998-US8677	W 19980429
AB	<p>The present invention discloses DNA enzymes -- catalytic or enzymic DNA mols. -- capable of cleaving nucleic acid sequences or mols., particularly RNA, in a site-specific manner, as well as compns. including same. The catalytic DNAs have first and substrate binding regions flanks a core region, wherein the first substrate binding region has a sequence complementary to a first portion of the preselected substrate nucleic acid sequence, and the second substrate binding region has a sequence complementary to a second portion of the preselected substrate nucleic acid sequence. The core region has a sequence according to the formula T(stem)'AGC(stem)"Z, where the (stem)' and (stem)" are each 3 sequential nucleotides which when hybridized as a (stem)':(stem)" pair comprise 3 base pairs including at least two G:C pairs and wherein Z = WCGR or WCGAA, and W = A or T and R = A or G. Also contemplated is a core region having a sequence RGGCTAGCXACAACGA, wherein X = T, C or A, and R = A or G. Methods of making and using the disclosed enzymes and compns. are also disclosed. An exemplary method of engineering enzymic DNA mols. that cleave phosphoester bonds comprises the following in vitro selection/evolution steps: (1) obtaining a population of single-stranded DNA mols.; (2) introducing genetic variation into the population to produce a variant population; (3) selecting individuals from the variant population that meet predetd. selection criteria; (4) separating the selected individuals from the remainder of the variant population; and (5) amplifying the selected individuals. Deoxyribozymes variants designated 8-17 (core region 5'-cttccaccttccgagccggaaggaagttttt-3') and 10-23 (core region 5'-cttttggttaggctagctacaacgatttttcc-3') have turnover nos. and kobs of 0.5 and 1 h-1, 0.002 and 0.01 min-1, resp., in 10 mM Mg2+, pH 7.5 and 37°.</p>			
IT	215727-35-8P, Deoxyribozyme (synthetic clone 10-38)			

THIS PAGE BLANK (USPTO)

09/423035

RL: BAC (Biological activity or effector, except adverse); BPN
(Biosynthetic preparation); BSU (Biological study, unclassified);
PRP (Properties); BIOL (Biological study); PREP (Preparation)
(design and catalytic activity of enzymic DNA mols.)

REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR
THIS RECORD. ALL CITATIONS AVAILABLE IN
THE RE FORMAT

L8 ANSWER 26 OF 26 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1997:308152 HCAPLUS

DOCUMENT NUMBER: 127:30832

TITLE: A general purpose RNA-cleaving DNA enzyme

AUTHOR(S): Santoro, Stephen W.; Joyce, Gerald F.

CORPORATE SOURCE: Departments of Chemistry and Molecular Biology
and the Skaggs Institute for Chemical Biology,
The Scripps Research Institute, La Jolla, CA,
92037, USA

SOURCE: Proceedings of the National Academy of Sciences
of the United States of America (1997), 94(9),
4262-4266

CODEN: PNASA6; ISSN: 0027-8424

PUBLISHER: National Academy of Sciences

DOCUMENT TYPE: Journal

LANGUAGE: English

AB An in vitro selection procedure was used to develop a DNA enzyme
that can be made to cleave almost any targeted RNA substrate under
simulated physiol. conditions. The enzyme is comprised of a
catalytic domain of 15 deoxynucleotides, flanked by two
substrate-recognition domains of seven to eight deoxynucleotides
each. The RNA substrate is bound through Watson-Crick base pairing
and is cleaved at a particular phosphodiester located between an
unpaired purine and a paired pyridine residue. Despite its small
size, the DNA enzyme has a catalytic efficiency (Kcat/Km) of
 $\approx 10^9$ M⁻¹min⁻¹ under multiple turnover conditions, exceeding
that of any other known nucleic acid enzyme. Its activity is
dependent on the presence of Mg²⁺ ion. By changing the sequence of
the substrate-recognition domains, the DNA enzyme can be made to
target different RNA substrates. In this study, for example, it was
directed to cleave synthetic RNAs corresponding to the start codon
region of HIV-1 gag/pol, env, vpr, tat, and nef mRNAs.

IT 190795-31-4

RL: BAC (Biological activity or effector, except adverse); BPR
(Biological process); BSU (Biological study, unclassified); RCT
(Reactant); BIOL (Biological study); PROC (Process); RACT (Reactant
or reagent)

(general purpose RNA-cleaving DNA enzyme)

E1 THROUGH E28 ASSIGNED

FILE 'REGISTRY' ENTERED AT 12:41:44 ON 21 JAN 2004

L9 28 SEA FILE=REGISTRY ABB=ON PLU=ON (190795-31-4/BI OR
215727-35-8/BI OR 223694-53-9/BI OR 292890-11-0/BI OR
300756-64-3/BI OR 300756-65-4/BI OR 334544-13-7/BI OR
334544-14-8/BI OR 345373-30-0/BI OR 345373-31-1/BI OR
400185-65-1/BI OR 403777-66-2/BI OR 444035-98-7/BI OR
478129-01-0/BI OR 479786-61-3/BI OR 483392-16-1/BI OR
484802-52-0/BI OR 491672-93-6/BI OR 493068-33-0/BI OR
503875-66-9/BI OR 504513-55-7/BI OR 506617-43-2/BI OR

Searcher : Shears 571-272-2528

THIS PAGE BLANK (USPTO)

09/423035

543745-67-1/BI OR 557143-59-6/BI OR 591261-44-8/BI OR
613321-58-7/BI OR 633370-08-8/BI OR 638223-95-7/BI)

L10 28 S L9 AND L1

L10 ANSWER 1 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN
RN 638223-95-7 REGISTRY
CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)
CI MAN
SQL 16

SEQ 1 rggctagcta caacga
=====
HITS AT: 1-16

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L10 ANSWER 2 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN
RN 633370-08-8 REGISTRY
CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 12: PN: US20030228590 SEQID: 14 unclaimed DNA
CI MAN
SQL 16

SEQ 1 rggctagcta caacga
=====
HITS AT: 1-16

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 140:26917

L10 ANSWER 3 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN
RN 613321-58-7 REGISTRY
CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 2617: PN: US20030203870 SEQID: 2617 unclaimed DNA
CI MAN
SQL 16

SEQ 1 rggctagcta caacga
=====
HITS AT: 1-16

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 139:317479

L10 ANSWER 4 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN
RN 591261-44-8 REGISTRY
CN DNA, d(N-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 63: PN: US2003171311 SEQID: 9700 unclaimed DNA
CI MAN
SQL 16

Searcher : Shears 571-272-2528

THIS PAGE BLANK (USPTO)

09/423035

SEQ 1 nggctagcta caacga
=====

HITS AT: 1-16

REFERENCE 1: 139:224402

L10 ANSWER 5 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN
RN 557143-59-6 REGISTRY
CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1913: PN: US20030125270 FIGURE: 5 unclaimed DNA
CI MAN
SQL 16

SEQ 1 rggctagcta caacga
=====

HITS AT: 1-16

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 139:358722

L10 ANSWER 6 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN
RN 543745-67-1 REGISTRY
CN DNA, d(A-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-(3'→3')-G) (9CI) (CA INDEX NAME)
CI MAN
SQL 17

SEQ 1 aggctagcta caacgag
=====

HITS AT: 1-16

REFERENCE 1: 139:46323

L10 ANSWER 7 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN
RN 506617-43-2 REGISTRY
CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 4771: PN: US20030073207 SEQID: 9645 unclaimed DNA
CI MAN
SQL 16

SEQ 1 rggctagcta caacga
=====

HITS AT: 1-16

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 139:143909

L10 ANSWER 8 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN
RN 504513-55-7 REGISTRY
CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 21: PN: US20030065155 SEQID: 21 unclaimed DNA
CI MAN
SQL 16

THIS PAGE BLANK (USPTO)

09/423035

SEQ 1 rggctagcta caacga
=====

HITS AT: 1-16

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:282290

L10 ANSWER 9 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN
RN 503875-66-9 REGISTRY
CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 445: PN: US20030064945 SEQID: 445 claimed DNA
CI MAN
SQL 16

SEQ 1 rggctagcta caacga
=====

HITS AT: 1-16

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:292713

L10 ANSWER 10 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN
RN 493068-33-0 REGISTRY
CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 13: PN: WO03008628 SEQID: 13 unclaimed DNA
CI MAN
SQL 16

SEQ 1 rggctagcta caacga
=====

HITS AT: 1-16

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:142441

L10 ANSWER 11 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN
RN 491672-93-6 REGISTRY
CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1774: PN: WO02081494 SEQID: 16197 unclaimed DNA
CI MAN
SQL 16

SEQ 1 rggctagcta caacga
=====

HITS AT: 1-16

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:314544

L10 ANSWER 12 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN

THIS PAGE BLANK (USPTO)

09/423035

RN 484802-52-0 REGISTRY
CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 80: PN: WO02081628 SEQID: 13274 unclaimed DNA
CI MAN
SQL 16

SEQ 1 rggctagcta caacga
=====
HITS AT: 1-16

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:265678

L10 ANSWER 13 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN
RN 483392-16-1 REGISTRY
CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 21: PN: US20030008295 SEQID: 21 unclaimed DNA
CI MAN
SQL 16

SEQ 1 rggctagcta caacga
=====
HITS AT: 1-16

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:84437

L10 ANSWER 14 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN
RN 479786-61-3 REGISTRY
CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 2122: PN: WO02068637 SEQID: 37054 unclaimed RNA
CI MAN
SQL 16

SEQ 1 rggctagcta caacga
=====
HITS AT: 1-16

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:66656

L10 ANSWER 15 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN
RN 478129-01-0 REGISTRY
CN DNA, d(Y-R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-R) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1332: PN: WO02097114 SEQID: 6810 unclaimed RNA
CI MAN
SQL 18

SEQ 1 yrggctagct acaacgar
=====
HITS AT: 2-17

Searcher : Shears 571-272-2528

THIS PAGE BLANK (USPTO)

09/423035

REFERENCE 1: 138:19530

L10 ANSWER 16 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN
RN 444035-98-7 REGISTRY
CN DNA, d(G-A-G-C-T-G-G-A-G-G-A-A-A-C-G-G-C-A-G-T-C), complex with DNA
d(G-G-G-C-A-A-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-C-T-A-A-A-T-T-G-G-A-G-G-
A-A-G-C-T-C) and RNA (G-A-C-U-G-C-C-G-U-A-G-G-U-U-G-C-C-C) (1:1:1)
(9CI) (CA INDEX NAME)
CI MAN
SQL 78,39,21,18

SEQ 1 gggcaaggct agctacaacg actaaattgg aggaagctc
=====

HITS AT: 6-21

SEQ 1 gagctggagg aaacggcagt c

SEQ 1 gacugccgua gguugccc

REFERENCE 1: 137:121425

L10 ANSWER 17 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN
RN 403777-66-2 REGISTRY
CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)
CI MAN
SQL 16

SEQ 1 rggctagcta caacga
=====

HITS AT: 1-16

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 136:241681

L10 ANSWER 18 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN
RN 400185-65-1 REGISTRY
CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 449: PN: WO0211674 SEQID: 5447 unclaimed DNA
CI MAN
SQL 16

SEQ 1 rggctagcta caacga
=====

HITS AT: 1-16

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 136:194272

L10 ANSWER 19 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN
RN 345373-31-1 REGISTRY
CN DNA, d(A-T-C-T-T-G-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-A-C-C-A-T-G),
complex with RNA (C-A-U-G-G-U-A-C-A-A-G-A-U) (1:1) (9CI) (CA INDEX
NAME)
OTHER CA INDEX NAMES:

THIS PAGE BLANK (USPTO)

09/423035

CN RNA, (C-A-U-G-G-U-A-C-A-A-G-A-U), complex with DNA
d(A-T-C-T-T-G-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-A-C-C-A-T-G) (1:1) (9CI)
CI MAN
SQL 40,27,13

SEQ 1 atcttgggct agctacaacg aaccatg
=====

HITS AT: 6-21

SEQ 1 caugguacaa gau

REFERENCE 1: 135:57661

L10 ANSWER 20 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN

RN 345373-30-0 REGISTRY

CN DNA, d(C-G-G-A-G-A-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-A-C-A-A-G-C),
complex with RNA (G-C-U-U-G-U-A-U-C-U-C-C-G) (1:1) (9CI) (CA INDEX
NAME)

OTHER CA INDEX NAMES:

CN RNA, (G-C-U-U-G-U-A-U-C-U-C-C-G), complex with DNA
d(C-G-G-A-G-A-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-A-C-A-A-G-C) (1:1) (9CI)

CI MAN

SQL 40,27,13

SEQ 1 cggagaggct agctacaacg aacaagc
=====

HITS AT: 6-21

SEQ 1 gcuuguaucu ccg

REFERENCE 1: 135:57661

L10 ANSWER 21 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN

RN 334544-14-8 REGISTRY

CN DNA, d(A-G-T-G-T-C-G-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-T-C-C-T-G-G-T),
complex with RNA (A-C-C-A-G-G-A-G-C-G-A-C-A-C-U) (1:1) (9CI) (CA
INDEX NAME)

OTHER CA INDEX NAMES:

CN RNA, (A-C-C-A-G-G-A-G-C-G-A-C-A-C-U), complex with DNA
d(A-G-T-G-T-C-G-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-T-C-C-T-G-G-T) (1:1)
(9CI)

CI MAN

SQL 44,29,15

SEQ 1 agtgtcgggc tagctacaac gatcctggt
=====

HITS AT: 7-22

SEQ 1 accaggagcg acacu

REFERENCE 1: 134:291623

L10 ANSWER 22 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN

RN 334544-13-7 REGISTRY

CN DNA, d(C-C-T-G-A-C-A-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-G-C-T-G-T-C-A),
complex with RNA (U-G-A-C-A-G-C-A-U-G-U-C-A-G-G) (1:1) (9CI) (CA
INDEX NAME)

OTHER CA INDEX NAMES:

THIS PAGE BLANK (USPTO)

09/423035

CN RNA, (U-G-A-C-A-G-C-A-U-G-U-C-A-G-G), complex with DNA
d(C-C-T-G-A-C-A-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-G-C-T-G-T-C-A) (1:1)
(9CI)
CI MAN
SQL 44,29,15

SEQ 1 cctgacaggc tagctacaac gagctgtca
=====

HITS AT: 7-22

SEQ 1 ugacagcaug ucagg

REFERENCE 1: 134:291623

L10 ANSWER 23 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN
RN 300756-65-4 REGISTRY
CN 14: PN: WO0060115 SEQID: 20 unclaimed DNA (9CI) (CA INDEX NAME)
CI MAN
SQL 16

SEQ 1 gggctagcta caacga
=====

HITS AT: 1-16

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 133:291920

L10 ANSWER 24 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN
RN 300756-64-3 REGISTRY
CN 13: PN: WO0060115 SEQID: 19 unclaimed DNA (9CI) (CA INDEX NAME)
CI MAN
SQL 16

SEQ 1 aggctagcta caacga
=====

HITS AT: 1-16

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 133:291920

L10 ANSWER 25 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN
RN 292890-11-0 REGISTRY
CN DNA, d(C-T-C-G-C-A-C-C-C-A-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-C-T-C-T-C-T-C-C-T), complex with RNA (A-G-G-A-G-A-G-A-G-A-U-G-G-G-U-G-C-G-A-G) (1:1) (9CI) (CA INDEX NAME)

OTHER CA INDEX NAMES:

CN RNA, (A-G-G-A-G-A-G-A-G-A-U-G-G-G-U-G-C-G-A-G), complex with DNA
d(C-T-C-G-C-A-C-C-C-A-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-C-T-C-T-C-T-C-C-T) (1:1) (9CI)

OTHER NAMES:

CN DNA (synthetic DNA-RNA four-way junction)

CN DNA (synthetic DNA-RNA Holliday junction)

CI MAN

SQL 54,34,20

SEQ 1 ctcgcaccca ggctagctac aacgactctc tcct

Searcher : Shears 571-272-2528

THIS PAGE BLANK (USPTO)

09/423035

HITS AT: 10-25

SEQ 1 aggagagaga ugggugcgag

REFERENCE 1: 133:234043

L10 ANSWER 26 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN
RN 223694-53-9 REGISTRY
CN DNA, d(G-C-T-C-C-C-A-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-C-T-G-T-C-C),
complex with RNA (G-G-A-C-A-G-A-U-G-G-G-A-G) (1:1) (9CI) (CA INDEX
NAME)

OTHER CA INDEX NAMES:

CN RNA, (G-G-A-C-A-G-A-U-G-G-G-A-G), complex with DNA
d(G-C-T-C-C-C-A-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A-C-T-G-T-C-C) (1:1)
(9CI)

CI MAN
SQL 82,28,28,13,13

SEQ 1 gctcccaggc tagctacaac gactgtcc
=====

HITS AT: 7-22

SEQ 1 gctcccaggc tagctacaac gactgtcc
=====

HITS AT: 7-22

SEQ 1 ggacagaugg gag

SEQ 1 ggacagaugg gag

REFERENCE 1: 130:321986

L10 ANSWER 27 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN
RN 215727-35-8 REGISTRY
CN Deoxyribozyme (synthetic clone 10-38) (9CI) (CA INDEX NAME)
CI MAN
SQL 16

SEQ 1 rggctagcha caacga
=====

HITS AT: 1-16

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 130:1776

L10 ANSWER 28 OF 28 REGISTRY COPYRIGHT 2004 ACS on STN
RN 190795-31-4 REGISTRY
CN DNA, d(R-G-G-C-T-A-G-C-T-A-C-A-A-C-G-A) (9CI) (CA INDEX NAME)
CI MAN
SQL 16

SEQ 1 rggctagcta caacga
=====

HITS AT: 1-16

RELATED SEQUENCES AVAILABLE WITH SEQLINK

THIS PAGE BLANK (USPTO)

09/423035

REFERENCE 1: 135:175355

REFERENCE 2: 127:30832

FILE 'HOME' ENTERED AT 12:42:16 ON 21 JAN 2004

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 06:26:43 ; Search time 1380 Seconds

(without alignments)
281.791 Million cell updates/sec

Title: US-09-423-035B-121

Perfect score: 16

Sequence: 1 rgcgtagctacaaga 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 1215238056 residues

Total number of hits satisfying chosen parameters: 452990

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Database :

EST:*

1: em_estba:*
2: em_estbun:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hnc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hnc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vit1:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	ID	Description
1	13	81.2	80	14	CA798147	Cac BL 54	
2	12.6	78.8	100	28	AZ658330	1M0535M02	
3	12.4	77.5	44	10	BG422154	60248881	
4	12	75.0	26	28	BH901408	SAUK_0790	

C	5	12	75.0	75	13	BH866082	BH866082 S062E01 P
C	6	12	75.0	95	13	BH867160	BH867160 S075A07 P
C	7	12	75.0	96	13	BH862306	BH862306 S014A04 P
C	8	12	75.0	100	13	BH861867	BH861867 S007G10 P
C	9	11.6	72.5	80	28	AZ619815	AZ619815 1M0452D18
C	10	11.4	71.2	52	14	H08942	H08942 Y193e05.r1
C	11	11.4	71.2	74	14	N98196	N98196 0266C3 czap
C	12	11.4	71.2	76	29	BX535085	BX535085 Arabidops
C	13	11.4	71.2	95	9	AI461140	AI461140 B875F01.Y
C	14	11.4	71.2	95	13	BQ823860	BQ823860 1030113D0
C	15	11.4	71.2	96	28	AZ916132	AZ916132 Pat1_3_a8
C	16	11	68.8	58	29	BX288422	BX288422 Arabidops
C	17	11	68.8	73	14	H62825	H62825 Y146e04.s1
C	18	11	68.8	82	12	B1865456	B1865456 fc22h12.x
C	19	11	68.8	84	28	AZ946645	AZ946645 2M0208H05
C	20	11	68.8	90	9	AI937714	AI937714 wp3a12.x
C	21	11	68.8	90	28	BH861753	BH861753 SALK_0879
C	22	11	68.8	91	29	AG224693	AG224693 locut_jap
C	23	11	68.8	96	28	AZ431360	AZ431360 1M0216F14
C	24	10.8	67.5	49	9	AI681141	AI681141 tx44d07.x
C	25	10.8	67.5	50	9	AU106358	AU106358 AU106358
C	26	10.8	67.5	52	9	AA425092	AA425092 zw11f11.r
C	27	10.8	67.5	52	29	BZ765391	BZ765391 SALK_1311
C	28	10.8	67.5	58	9	AA433099	AA433099 v04e08.r
C	29	10.8	67.5	59	28	AZ342599	AZ342599 1M0075C18
C	30	10.8	67.5	60	29	CNS0682T	AL394587 T3 end of
C	31	10.8	67.5	61	9	AA070413	AA070413 zme6c11.r
C	32	10.8	67.5	62	14	D12015	D12015 HUM0005149
C	33	10.8	67.5	65	9	AA494566	AA494566 v185904.r
C	34	10.8	67.5	65	28	BH414369	BH414369 1007037G0
C	35	10.8	67.5	65	29	TA184A08Q	TA184A08Q
C	36	10.8	67.5	67	10	BG447495	BG447495 EST000018
C	37	10.8	67.5	67	9	AA771119	AA771119 vt16h01.r
C	38	10.8	67.5	67	14	CB366166	CB366166 ZF001-P00
C	39	10.8	67.5	69	14	D11778	D11778 HUM001B11
C	40	10.8	67.5	71	9	AW104004	AW104004 x63h05.x
C	41	10.8	67.5	72	28	BH911226	BH911226 SALK_0670
C	42	10.8	67.5	72	29	BZ287687	BZ287687 SALK_0210
C	43	10.8	67.5	72	29	AL755673	AL755673 Arabidops
C	44	10.8	67.5	73	13	BH870558	BH870558 Q015B11 P
C	45	10.8	67.5	73	14	R46193	R46193 Yj53a03.s1
C	46	10.8	67.5	74	9	AW597442	AW597442 s18a11.Y
C	47	10.8	67.5	74	28	BH864812	BH864812 SALK_0675
C	48	10.8	67.5	76	9	AI353603	AI353603 zeh0736.8
C	49	10.8	67.5	79	9	AA445499	AA445499 v157f08.r
C	50	10.8	67.5	79	28	BH852365	BH852365 SALK_0745
C	51	10.8	67.5	79	29	AL757069	AL757069 Arabidops
C	52	10.8	67.5	80	9	AI371107	AI371107 ta30a05.x
C	53	10.8	67.5	80	10	BG447497	BG447497 EST000023
C	54	10.8	67.5	82	9	AA754818	AA754818 vt51b02.r
C	55	10.8	67.5	83	14	R86482	R86482 RABST056M
C	56	10.8	67.5	85	9	AA815657	AA815657 vt03f06.r
C	57	10.8	67.5	85	9	AA466155	AA466155 vq73g10.r
C	58	10.8	67.5	86	29	TA87H09Q	TA87H09Q
C	59	10.8	67.5	87	9	AI210682	AI210682 k0d02a1.r
C	60	10.8	67.5	88	9	AA935865	AA935865 on76a12.8
C	61	10.8	67.5	88	9	AA174733	AA174733 mt12c11.r
C	62	10.8	67.5	90	10	BE568667	BE568667 601342684
C	63	10.8	67.5	90	28	AZ602406	AZ602406 1M0421H09
C	64	10.8	67.5	93	9	AI680424	AI680424 tw63a03.x
C	65	10.8	67.5	93	28	BH215494	BH215494 1006027C1
C	66	10.8	67.5	94	9	AA420062	AA420062 v150b06.r
C	67	10.8	67.5	94	9	AA435359	AA435359 ve15e06.r
C	68	10.8	67.5	94	9	AA512503	AA512503 vj17h04.r
C	69	10.8	67.5	94	29	BZ291056	BZ291056 SALK_1123
C	70	10.8	67.5	94	29	AG219003	AG219003 Drosoph11
C	71	10.8	67.5	95	9	AA919502	AA919502 vz20g11.r
C	72	10.8	67.5	95	12	BI972059	BI972059 s8g85g03.
C	73	10.8	67.5	95	14	CA337825	CA337825 N1SC_1W06
C	74	10.8	67.5	95	14	T81028	T81028 yd25c05.s1
C	75	10.8	67.5	95	28	BH812878	BH812878 SALK_0633
C	76	10.8	67.5	96	28	B42033	B42033 HS-1055-A1-
C	77	10.8	67.5	97	9	AA691488	AA691488 vt15h04.r

C 78	10.8	67.5	97	9	AA797348	AA797348	151	10.4	65.0	92	9	AM714722	AM714722	120404e.r
C 79	10.8	67.5	97	9	AI581819	AI581819	152	10.4	65.0	92	9	AM722670	AM722670	C4903mm.r
C 80	10.8	67.5	97	9	AM064307	AM064307	153	10.4	65.0	92	28	AZ362937	IM0108B18	AZ362937
C 81	10.8	67.5	97	28	AZ916331	AZ916331	154	10.4	65.0	92	28	AZ348999	IM0229H19	AZ348999
C 82	10.8	67.5	99	9	AM271170	AM271170	155	10.4	65.0	92	29	BZ291268	SAUK 1200	BZ291268
C 83	10.8	67.5	99	10	BG695449	BG695449	156	10.4	65.0	93	10	BG409079	gpb9503.y	BG409079
C 84	10.8	67.5	99	12	BI421049	BI421049	157	10.4	65.0	93	29	AL752909	ArabiIdops	AL752909
C 85	10.8	67.5	99	28	BH418153	BH418153	158	10.4	65.0	93	29	AL753208	ArabiIdops	AL753208
C 86	10.8	67.5	100	9	AI934888	AI934888	159	10.4	65.0	94	23	DME546996	ArabiIdops	AJ546996
C 87	10.8	67.5	100	10	AA465654	AA465654	160	10.4	65.0	94	18	B0869084	MJ25H05.P	B0869084
C 88	10.8	67.5	100	10	BF874679	BF874679	161	10.4	65.0	94	28	AZ508919	IM0351C11	AZ508919
C 89	10.8	67.5	100	13	BO625306	BO625306	162	10.4	65.0	94	29	BX291595	ArabiIdops	BX291595
C 90	10.6	66.2	76	13	BO764143	BO764143	163	10.4	65.0	95	10	BG154716	ArabiIdops	BG154716
C 91	10.6	66.2	93	13	BO766868	BO766868	164	10.4	65.0	98	10	AMS96808	g1ch11.y	AMS96808
C 92	10.6	66.2	95	13	BO764114	BO764114	165	10.4	65.0	98	9	AM709081	d2106e.x	AM709081
C 93	10.6	66.2	98	13	BQ815594	BQ815594	166	10.4	65.0	98	28	AZ918923	100601e.r	AZ918923
C 94	10.4	65.0	34	28	AQ025306	AQ025306	167	10.4	65.0	99	9	AU244075	AU244075	AU244075
C 95	10.4	65.0	40	29	AL754614	AL754614	168	10.4	65.0	99	14	R79054	R79054	R79054
C 96	10.4	65.0	43	28	AZ502070	AZ502070	169	10.4	65.0	99	28	BH214808	1006004G0	BH214808
C 97	10.4	65.0	43	29	AL755593	AL755593	170	10.4	65.0	100	9	AM797834	CMO-UM04	AM797834
C 98	10.4	65.0	48	28	BH807268	BH807268	171	10.4	65.0	100	12	BM328423	PIC1_29.B	BM328423
C 99	10.4	65.0	49	28	BH861777	BH861777	172	10.2	63.7	42	10	BF527907	602041058	BF527907
C 100	10.4	65.0	49	28	BH861778	BH861778	173	10.2	63.7	53	28	AZ625652	1M0465A24	AZ625652
C 101	10.4	65.0	49	29	BZ586070	BZ586070	174	10.2	63.7	57	9	AI973877	sd13a08.y	AI973877
C 102	10.4	65.0	50	9	AU107549	AU107549	175	10.2	63.7	60	14	M85304	M85304	M85304
C 103	10.4	65.0	50	28	AZ921814	AZ921814	176	10.2	63.7	65	9	AV671702	AV671702	AV671702
C 104	10.4	65.0	53	9	AI161613	AI161613	177	10.2	63.7	68	9	AU256518	AU256518	AU256518
C 105	10.4	65.0	53	9	AM102062	AM102062	178	10.2	63.7	68	28	BH644273	1008043C0	BH644273
C 106	10.4	65.0	53	14	H18867	H18867	179	10.2	63.7	74	29	CC1179318	SAUK 0678	CC1179318
C 107	10.4	65.0	53	29	BZ63828	BZ63828	180	10.2	63.7	75	12	BI909149	603069150	BI909149
C 108	10.4	65.0	54	29	AL756050	AL756050	181	10.2	63.7	76	10	BE058589	sm18B03.y	BE058589
C 109	10.4	65.0	55	9	AA142563	AA142563	182	10.2	63.7	79	14	U44372	ENU44372.AB	U44372
C 110	10.4	65.0	58	29	BX288876	BX288876	183	10.2	63.7	80	9	AA836179	cd21905.B	AA836179
C 111	10.4	65.0	63	28	AZ435853	AZ435853	184	10.2	63.7	82	9	AA594999	no31e06.B	AA594999
C 112	10.4	65.0	63	29	BX188578	BX188578	185	10.2	63.7	83	10	BF463412	UI-M-CG0P	BF463412
C 113	10.4	65.0	64	9	AA25961	AA25961	186	10.2	63.7	85	9	AL896449	AL896449	AL896449
C 114	10.4	65.0	66	28	BH894070	BH894070	187	10.2	63.7	86	9	AA236075	z805a05.x	AA236075
C 115	10.4	65.0	67	28	AZ759905	AZ759905	188	10.2	63.7	88	14	R22567	yh24a08.e1	R22567
C 116	10.4	65.0	67	28	BH908636	BH908636	189	10.2	63.7	91	14	CB394112	OSTR131H4	CB394112
C 117	10.4	65.0	69	29	AL752981	AL752981	190	10.2	63.7	91	28	BH851397	SAUK 0729	BH851397
C 118	10.4	65.0	70	29	AL753206	AL753206	191	10.2	63.7	92	28	AZ778554	2M0013M10	AZ778554
C 119	10.4	65.0	70	29	CNS03W6S	CNS03W6S	192	10.2	63.7	92	28	BH220609	1006095G0	BH220609
C 120	10.4	65.0	73	3	AM251001	AM251001	193	10.2	63.7	94	28	AZ822068	2M0095D02	AZ822068
C 121	10.4	65.0	73	13	BH970558	BH970558	194	10.2	63.7	95	29	AL943193	ArabiIdops	AL943193
C 122	10.4	65.0	73	14	CB832613	CB832613	195	10.2	63.7	97	9	AA429118	zw19c01.r	AA429118
C 123	10.4	65.0	74	9	AA832576	AA832576	196	10.2	63.7	98	14	CA843512	1748a01.y	CA843512
C 124	10.4	65.0	74	29	CNS0217A	CNS0217A	197	10.2	63.7	100	10	BE330980	8092a05.y	BE330980
C 125	10.4	65.0	75	10	BE368978	BE368978	198	10.2	62.5	28	9	A1625681	ty59c06.x	A1625681
C 126	10.4	65.0	76	29	AL753252	AL753252	199	10.2	62.5	33	29	BZ358119	SAUK 1319	BZ358119
C 127	10.4	65.0	76	29	BSA275805	BSA275805	200	10.2	62.5	37	9	AA864329	ch56f12.B	AA864329
C 128	10.4	65.0	77	14	CA819431	CA819431	201	10.2	62.5	37	9	AA985715	ue13d01.y	AA985715
C 129	10.4	65.0	78	10	BE023116	BE023116	202	10.2	62.5	37	9	AA238798	mx93c01.r	AA238798
C 130	10.4	65.0	79	14	CB367939	CB367939	203	10.2	62.5	40	14	W53067	md14f07.x1	W53067
C 131	10.4	65.0	80	9	AL820251	AL820251	204	10.2	62.5	43	28	AZ789583	2M0037F01	AZ789583
C 132	10.4	65.0	81	13	BO823042	BO823042	205	10.2	62.5	46	28	BH635864	1008007F0	BH635864
C 133	10.4	65.0	81	29	CC457634	CC457634	206	10.2	62.5	47	29	TA359H02Q	ArabiIdops	TA359H02Q
C 134	10.4	65.0	81	29	CC457635	CC457635	207	10.2	62.5	48	28	BH907194	SAUK 0386	BH907194
C 135	10.4	65.0	81	29	CC457636	CC457636	208	10.2	62.5	51	14	CB053396	g114	CB053396
C 136	10.4	65.0	82	9	AM598481	AM598481	209	10.2	62.5	52	9	A1287257	qv22e08.g114	A1287257
C 137	10.4	65.0	82	9	AM598483	AM598483	210	10.2	62.5	55	12	BI447971	dash90d02.	BI447971
C 138	10.4	65.0	83	12	BJ0000334	BJ0000334	211	10.2	62.5	55	28	B45110	HS-1060-B1-	B45110
C 139	10.4	65.0	84	9	AM722919	AM722919	212	10.2	62.5	58	9	AI195289	ue71a03.r	AI195289
C 140	10.4	65.0	85	9	AA183068	AA183068	213	10.2	62.5	58	9	AA480462	ne70d10.B	AA480462
C 141	10.4	65.0	85	9	AV842614	AV842614	214	10.2	62.5	58	12	BI944424	sbd21d05.	BI944424
C 142	10.4	65.0	87	9	AM722677	AM722677	215	10.2	62.5	58	29	BZ360332	SAUK 1149	BZ360332
C 143	10.4	65.0	88	28	BH228507	BH228507	216	10.2	62.5	60	10	BF471331	UI-M-BH3-	BF471331
C 144	10.4	65.0	89	14	CA797738	CA797738	217	10.2	62.5	60	29	BX232154	Danio.fex	BX232154
C 145	10.4	65.0	89	28	AZ495357	AZ495357	218	10.2	62.5	61	13	B0759608	EBD103-SQ	B0759608
C 146	10.4	65.0	90	9	AI320073	AI320073	219	10.2	62.5	65	9	AI926212	w054a05.x	AI926212
C 147	10.4	65.0	90	12	BM069470	BM069470	220	10.2	62.5	67	28	AZ588886	1M0397D06	AZ588886
C 148	10.4	65.0	90	13	B0824532	B0824532	221	10.2	62.5	68	10	BE463636	h696c11.x	BE463636
C 149	10.4	65.0	90	14	D20584	D20584	222	10.2	62.5	68	10	BE463636	h696c11.x	BE463636
C 150	10.4	65.0	90	28	BH217012	BH217012	223	10.2	62.5	70	9	AA271393	vab4e05.r	AA271393

C 224	10	62.5	74	9	AA066266	mm08b02.r	297	9.8	61.3	44	9	AV845599	AV845599
C 225	10	62.5	75	28	A1355788	qt94f02.x	C 298	9.8	61.3	45	12	B1761191	B1761191
C 226	10	62.5	76	28	AZ960154	2M0228A10	C 299	9.8	61.3	45	28	AZ832673	AZ832673
C 227	10	62.5	76	29	CC156096	NPX002.Ba	C 300	9.8	61.3	45	28	TA17A05Q	TA17A05Q
C 228	10	62.5	77	29	AG226570	Locus_jap	301	9.8	61.3	46	28	AZ603730	AZ603730
C 229	10	62.5	79	19	BF507191	2912P-22d	302	9.8	61.3	46	28	BH789255	BH789255
C 230	10	62.5	80	29	TAB1G040	bruce1	303	9.8	61.3	47	29	BZ382871	BZ382871
C 231	10	62.5	85	28	BH866791	3526.1.5	C 304	9.8	61.3	48	12	B1757791	B1757791
C 232	10	62.5	85	29	AL947273	ArabiIdops	305	9.8	61.3	48	28	AZ767769	AZ767769
C 233	10	62.5	89	14	CB686411	Bn01D_04h	C 306	9.8	61.3	49	28	B1407152	B1407152
C 234	10	62.5	89	28	AZ921956	HRC02G04	C 307	9.8	61.3	49	12	CC459657	CC459657
C 235	10	62.5	91	10	AA814152	cb25e02.s	C 308	9.8	61.3	50	9	AU102609	AU102609
C 236	10	62.5	91	10	BE399488	WHE0036.H	C 309	9.8	61.3	50	9	AU102610	AU102610
C 237	10	62.5	91	10	CB884950	Ma17065.H	C 310	9.8	61.3	50	9	AU102612	AU102612
C 238	10	62.5	91	28	AZ483571	IM0309D20	C 311	9.8	61.3	50	9	AU102613	AU102613
C 239	10	62.5	92	14	W17739	mb77902.r1	C 312	9.8	61.3	50	9	AU102614	AU102614
C 240	10	62.5	94	28	BH901682	SA1K_0844	C 313	9.8	61.3	50	9	AU103873	AU103873
C 241	10	62.5	95	29	BZ706369	SM276B2-G	C 314	9.8	61.3	50	9	AU107477	AU107477
C 242	10	62.5	97	28	AA936843	oh89f08.s	C 315	9.8	61.3	50	9	AU107480	AU107480
C 243	10	62.5	97	28	BH906651	SA1K_0351	C 316	9.8	61.3	50	9	AW783902	AW783902
C 244	10	62.5	98	28	AZ777342	2M001M07	C 317	9.8	61.3	50	29	BZ769258	BZ769258
C 245	10	62.5	99	9	AA785099	g5a02a1.f	C 318	9.8	61.3	50	29	BZ769259	BZ769259
C 246	10	62.5	99	9	AL826677	AL826677	C 319	9.8	61.3	52	28	BH809438	BH809438
C 247	10	62.5	99	10	BG152001	nae72e07.	C 320	9.8	61.3	54	29	CC054970	CC054970
C 248	10	62.5	99	14	H92491	Y8B6C10..81	C 321	9.8	61.3	55	9	AU235741	AU235741
C 249	10	62.5	100	9	AA196242	zP98f04.r	C 322	9.8	61.3	55	28	AZ759826	AZ759826
C 250	10	62.5	100	29	BZ355837	SA1K_1276	C 323	9.8	61.3	55	28	AZ845377	AZ845377
C 251	9.8	61.3	19	9	A1318366	q053b01.x	C 324	9.8	61.3	55	28	BF312405	BF312405
C 252	9.8	61.3	20	29	TA384D04P	bruce1	C 325	9.8	61.3	56	10	BF315275	BF315275
C 253	9.8	61.3	30	10	BE274322	601121015	C 326	9.8	61.3	56	10	BF315275	BF315275
C 254	9.8	61.3	30	10	BE276865	601178428	C 327	9.8	61.3	56	12	BF1906543	BF1906543
C 255	9.8	61.3	30	10	BE277260	601178250	C 328	9.8	61.3	58	28	AF219062	AF219062
C 256	9.8	61.3	30	10	BE279576	601157461	C 329	9.8	61.3	58	28	BZ52795	BZ52795
C 257	9.8	61.3	30	10	BE280898	601155490	C 330	9.8	61.3	59	12	BJ036242	BJ036242
C 258	9.8	61.3	30	10	BE384678	60127335	C 331	9.8	61.3	59	12	A1857338	A1857338
C 259	9.8	61.3	30	10	BE384733	60127335	C 332	9.8	61.3	61	9	AA189463	AA189463
C 260	9.8	61.3	30	10	BE386356	601273503	C 333	9.8	61.3	62	9	AA149923	AA149923
C 261	9.8	61.3	30	10	BE389833	601284336	C 334	9.8	61.3	63	9	AU009048	AU009048
C 262	9.8	61.3	30	10	BE359533	601345383	C 335	9.8	61.3	63	9	AU009049	AU009049
C 263	9.8	61.3	30	10	BE5561270	601344283	C 336	9.8	61.3	63	9	AU009103	AU009103
C 264	9.8	61.3	30	10	BE727688	601564370	C 337	9.8	61.3	63	9	AU009104	AU009104
C 265	9.8	61.3	30	10	BE731660	601594894	C 338	9.8	61.3	63	9	AW762943	AW762943
C 266	9.8	61.3	30	10	BE741581	601594894	C 339	9.8	61.3	63	29	TA393B01P	TA393B01P
C 267	9.8	61.3	30	10	BE900191	601673121	C 340	9.8	61.3	64	9	AA980801	AA980801
C 268	9.8	61.3	31	10	BE261494	601148665	C 341	9.8	61.3	64	13	BU060104	BU060104
C 269	9.8	61.3	31	10	BE384502	601277869	C 342	9.8	61.3	65	9	AA650570	AA650570
C 270	9.8	61.3	31	10	BE409249	601301117	C 343	9.8	61.3	65	12	B1828339	B1828339
C 271	9.8	61.3	31	10	BE729154	601561047	C 344	9.8	61.3	65	29	AL758072	AL758072
C 272	9.8	61.3	31	10	BE731925	601568932	C 345	9.8	61.3	65	29	BX287248	BX287248
C 273	9.8	61.3	31	28	AZ386571	IM0145C09	C 346	9.8	61.3	66	9	AA122247	AA122247
C 274	9.8	61.3	31	29	TA235H03Q	bruce1	C 347	9.8	61.3	66	9	AA063368	AA063368
C 275	9.8	61.3	32	10	BE277724	601119330	C 348	9.8	61.3	67	9	AA098036	AA098036
C 276	9.8	61.3	32	10	BE561225	601344209	C 349	9.8	61.3	67	9	A1931601	A1931601
C 277	9.8	61.3	32	10	BE901763	601675392	C 350	9.8	61.3	67	9	AA592240	AA592240
C 278	9.8	61.3	32	28	AZ631344	IM0485A05	C 351	9.8	61.3	67	28	AZ426659	AZ426659
C 279	9.8	61.3	32	28	AZ639727	IM0501D21	C 352	9.8	61.3	67	28	AZ505102	AZ505102
C 280	9.8	61.3	33	10	BE385013	601276895	C 353	9.8	61.3	67	29	AL945283	AL945283
C 281	9.8	61.3	33	10	BF026570	601672580	C 354	9.8	61.3	68	10	BF026620	BF026620
C 282	9.8	61.3	34	10	BE268227	601125649	C 355	9.8	61.3	68	10	AG228238	AG228238
C 283	9.8	61.3	34	10	BE277022	601178905	C 356	9.8	61.3	69	29	AL768203	AL768203
C 284	9.8	61.3	34	10	BE277727	601119937	C 357	9.8	61.3	69	29	BE729541	BE729541
C 285	9.8	61.3	34	10	BE561483	601346552	C 358	9.8	61.3	70	10	BE729541	BE729541
C 286	9.8	61.3	35	28	AZ666284	IM0548P10	C 359	9.8	61.3	70	10	AZ807035	AZ807035
C 287	9.8	61.3	36	10	BE408356	601302740	C 360	9.8	61.3	71	28	B02627	B02627
C 288	9.8	61.3	37	14	CB305210	3'EST_ncl1	C 361	9.8	61.3	72	9	AV848928	AV848928
C 289	9.8	61.3	37	29	TA15F1P	bruce1	C 362	9.8	61.3	72	9	AV848928	AV848928
C 290	9.8	61.3	39	10	BE393354	601308575	C 363	9.8	61.3	72	13	B0759977	B0759977
C 291	9.8	61.3	41	28	AZ467358	IM0278M07	C 364	9.8	61.3	72	14	F30685	F30685
C 292	9.8	61.3	41	28	AZ804585	2M0065B10	C 365	9.8	61.3	72	14	U25930	U25930
C 293	9.8	61.3	42	9	AU006856	AV006856	C 366	9.8	61.3	72	28	BH617862	BH617862
C 294	9.8	61.3	43	9	AV962413	AV962413	C 367	9.8	61.3	72	28	BX187211	BX187211
C 295	9.8	61.3	43	12	B1829531	603080362	C 368	9.8	61.3	73	28	BH804456	BH804456
C 296	9.8	61.3	43	29	AL756475	ArabiIdops	C 369	9.8	61.3	73	29	BX146393	BX146393

AV845599 AV845599
B1761191 603043417
AZ832673 2M0113G22
AL452403 T. bruce1
AZ603730 IM0423A18
BH789255 SA1K_0013
BZ382871 SA1K_1190
B1757791 603029775
AZ767769 IM0567H13
B1407152 602919431
CC459657 SA1K_1379
AU102609 AU102609
AU102610 AU102610
AU102612 AU102612
AU102613 AU102613
AU102614 AU102614
AU103873 AU103873
AU107477 AU107477
AU107480 AU107480
AW783902 5. A12 G11
BZ769258 SA1K_1418
BZ769259 SA1K_1418
BH809438 KC03411-5
CC054970 SA1K_0804
AU235741 AU235741
AA669546 v6f6d07.r
AZ759826 IM052N20
AZ845377 2M0145H09
BF312405 601898946
BF315275 601902673
B1906543 603064110
AF219062 AF219062
BZ52795 SA1K_0291
BJ036242 BJ036242
A1857338 m02h07.x
AA189463 m79f06.r
A1149923 qf33d06.x
AU009048 AU009048
AU009049 AU009049
AU009103 AU009103
AU009104 AU009104
AW762943 u6f6g08.y
AL986693 T. bruce1
AA980801 u445g07.r
BU060104 F9r-C_0.L
AA650570 n06a06.b
B1828339 603078350
AL758072 ArabiIdops
BX287248 ArabiIdops
AA122247 z029e03.s
AA063368 TN0743 KR
AA098036 mn84d01.r
A1931601 u171c02.y
AA592240 v020a06.r
AZ426659 IM0208N14
AZ505102 IM0345D12
AL945283 ArabiIdops
AA610931 AY324 ANY
BF026620 601672788
AG228238 Locus_jap
AL768203 ArabiIdops
BE729541 601564626
AZ807035 2M0065C01
B02627 CSRL-15788-
AV848928 AV848928
AV848928 6k17g11.y
B0759977 EBD107 SQ
F30685 HSPD21285 H
U25930 HSU25930 HU
BH617862 SA1K_0380
BX187211 Danilo rer
BH804456 100810280
BX146393 Danilo rer

C 370	9.8	61.3	74	13	BUE63073	5023E06 P	443	9.8	61.3	95	28	A2823238
C 371	9.8	61.3	74	28	A2490925	IM0324N10	444	9.8	61.3	96	28	BH219479
C 372	9.8	61.3	74	29	AL764987	ArabiDops	445	9.8	61.3	97	9	AI125129
C 373	9.8	61.3	75	29	AM057152	AM057152 ca01d2.y	446	9.8	61.3	97	9	AI1401740
C 374	9.8	61.3	75	29	TR246602Q	AL48810 T. brucei	447	9.8	61.3	97	9	AI1858905
C 375	9.8	61.3	78	10	BE057811	BE057811 BUE09.Y	448	9.8	61.3	97	9	AI1858905
C 376	9.8	61.3	78	10	BE408724	BE408724 601304095	449	9.8	61.3	97	9	AI1858905
C 377	9.8	61.3	78	10	H73809	H73809 YH1308.B1	450	9.8	61.3	97	9	AI1858905
C 378	9.8	61.3	78	28	BH251148	BH251148 MSMD P06.	451	9.8	61.3	98	9	AI1858905
C 379	9.8	61.3	79	9	AI133764	AI133764 mmlh09.x	452	9.8	61.3	98	9	AI1858905
C 380	9.8	61.3	79	10	BE386358	BE386358 sb13c03.Y	453	9.8	61.3	98	9	AI1858905
C 381	9.8	61.3	79	10	BE732944	BE732944 601569704	454	9.8	61.3	98	9	AI1858905
C 382	9.8	61.3	79	28	BZ580914	BZ580914 STCCr4H04	455	9.8	61.3	98	9	AI1858905
C 383	9.8	61.3	80	13	BQ758161	BQ758161 3590_141	456	9.8	61.3	99	9	AI1858905
C 384	9.8	61.3	80	14	N84008	N84008 KK4294F Hum	457	9.8	61.3	99	9	AI1858905
C 385	9.8	61.3	80	28	AE761677	AE761677 IM0556D08	458	9.8	61.3	99	9	AI1858905
C 386	9.8	61.3	81	9	AI593729	AI593729 VL64C03.X	459	9.8	61.3	99	9	AI1858905
C 387	9.8	61.3	81	9	AL647524	AL647524 AL647524	460	9.8	61.3	99	9	AI1858905
C 388	9.8	61.3	81	9	CA592527	CA592527 bsn1.PK00	461	9.8	61.3	99	9	AI1858905
C 389	9.8	61.3	81	28	BH24699	BH24699 1006120G0	462	9.8	61.3	99	9	AI1858905
C 390	9.8	61.3	81	28	AF219090	AF219090 mmlh09.x	463	9.8	61.3	99	9	AI1858905
C 391	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	464	9.8	61.3	99	9	AI1858905
C 392	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	465	9.8	61.3	99	9	AI1858905
C 393	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	466	9.8	61.3	99	9	AI1858905
C 394	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	467	9.8	61.3	99	9	AI1858905
C 395	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	468	9.8	61.3	99	9	AI1858905
C 396	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	469	9.8	61.3	99	9	AI1858905
C 397	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	470	9.8	61.3	99	9	AI1858905
C 398	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	471	9.8	61.3	99	9	AI1858905
C 399	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	472	9.8	61.3	99	9	AI1858905
C 400	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	473	9.8	61.3	99	9	AI1858905
C 401	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	474	9.8	61.3	99	9	AI1858905
C 402	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	475	9.8	61.3	99	9	AI1858905
C 403	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	476	9.8	61.3	99	9	AI1858905
C 404	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	477	9.8	61.3	99	9	AI1858905
C 405	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	478	9.8	61.3	99	9	AI1858905
C 406	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	479	9.8	61.3	99	9	AI1858905
C 407	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	480	9.8	61.3	99	9	AI1858905
C 408	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	481	9.8	61.3	99	9	AI1858905
C 409	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	482	9.8	61.3	99	9	AI1858905
C 410	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	483	9.8	61.3	99	9	AI1858905
C 411	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	484	9.8	61.3	99	9	AI1858905
C 412	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	485	9.8	61.3	99	9	AI1858905
C 413	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	486	9.8	61.3	99	9	AI1858905
C 414	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	487	9.8	61.3	99	9	AI1858905
C 415	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	488	9.8	61.3	99	9	AI1858905
C 416	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	489	9.8	61.3	99	9	AI1858905
C 417	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	490	9.8	61.3	99	9	AI1858905
C 418	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	491	9.8	61.3	99	9	AI1858905
C 419	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	492	9.8	61.3	99	9	AI1858905
C 420	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	493	9.8	61.3	99	9	AI1858905
C 421	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	494	9.8	61.3	99	9	AI1858905
C 422	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	495	9.8	61.3	99	9	AI1858905
C 423	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	496	9.8	61.3	99	9	AI1858905
C 424	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	497	9.8	61.3	99	9	AI1858905
C 425	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	498	9.8	61.3	99	9	AI1858905
C 426	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	499	9.8	61.3	99	9	AI1858905
C 427	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	500	9.8	61.3	99	9	AI1858905
C 428	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	501	9.8	61.3	99	9	AI1858905
C 429	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	502	9.8	61.3	99	9	AI1858905
C 430	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	503	9.8	61.3	99	9	AI1858905
C 431	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	504	9.8	61.3	99	9	AI1858905
C 432	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	505	9.8	61.3	99	9	AI1858905
C 433	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	506	9.8	61.3	99	9	AI1858905
C 434	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	507	9.8	61.3	99	9	AI1858905
C 435	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	508	9.8	61.3	99	9	AI1858905
C 436	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	509	9.8	61.3	99	9	AI1858905
C 437	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	510	9.8	61.3	99	9	AI1858905
C 438	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	511	9.8	61.3	99	9	AI1858905
C 439	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	512	9.8	61.3	99	9	AI1858905
C 440	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	513	9.8	61.3	99	9	AI1858905
C 441	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	514	9.8	61.3	99	9	AI1858905
C 442	9.8	61.3	82	28	AA170093	AA170093 mmlh09.x	515	9.8	61.3	99	9	AI1858905

516	9.4	58.8	51	14	CAB19249	SAUT1D08.	589	9.4	58.8	72	10	BE729054	BE729054	601561245
517	9.4	58.8	51	28	AZ377404	1M031B15	590	9.4	58.8	72	12	BM023144	BM023144	i-e80b09.x
518	9.4	58.8	52	9	AA490834	AA490834	591	9.4	58.8	72	28	AZ826761	AZ826761	2M0102C17
519	9.4	58.8	52	28	AZ591884	AZ591884	592	9.4	58.8	72	29	BX288010	BX288010	ArabiDops
520	9.4	58.8	53	29	BX87634	ArabiDops	593	9.4	58.8	73	9	AA730934	AA730934	nw55a01.s
521	9.4	58.8	53	29	AA502082	AA502082	594	9.4	58.8	73	9	AF211624	AF211624	AF211624
522	9.4	58.8	53	29	AG5252874	Lotus_jap	595	9.4	58.8	73	9	AI368998	AI368998	qwl7f02.x
523	9.4	58.8	54	14	CB019050	CB019050	596	9.4	58.8	73	14	CB832357	CB832357	SWMBFCAY
524	9.4	58.8	54	28	AZ581916	IM0374B10	597	9.4	58.8	73	14	CB832488	CB832488	SWMBFCAY
525	9.4	58.8	54	28	BH220866	BH220866	598	9.4	58.8	74	10	BF507235	BF507235	4682P-18a
526	9.4	58.8	54	29	DME546441	AS456441	599	9.4	58.8	74	13	BU761013	BU761013	sa661902.
527	9.4	58.8	55	14	CA913529	CA913529	600	9.4	58.8	74	14	CB019138	CB019138	px73h03.y
528	9.4	58.8	55	14	U44321	U44321	601	9.4	58.8	74	29	CC455019	CC455019	0282035-0
529	9.4	58.8	55	28	AO107792	HS_3109_A	602	9.4	58.8	74	29	AC226279	AC226279	Lotus_jap
530	9.4	58.8	55	28	BH911635	BH911635	603	9.4	58.8	75	28	AZ449752	AZ449752	IM0246007
531	9.4	58.8	55	29	BZ664325	SALK_0698	604	9.4	58.8	76	9	AI213259	AI213259	y8g10a1.f
532	9.4	58.8	56	9	AJ237104	AJ237104	605	9.4	58.8	76	13	BQ758159	BQ758159	EBma01.SQ
533	9.4	58.8	56	9	AV858811	AV858811	606	9.4	58.8	76	14	R52188	R52188	Y985d03.r1
534	9.4	58.8	56	29	BZ380795	BZ380795	607	9.4	58.8	76	14	W42696	W42696	zc24G06.r1
535	9.4	58.8	56	29	TA209B01P	TA209B01P	608	9.4	58.8	77	28	BH856483	BH856483	SAUK_0796
536	9.4	58.8	58	9	AI302327	AI302327	609	9.4	58.8	77	10	EG315199	EG315199	FOI_0.175
537	9.4	58.8	58	10	BF206095	BF206095	610	9.4	58.8	77	14	C00491	C00491	HUMGS000801
538	9.4	58.8	58	14	H68254	H68254	611	9.4	58.8	77	14	U44224	U44224	ENU44224.AS
539	9.4	58.8	58	29	BX288422	BX288422	612	9.4	58.8	77	28	AZ659686	AZ659686	IM0537D13
540	9.4	58.8	59	9	AM245782	AM245782	613	9.4	58.8	77	29	AL757611	AL757611	ArabiDops
541	9.4	58.8	60	10	BF639034	NP064G04P	614	9.4	58.8	78	9	AB036473	AB036473	AB036473
542	9.4	58.8	60	14	CA330654	CA330654	615	9.4	58.8	78	28	BH863739	BH863739	SAUK_0944
543	9.4	58.8	60	14	CB912855	CB912855	616	9.4	58.8	79	13	BQ758356	BQ758356	EBma04.SQ
544	9.4	58.8	60	29	BX003940	BX003940	617	9.4	58.8	79	14	CD346390	CD346390	ESTESTe01
545	9.4	58.8	60	29	BX293075	BX293075	618	9.4	58.8	79	28	AZ822008	AZ822008	2M0095G20
546	9.4	58.8	61	9	AI138514	AI138514	619	9.4	58.8	79	28	BH176333	BH176333	006_E_04-
547	9.4	58.8	61	9	AI306736	AI306736	620	9.4	58.8	79	29	CNS0707Q	CNS0707Q	end of
548	9.4	58.8	61	12	BG824696	BG824696	621	9.4	58.8	80	9	AI571712	AI571712	lr87h03.x
549	9.4	58.8	61	28	AQ050887	AQ050887	622	9.4	58.8	80	11	CNS08D0A	CNS08D0A	Single re
550	9.4	58.8	61	28	BH636149	BH636149	623	9.4	58.8	80	14	CB549291	CB549291	MMP10024
551	9.4	58.8	61	28	BH847946	BH847946	624	9.4	58.8	81	9	AA105549	AA105549	mo57G07.x
552	9.4	58.8	61	28	BH848228	BH848228	625	9.4	58.8	81	9	AI510696	AI510696	ar75b02.x
553	9.4	58.8	62	13	BQ563196	BQ563196	626	9.4	58.8	81	9	AU256415	AU256415	AU256415
554	9.4	58.8	62	29	AG022515	AG022515	627	9.4	58.8	81	9	AV916479	AV916479	AV916479
555	9.4	58.8	62	29	AL758849	ArabiDops	628	9.4	58.8	81	10	BE226221	BE226221	1a17b02.y
556	9.4	58.8	63	10	BF638564	BF638564	629	9.4	58.8	81	28	AZ586406	AZ586406	IM0392J16
557	9.4	58.8	63	10	BG362029	BG362029	630	9.4	58.8	81	28	BH635784	BH635784	1008007A0
558	9.4	58.8	63	28	AZ622892	IM0460B05	631	9.4	58.8	81	29	AG241454	AG241454	Lotus_jap
559	9.4	58.8	63	29	BZ595944	SAUK_0904	632	9.4	58.8	82	14	CB221835	CB221835	11i20E7.B
560	9.4	58.8	63	29	AL769268	AL769268	633	9.4	58.8	82	28	AZ800630	AZ800630	2M0058B14
561	9.4	58.8	64	9	AU076645	AU076645	634	9.4	58.8	82	29	BZ764336	BZ764336	SAUK_1244
562	9.4	58.8	64	9	AM161265	AM161265	635	9.4	58.8	83	11	CNS0916T	CNS0916T	Single re
563	9.4	58.8	64	11	CNS09MTR	CNS09MTR	636	9.4	58.8	83	13	BQ754434	BQ754434	EBed01.SQ
564	9.4	58.8	64	28	BH852825	BH852825	637	9.4	58.8	83	28	BH609150	BH609150	23h17.TL1
565	9.4	58.8	64	29	AL763885	ArabiDops	638	9.4	58.8	83	29	AG250348	AG250348	Lotus_jap
566	9.4	58.8	65	12	B1420923	B1420923	639	9.4	58.8	84	12	BM284355	BM284355	k157d06.y
567	9.4	58.8	65	28	BH813114	SAUK_0637	640	9.4	58.8	84	29	BZ831311	BZ831311	SAUK_1210
568	9.4	58.8	66	14	CA330071	CA330071	641	9.4	58.8	84	29	TA73C01P	TA73C01P	T. brucei
569	9.4	58.8	66	28	BH795866	1008091P0	642	9.4	58.8	85	10	BE138392	BE138392	xr74C08.x
570	9.4	58.8	67	9	AL682081	AL682081	643	9.4	58.8	85	14	H40981	H40981	yr93e12.B1
571	9.4	58.8	67	12	BO066489	BO066489	644	9.4	58.8	85	14	R09677	R09677	yf27h07.r1
572	9.4	58.8	68	9	AA646188	AA646188	645	9.4	58.8	85	29	BZ286725	BZ286725	SAUK_0200
573	9.4	58.8	68	9	AA906482	AA906482	646	9.4	58.8	85	29	CC156125	CC156125	DTW072.Ba
574	9.4	58.8	68	9	AV834246	AV834246	647	9.4	58.8	86	9	AV561505	AV561505	AV561505
575	9.4	58.8	68	11	CNS08M76	CNS08M76	648	9.4	58.8	86	13	BU891532	BU891532	P051G02.P
576	9.4	58.8	68	28	AZ659333	AX018190	649	9.4	58.8	86	29	BZ662007	BZ662007	SAUK_0254
577	9.4	58.8	68	29	CC177925	CC177925	650	9.4	58.8	87	9	AA090193	AA090193	CCDP0520.
578	9.4	58.8	69	14	CB910918	CB910918	651	9.4	58.8	87	9	AM197942	AM197942	xo27d11.x
579	9.4	58.8	69	28	BH256331	SAUK_0151	652	9.4	58.8	87	9	AA447716	AA447716	a220C07.s
580	9.4	58.8	69	28	BH798590	1008121A0	653	9.4	58.8	87	9	AA536680	AA536680	vj87h08.r
581	9.4	58.8	69	29	BZ356429	SAUK_1289	654	9.4	58.8	88	9	AV911279	AV911279	AV911279
582	9.4	58.8	70	9	AA883591	AA883591	655	9.4	58.8	88	9	AM064494	AM064494	SP1094.XR
583	9.4	58.8	70	9	AA953289	AA953289	656	9.4	58.8	88	9	AA522214	AA522214	vi43a04.r
584	9.4	58.8	70	12	BO084169	BO084169	657	9.4	58.8	88	9	AA534719	AA534719	ni79b02.s
585	9.4	58.8	70	28	AG263877	Locus_jap	658	9.4	58.8	88	13	BU087452	BU087452	M10C07.P
586	9.4	58.8	71	29	BH856644	SAUK_0793	659	9.4	58.8	88	28	AZ409014	AZ409014	IM0180K22
587	9.4	58.8	72	10	BF507113	BF507113	660	9.4	58.8	88	29	BZ288474	BZ288474	SAUK_0218
588	9.4	58.8	72	10	BB655522	BB655522	661	9.4	58.8	88	29	BZ662920	BZ662920	SAUK_0264

C 662	9.4	58.8	88	29	AG217414	C 735	9.4	58.8	100	9	AU083178
C 663	9.4	58.8	88	29	AL753134	C 736	9.4	58.8	100	9	AV954305
C 664	9.4	58.8	88	29	BX001307	C 737	9.4	58.8	100	9	AA545643
C 665	9.4	58.8	89	9	AA011169	C 738	9.4	58.8	100	10	BG552751
C 666	9.4	58.8	89	9	AA861138	C 739	9.4	58.8	100	10	BE154960
C 667	9.4	58.8	89	9	AU014403	C 740	9.4	58.8	100	10	BF023697
C 668	9.4	58.8	89	9	AM133499	C 741	9.4	58.8	100	12	BF372034
C 669	9.4	58.8	89	29	AG233862	C 742	9.4	58.8	100	12	BM374004
C 670	9.4	58.8	90	9	AA653697	C 743	9.4	58.8	100	12	BQ621255
C 671	9.4	58.8	90	9	AA200414	C 744	9.4	58.8	100	13	BQ621255
C 672	9.4	58.8	90	9	AU180944	C 745	9.4	58.8	100	13	BQ621255
C 673	9.4	58.8	90	11	AA279965	C 746	9.4	58.8	100	14	CB274278
C 674	9.4	58.8	90	11	CNS03692	C 747	9.4	58.8	100	14	CB274278
C 675	9.4	58.8	90	28	AZ986258	C 748	9.4	58.8	100	14	CB956291
C 676	9.4	58.8	90	29	BZ292762	C 749	9.4	58.8	100	14	AZ307591
C 677	9.4	58.8	91	9	AA845242	C 750	9.4	58.8	100	28	AZ410813
C 678	9.4	58.8	91	9	AA878704	C 751	9.4	58.8	100	28	AZ957930
C 679	9.4	58.8	91	9	AA954734	C 752	9.4	58.8	100	28	BH218122
C 680	9.4	58.8	91	9	AI941365	C 753	9.4	58.8	100	29	BZ597284
C 681	9.4	58.8	91	9	AA89178	C 754	9.2	57.5	22	9	AA912639
C 682	9.4	58.8	91	10	BG142757	C 755	9.2	57.5	22	29	TA53H020
C 683	9.4	58.8	91	14	W35852	C 756	9.2	57.5	23	28	AZ303987
C 684	9.4	58.8	91	28	BH216058	C 757	9.2	57.5	24	11	CNS08018
C 685	9.4	58.8	92	9	AT000234	C 758	9.2	57.5	26	29	BZ358021
C 686	9.4	58.8	92	10	BF676997	C 759	9.2	57.5	27	28	AZ799014
C 687	9.4	58.8	92	14	CB006075	C 760	9.2	57.5	28	28	BH911462
C 688	9.4	58.8	92	14	CB402602	C 761	9.2	57.5	30	10	BE278221
C 689	9.4	58.8	92	28	AZ310800	C 762	9.2	57.5	30	10	BE278715
C 690	9.4	58.8	92	28	BH217859	C 763	9.2	57.5	30	10	BE385997
C 691	9.4	58.8	92	29	BZ764434	C 764	9.2	57.5	30	10	BE386027
C 692	9.4	58.8	92	29	AG220799	C 765	9.2	57.5	30	10	BE386094
C 693	9.4	58.8	92	29	AG257737	C 766	9.2	57.5	30	10	BE386937
C 694	9.4	58.8	92	29	AL770432	C 767	9.2	57.5	30	10	BE900457
C 695	9.4	58.8	93	9	AV909387	C 768	9.2	57.5	30	28	BH909028
C 696	9.4	58.8	93	14	CB827185	C 769	9.2	57.5	31	10	BE274171
C 697	9.4	58.8	93	28	BH848820	C 770	9.2	57.5	31	10	BE277749
C 698	9.4	58.8	93	29	BZ383142	C 771	9.2	57.5	31	10	BE280621
C 699	9.4	58.8	93	29	BX201107	C 772	9.2	57.5	31	10	BE298405
C 700	9.4	58.8	94	9	AA215254	C 773	9.2	57.5	31	10	BE388076
C 701	9.4	58.8	94	28	AZ920726	C 774	9.2	57.5	31	10	BE408963
C 702	9.4	58.8	95	12	BM306418	C 775	9.2	57.5	32	10	BE729734
C 703	9.4	58.8	95	12	BM306418	C 776	9.2	57.5	32	29	TA227H06Q
C 704	9.4	58.8	95	28	AZ388579	C 777	9.2	57.5	33	10	BF025659
C 705	9.4	58.8	96	9	AA845963	C 778	9.2	57.5	33	10	BE296540
C 706	9.4	58.8	96	9	AI869450	C 779	9.2	57.5	34	10	BE298772
C 707	9.4	58.8	96	28	AZ432614	C 780	9.2	57.5	34	10	BE384902
C 708	9.4	58.8	97	10	BF426038	C 781	9.2	57.5	34	28	AZ810771
C 709	9.4	58.8	97	13	BF426038	C 782	9.2	57.5	35	10	BE385175
C 710	9.4	58.8	97	14	CB356166	C 783	9.2	57.5	35	10	BE409354
C 711	9.4	58.8	97	14	H48944	C 784	9.2	57.5	35	28	AZ430239
C 712	9.4	58.8	97	28	AZ598831	C 785	9.2	57.5	36	28	BH911899
C 713	9.4	58.8	97	29	AG261655	C 786	9.2	57.5	36	28	BH911900
C 714	9.4	58.8	97	29	DR33012T	C 787	9.2	57.5	37	28	AZ873706
C 715	9.4	58.8	97	29	AL86217	C 788	9.2	57.5	37	28	AZ873706
C 716	9.4	58.8	98	9	AV525314	C 789	9.2	57.5	38	10	BE732314
C 717	9.4	58.8	98	9	AV525314	C 790	9.2	57.5	38	28	AZ660837
C 718	9.4	58.8	98	14	Z20006	C 791	9.2	57.5	38	28	AZ660837
C 719	9.4	58.8	98	29	CNS0336B	C 792	9.2	57.5	38	28	AZ806182
C 720	9.4	58.8	99	9	AJ499407	C 793	9.2	57.5	38	28	AL76173
C 721	9.4	58.8	99	9	AL957894	C 794	9.2	57.5	38	29	AG020646
C 722	9.4	58.8	99	10	BF807307	C 795	9.2	57.5	39	14	D74281
C 723	9.4	58.8	99	10	BF850128	C 796	9.2	57.5	40	9	AI959899
C 724	9.4	58.8	99	12	BI942335	C 797	9.2	57.5	40	9	AI959899
C 725	9.4	58.8	99	12	BM698165	C 798	9.2	57.5	40	9	AI959899
C 726	9.4	58.8	99	14	R88374	C 799	9.2	57.5	40	29	AL994126
C 727	9.4	58.8	99	28	BH901247	C 800	9.2	57.5	40	29	AL953755
C 728	9.4	58.8	99	28	AG337710	C 801	9.2	57.5	41	28	BH906036
C 729	9.4	58.8	99	29	AG255479	C 802	9.2	57.5	41	28	BH906037
C 730	9.4	58.8	99	29	AA013890	C 803	9.2	57.5	41	29	BZ762860
C 731	9.4	58.8	100	9	AA013890	C 804	9.2	57.5	41	29	BZ762860
C 732	9.4	58.8	100	9	AI558976	C 805	9.2	57.5	42	9	AV833522
C 733	9.4	58.8	100	9	AA175673	C 806	9.2	57.5	42	10	BF206391
C 734	9.4	58.8	100	9	AA175673	C 807	9.2	57.5	42	28	AZ649663

808	9.2	57.5	42	29	AL947757	Arabidops	c 881	9.2	57.5	54	10	BE022588	BE022588 em86h08.y
809	9.2	57.5	43	9	AA948228	ocq2h11.s	c 882	9.2	57.5	54	13	BI261027	BI261027 602972214
810	9.2	57.5	43	9	AT1795121	bb77a11.y	c 883	9.2	57.5	54	13	BQ592460	BQ592460 S013686-0
811	9.2	57.5	43	9	AW566030	EST00022	c 884	9.2	57.5	54	28	BH906866	BH906866 SALK_0362
812	9.2	57.5	43	28	AZ349590	IM0086H09	c 885	9.2	57.5	54	29	BZ769887	BZ769887 SALK_1428
813	9.2	57.5	44	10	BF102281	601752583	c 886	9.2	57.5	54	29	DR102E23T	DR102E23T
814	9.2	57.5	44	14	CA907055	PCSC06467	c 887	9.2	57.5	55	9	AM306630	AM306630 se53c11.y
815	9.2	57.5	44	14	W66525	EST083_chic	c 888	9.2	57.5	55	13	B0068713	B0068713 2565.G01
816	9.2	57.5	44	28	AZ470514	IM0284E10	c 889	9.2	57.5	55	29	AL753005	AL753005 Arabidops
817	9.2	57.5	44	29	AL764168	Arabidops	c 890	9.2	57.5	55	29	BX204435	BX204435 Danio rer
818	9.2	57.5	46	9	AA758346	ah65h06.s	c 891	9.2	57.5	56	9	AA906034	AA906034 o390b02.s
819	9.2	57.5	46	9	AA916137	cg32c10.s	c 892	9.2	57.5	56	10	BE280329	BE280329 601157870
820	9.2	57.5	46	9	AT1789691	uh19h03.r	c 893	9.2	57.5	56	14	CB274974	CB274974 kg74h09.y
821	9.2	57.5	47	9	AT012362	AT012362	c 894	9.2	57.5	56	28	AZ645965	AZ645965 IM0511E17
822	9.2	57.5	47	28	BH891856	3526_119	c 895	9.2	57.5	56	28	BH852317	BH852317 SALK_0744
823	9.2	57.5	47	28	AG216926	Drosophila	c 896	9.2	57.5	56	28	BZ663353	BZ663353 SALK_0269
824	9.2	57.5	48	28	AZ639981	IM0501D16	c 897	9.2	57.5	57	13	BQ382141	BQ382141 Kk42902.y
825	9.2	57.5	48	29	AG218322	Drosophila	c 898	9.2	57.5	57	13	BQ382493	BQ382493 Kk51d04.y
826	9.2	57.5	48	29	BX209797	Danio rer	c 899	9.2	57.5	57	14	W00883	W00883 z455a02.x1
827	9.2	57.5	49	9	AT200287	qf66a10.x	c 900	9.2	57.5	57	29	BZ762555	BZ762555 SALK_1053
828	9.2	57.5	49	28	AZ586447	IM0392B22	c 901	9.2	57.5	58	9	AT208634	AT208634 q934b06.x
829	9.2	57.5	50	9	AT0103863	AT0103863	c 902	9.2	57.5	58	9	AA138639	AA138639 m162d11.r
830	9.2	57.5	50	9	AT0103864	AT0103864	c 903	9.2	57.5	58	9	AT453341	AT453341 t377a08.x
831	9.2	57.5	50	9	AT0103865	AT0103865	c 904	9.2	57.5	58	9	AA458540	AA458540 sh10d12.y
832	9.2	57.5	50	9	AT0103867	AT0103867	c 905	9.2	57.5	58	10	BE733638	BE733638 601567537
833	9.2	57.5	50	9	AT0103870	AT0103870	c 906	9.2	57.5	58	12	BI493871	BI493871 df106409.y
834	9.2	57.5	50	9	AT0103874	AT0103874	c 907	9.2	57.5	58	14	CB003153	CB003153 VVB027A03
835	9.2	57.5	50	9	AT0103875	AT0103875	c 908	9.2	57.5	58	14	CB003932	CB003932 VVB030H05
836	9.2	57.5	50	9	AT0103876	AT0103876	c 909	9.2	57.5	58	28	AZ591317	AZ591317 IM0401B24
837	9.2	57.5	50	9	AT0103877	AT0103877	c 910	9.2	57.5	58	28	AZ917758	AZ917758 1060602A0
838	9.2	57.5	50	9	AT0103880	AT0103880	c 911	9.2	57.5	58	29	AL942095	AL942095 Arabidops
839	9.2	57.5	50	9	AT0103881	AT0103881	c 912	9.2	57.5	58	29	DR4B125	DR4B125 Arabidops
840	9.2	57.5	50	9	AT0103883	AT0103883	c 913	9.2	57.5	58	29	TA113A05Q	TA113A05Q
841	9.2	57.5	50	9	AT0103885	AT0103885	c 914	9.2	57.5	59	9	AT451268	AT451268 m175c01.x
842	9.2	57.5	50	9	AT0103892	AT0103892	c 915	9.2	57.5	59	10	BF013445	BF013445 kR8f04.y
843	9.2	57.5	50	9	AT0104393	AT0104393	c 916	9.2	57.5	59	28	AQ254664	AQ254664 BP(3)0887
844	9.2	57.5	50	9	AT0104305	AT0104305	c 917	9.2	57.5	60	9	AW719257	AW719257 LjNEST96
845	9.2	57.5	50	9	AT0104386	AT0104386	c 918	9.2	57.5	60	14	CB277341	CB277341 ku64c10.y
846	9.2	57.5	50	9	AT0104387	AT0104387	c 919	9.2	57.5	60	14	CD028775	CD028775 mgc8002xH
847	9.2	57.5	50	9	AT0104486	AT0104486	c 920	9.2	57.5	60	28	BH865304	BH865304 SALK_0981
848	9.2	57.5	50	9	AT0105006	AT0105006	c 921	9.2	57.5	60	29	CC199567	CC199567 XE809 Bay
849	9.2	57.5	50	9	AT0105969	AT0105969	c 922	9.2	57.5	60	29	CC457394	CC457394 SALK_1096
850	9.2	57.5	50	9	AT0107634	AT0107634	c 923	9.2	57.5	60	29	BX535184	BX535184 Arabidops
851	9.2	57.5	50	9	AT108086	AT108086	c 924	9.2	57.5	60	29	DR102D22S	DR102D22S
852	9.2	57.5	50	12	B0035910	B0035910	c 925	9.2	57.5	61	9	AU012625	AU012625
853	9.2	57.5	50	14	CB218569	NISC_nb09	c 926	9.2	57.5	61	9	AA581081	AA581081 nd13b07.s
854	9.2	57.5	50	14	T73299	yc34b09.s1	c 927	9.2	57.5	61	9	AA586727	AA586727 nm767c10.s
855	9.2	57.5	50	29	BZ766844	SALK_1379	c 928	9.2	57.5	61	14	CB016864	CB016864 pgn1c.pk0
856	9.2	57.5	50	29	TA187C12P	AL477525.T_btuce1	c 929	9.2	57.5	61	14	CB016864	CB016864 pgn1c.pk0
857	9.2	57.5	51	9	AL873986	AL873986	c 930	9.2	57.5	62	10	BE278269	BE278269 601179416
858	9.2	57.5	51	9	AW156250	se21e05.y	c 931	9.2	57.5	62	13	BQ595222	BQ595222 E012711-0
859	9.2	57.5	51	28	AZ594400	IM0406K23	c 932	9.2	57.5	62	28	AZ920963	AZ920963 1006023A0
860	9.2	57.5	51	28	BH225854	1006128G0	c 933	9.2	57.5	62	28	BH219720	BH219720 100609080
861	9.2	57.5	51	28	BH861528	SALK_0817	c 934	9.2	57.5	62	29	BZ355855	BZ355855 SALK_1276
862	9.2	57.5	51	29	AL944876	Arabidops	c 935	9.2	57.5	62	29	BZ380489	BZ380489 SALK_1152
863	9.2	57.5	52	9	AA068274	mm53c01.r	c 936	9.2	57.5	62	29	BZ764789	BZ764789 SALK_1269
864	9.2	57.5	52	9	AA723687	ah85c05.s	c 937	9.2	57.5	62	29	AL762933	AL762933 Arabidops
865	9.2	57.5	52	9	AL143632	qf74c03.x	c 938	9.2	57.5	63	13	BQ636122	BQ636122 sh25g09.y
866	9.2	57.5	52	9	AW693197	PCSC08B15	c 939	9.2	57.5	63	13	BQ636122	BQ636122 sh25g09.y
867	9.2	57.5	52	9	AA499863	vg05g12.r	c 940	9.2	57.5	63	28	AZ836154	AZ836154 SMO130A20
868	9.2	57.5	52	12	B0075938	B0075938	c 941	9.2	57.5	63	29	BZ291038	BZ291038 SALK_1123
869	9.2	57.5	52	28	AZ495807	IM0331F21	c 942	9.2	57.5	63	29	BZ381526	BZ381526 SALK_1168
870	9.2	57.5	52	29	BZ769876	SALK_1428	c 943	9.2	57.5	64	9	AI1821064	AI1821064 qg90d10.x
871	9.2	57.5	52	29	CC248941	KX287 Bay	c 944	9.2	57.5	64	9	AW620167	AW620167 SMOVAFAP
872	9.2	57.5	53	13	BQ382839	kK56h09.y	c 945	9.2	57.5	64	9	AA626441	AA626441 SMOVAFAP
873	9.2	57.5	53	14	CA910469	PCSC08B67	c 946	9.2	57.5	64	9	AA432439	AA432439 v032e11.x
874	9.2	57.5	53	14	CB274957	ku73e02.y	c 947	9.2	57.5	64	9	AA572476	AA572476 v182d11.r
875	9.2	57.5	53	14	R88455	ym92d07.r1	c 948	9.2	57.5	64	9	AA572477	AA572477 v182d12.r
876	9.2	57.5	53	28	AZ353396	IM0092F18	c 949	9.2	57.5	64	11	CN609MTR	CN609MTR
877	9.2	57.5	53	28	AZ442528	IM0236H08	c 950	9.2	57.5	64	11	BI097356	BI097356 SMOVJMCM
878	9.2	57.5	53	28	BH790547	SALK_0573	c 951	9.2	57.5	64	12	BI912407	BI912407 603290867
879	9.2	57.5	53	29	BX004390	Arabidops	c 952	9.2	57.5	64	12	BI912407	BI912407 603290867
880	9.2	57.5	54	9	AU006791	AU006791	c 953	9.2	57.5	64	14	CB277338	CB277338 ku64b09.y


```

/sex="Male"
/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCIM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnars/). The DNA
was hydrodynamically sheared by repeated passages through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114[gb]/AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT      23 a      13 c      36 g      28 t
ORIGIN

Query Match      78.8%; Score 12.6; DB 28; Length 100;
Best Local Similarity 92.3%; Pred. No. 1.1e+04;
Matches 12; Conservative 1; Mismatches 0; Gaps 0;
Indels 0;

Cy 1 RGGCTAGCTACAA 13
   :|||||
   5 GGGCTAGCTACAA 17

RESULT 3
BG422154/c
LOCUS      44 bp      mRNA      linear      EST 14-MAR-2001
DEFINITION 602448881P1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4587189 5',
            mRNA sequence.
ACCESSION  BG422154
VERSION     BG422154.1 GI:13328660
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE   1 (bases 1 to 44)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished
            Contact: Robert Strausberg, Ph.D.
            Email: cgsapb@remail.nih.gov
            Tissue Procurement: DCTD/DRP
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMN)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LMN at:
            http://image.llnl.gov
            Plate: L1CM1317 row: b column: 22
            High quality sequence stop: 44.
            Location/Qualifiers
                1..44
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:4587189"
                /rissue_type="renal cell adenocarcinoma"
                /lab host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_14"
                /note="Organ: kidney; Vector: POTB7; Site 1: XhoI; Site 2:
                EcoRI; cDNA made by oligo-dT priming. Directionally
                cloned into EcoRI/XhoI sites using the following 5'

```

```

adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA Synthesis Kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT      6 a      10 c      21 g      7 t
ORIGIN

Query Match      77.5%; Score 12.4; DB 10; Length 44;
Best Local Similarity 81.2%; Pred. No. 1e+04;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy 1 RGGCTAGCTACAA 16
   :|||||
   39 AGGCAGCTACAGCA 24

RESULT 4
BH901408/c
LOCUS      26 bp      DNA      linear      GSS 04-SEP-2002
DEFINITION SALK_079024.36.15.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_079024.36.15.x, genomic
            survey sequence.
ACCESSION  BH901408
VERSION     BH901408.1 GI:22712289
KEYWORDS   GSS.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (bases 1 to 26)
            Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
            ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
            , Zimmerman,J. and Ecker,J.R.
            A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
            Unpublished
            Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
            Location/Qualifiers
                1..26
                /organism="Arabidopsis thaliana"
                /mol_type="genomic DNA"
                /strain="Columbia 0"
                /db_xref="taxon:3702"
                /clone="SALK_079024.36.15.x"
                /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                /note="PCR was performed on Arabidopsis thaliana lines
                each of which contains one or more TDNA insertion
                elements. The resultant fragment for each line was
                directly sequenced to determine the genomic sequence at
                the site of insertion. Details of the protocols used can
                be found at http://signal.salk.edu/cdna_protocols.html"

BASE COUNT      6 a      6 c      3 g      11 t
ORIGIN

Query Match      75.0%; Score 12; DB 28; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 2 GGCTAGCTACAA 13
   :|||||
   21 GGCTAGCTACAA 10

```

```

BASE COUNT      25 a      28 c      16 g      26 t
ORIGIN
Query Match      75.0%; Score 12; DB 13; Length 95;
Best Local Similarity 85.7%; Pred. No. 2.2e+04;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy      1 RGGCTAGTACAAC 14
      :|||||||
      Db      74 AGGCTAGTACAAC 61

RESULT 7
BU862306/c      96 bp      mRNA      linear      EST 16-OCT-2002
LOCUS DEFINITION S014A04 Populus imbibed seed cDNA library Populus tremula x Populus tremuloides
ACCESSION BU862306
VERSION BU862306.1 GI:24048366
KEYWORDS EST.
SOURCE Populus tremula x Populus tremuloides
ORGANISM Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Malpighiales; Salicaceae; Populus.
1 (bases 1 to 96)
Unenberger, P., Bhalerao, R. R., Jansson, S. and Sterky, F.
The poplar tree transcriptome: Analysis of expressed sequence tags
from multiple libraries
Unpublished
Contact: BHALERAO RUPALI R.
Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhalerao@plantphys.umu.se.
Location/Qualifiers
1..96
/organism="Populus tremula x Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:47664"
/rtissue_type="imbibed seed"
/clone_lib="Populus imbibed seed cDNA library"
BASE COUNT      27 a      27 c      16 g      26 t
ORIGIN
Query Match      75.0%; Score 12; DB 13; Length 96;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy      1 RGGCTAGTACAAC 14
      :|||||||
      Db      46 AGGCTAGTACAAC 33

RESULT 8
BU861867/c      100 bp      mRNA      linear      EST 16-OCT-2002
LOCUS DEFINITION S007G10 Populus imbibed seed cDNA library Populus tremula x Populus tremuloides
ACCESSION BU861867
VERSION BU861867.1 GI:24047927
KEYWORDS EST.
SOURCE Populus tremula x Populus tremuloides
ORGANISM Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Malpighiales; Salicaceae; Populus.

```

```

REFERENCE      1 (bases 1 to 100)
AUTHORS        Umeberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
TITLE          The poplar tree transcriptome: Analysis of expressed sequence tags
               from multiple libraries
JOURNAL        Unpublished
COMMENT        Contact: BHALERAO RUPALI R.
               Umea Plant Science Center
               Department of Plant Physiology
               University of Umea, 901 87 Umea, Sweden
               Tel: +46 90 786 5279
               Fax: +46 90 786 6676
               Email: rupali.bhalerao@plantphys.umu.se.
FEATURES       location/Qualifiers
SOURCE         1..100
               /organism="Populus tremula x Populus tremuloides"
               /mol_type="mRNA"
               /db_xref="taxon:47664"
               /tissue_type="imbibed seed"
               /clone_lib="Populus imbibed seed cDNA library"
BASE COUNT     22 a      25 c      20 g      29 t
ORIGIN
Query Match    75.0%; Score 12; DB 13; Length 100;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY      1 RGCTAGCTACAC 14
       :|||||||
       37 AGGCTAGCTAGAC 24

Db

RESULT 9
A261815/c      80 bp      DNA      linear      GSS 13-DEC-2000
LOCUS          1M0452D18F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION     clone UGCG1M0452D18 F, genomic survey sequence.
ACCESSION      A2619815
VERSION        A2619815
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 80)
AUTHORS        Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
               Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
               M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A.
               and Wright, D., Weiss, R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL        Unpublished
COMMENT        Contact: Robert B. Weiss
               University of Utah Genome Center
               University of Utah
               Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0452 row: D column: 18
               Seq primer: CGTTGTAAACGACGCGCAGT
               Class: plasmid ends
               High quality sequence stop: 80.
               location/Qualifiers
SOURCE         1..80
               /organism="Mus musculus"
               /mol_type="genomic DNA"
               /strain="CS7BL/6J"
               /db_xref="taxon:10090"
               /clone="UGCG1M0452D18"
               /sex="Male"
               /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
```

```

/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114[gb|AF129072.1]) a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

```

BASE COUNT     20 a      15 c      21 g      24 t
ORIGIN
Query Match    72.5%; Score 11.6; DB 28; Length 80;
Best Local Similarity 91.7%; Pred. No. 3.5e+04;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 RGCTAGCTACA 12
       :|||||||
       28 AGGCTAGCTACA 17

Db

RESULT 10
H08942         52 bp      mRNA      linear      EST 23-JUN-1995
LOCUS          Y13605.r1 Soares infant brain INB Homo sapiens cDNA clone
DEFINITION     IMAGE:45750 5', similar to gb|M87909|HUMANLN36 Human carcinoma
               cell-derived Alu RNA transcript, (rRNA); gb:M2315 TUMOR NECROSIS
               FACTOR RECEPTOR 2 PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION      H08942
VERSION        H08942.1 GI:873764
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 52)
AUTHORS        Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
               M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
               Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaekis, E., Waterston
               R., Williamson, A., Wohlmann, P. and Willson, R.
TITLE          The Washu-Merck EST Project
JOURNAL        Unpublished
COMMENT        Contact: Willson RK
               Washington University School of Medicine
               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
               Tel: 314 286 1800
               Fax: 314 286 1810
               Email: eest@watson.wustl.edu
               Insert Size: 1449
               High quality sequence starts: 1
               High quality sequence stops: 1
               Source: IMAGE Consortium, LNLN
               This clone is available royalty-free through LNLN; contact the
               IMAGE Consortium (info@image.llnl.gov) for further information.
               Trace considered overall poor quality
               Insert Length: 1449 Std Error: 0.00
               Seq primer: M13RP1
               High quality sequence stop: 1.
               location/Qualifiers
SOURCE         1..52
               /organism="Homo sapiens"
               /mol_type="mRNA"
```

```

/db_xref="GDB:418291"
/db_xref="taxon:9606"
/clone="IMAGB:45750"
/sex="female"
/dev stage="73 days post natal"
/lab host="DH10B (ampicillin resistant)"
/clone lib="Soares infant brain INTB"
/notes:Organ: whole brain; Vector: Lactid BA; Site 1: Not
1; Site 2: Hind III; 1st strand cDNA was primed with a Not
1 - oligo (dt) primer 5',
AAGCGAAGATTGCGCGCGAGCAATTTTCTTTTCTTTT 3';
double-stranded cDNA was ligated to Hind III adaptors
(pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the Lactid BA vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      8 a      16 c      11 g      11 t      6 others
ORIGIN

Query Match      71.2%; Score 11.4; DB 14; Length 52;
Best Local Similarity 92.3%; Pred. No. 3.8e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      2 GGCTAGCTACAC 14
      |||||
      30 GGCTCGCTACAC 42

RESULT 11
N98196      74 bp mRNA linear EST 18-NOV-1996
LOCUS      0266C3 czappdpd2.1, Debopam Chakrabarti Plasmodium falciparum cDNA
DEFINITION clone PF0266C, mRNA sequence.
ACCESSION  N98196
VERSION     N98196
KEYWORDS   EST.
SOURCE     Plasmodium falciparum (malaria parasite P. falciparum)
ORGANISM   Eukaryota; Alveolata; Apicomplexa; Hemosporidia; Plasmodium
REFERENCE  1 (bases 1 to 74)
AUTHORS   Dame,J.B., Arnot,D.E., Bouke,P., Chakrabarti,D., Christodoulou,Z.,
Coppel,R.R., Cowman,A., Craig,A., Fischer,K., Foster,J., Goodman,N.,
Hinterberg,K., Holder,A.A., Holt,D., Kemp,D., Lanzer,M., Lim,A.,
Newbold,C., Ravetch,J.V., Reddy,G.R., Rubio,J., Schuster,S.M., Su
,X.-Z., Thompson,J.K., Vitali,F., Williams,T.B. and Werner,E.
COMMENT    Current status of the Plasmodium falciparum genome project
JOURNAL    Mol. Biochem. Parasitol. 79, 1-12 (1996)
MEDLINE    97001675
PUBMED     8844667
TITLE      Contact: Debopam Chakrabarti
JOURNAL    Department of Molecular Biology and Microbiology
PUBMED     University of Central Florida
PUBMED     Orlando, FL 32816-2360
PUBMED     Tel: 407 384 2061
PUBMED     Fax: 407 384 3095
PUBMED     Email: dchak@pegasus.cc.ucf.edu
PUBMED     Seq primer: 73
PUBMED     Location/Qualifiers
PUBMED     1..74
PUBMED     /organism="Plasmodium falciparum"
PUBMED     /mol_type="mRNA"
PUBMED     /strain="Dd2"
PUBMED     /db_xref="taxon:5833"
PUBMED     /clone="PF0266C"
PUBMED     /lab host="E. coli XL-1 blue"
PUBMED     /note="Vector: lambda ZAP II; Site 1: EcoR I; Site 2: Xho
PUBMED     I; PolyA+ RNA, from asynchronous blood stage parasites of
PUBMED     using an oligo dT-Xho I primer. Second strand was
PUBMED     prepared using RNase H and DNA polymerase I. EcoR I
PUBMED     adapters were ligated to the cDNA, and it was digested
PUBMED     with Xho I. Prepared fragments were ligated into EcoR I +

```

```

Xho I digested lambda ZAP II vector. "
BASE COUNT      18 a      17 c      12 g      14 t      13 others
ORIGIN

Query Match      71.2%; Score 11.4; DB 14; Length 74;
Best Local Similarity 85.7%; Pred. No. 4.4e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      3 GCTAGCTACACGA 16
      |||||
      43 GCTANCTACACGA 56

RESULT 12
BX535085      76 bp DNA linear GSS 03-JUN-2003
LOCUS      Arabidopsis thaliana T-DNA flanking sequence GK-514H05-019924,
DEFINITION genomic survey sequence.
ACCESSION  BX535085
VERSION     BX535085.1 GI:31412215
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
REFERENCE  1
AUTHORS   Strizhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Saedler,H.
and Weishaar,B.
TITLE      A pipeline for automated high-throughput generation of FSTs
(Jflanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
JOURNAL     unpublished
PUBMED     2
PUBMED     Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weishaar,B.
PUBMED     A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
PUBMED     for flanking sequence tag based reverse genetics
PUBMED     Unpublished
PUBMED     3 (bases 1 to 76)
PUBMED     Li,Y., Strizhov,N., Rosso,M. and Weishaar,B.
PUBMED     Direct Submission
PUBMED     Submitted (02-JUN-2003) Weishaar B., Max-Planck-Institut fuer
PUBMED     Zuechunngsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
PUBMED     This sequence is recovered from the left border of the T-DNA. It
PUBMED     indicates an insertion close to or within gene At3g53040. The
PUBMED     sequences are generated at the MPI for Plant Breeding Research in
PUBMED     the context of the GABI-Kat project. GABI-Kat is part of the German
PUBMED     Plant Genomics program designated 'GABI'. Information on line
PUBMED     availability can be found at:
PUBMED     http://www.mpiz-koeln.mpg.de/GABI-Kat/.
PUBMED     Location/Qualifiers
PUBMED     1..76
PUBMED     /organism="Arabidopsis thaliana"
PUBMED     /mol_type="genomic DNA"
PUBMED     /strain="Columbia 0"
PUBMED     /db_xref="taxon:3702"
PUBMED     /clone="GK-514H05-019924"
PUBMED     /note="PCR was performed on DNA from Arabidopsis thaliana
PUBMED     plants (Ti) which were transformed with the T-DNA from
PUBMED     vector pAC161. The lines contain one or more T-DNA
PUBMED     insertions. The DNA fragment(s) resulting from the PCR
PUBMED     were directly sequenced to determine the genomic sequence
PUBMED     flanking the insertion. Sequences displaying significant
PUBMED     similarity to the A. thaliana nuclear genome sequence were
PUBMED     processed for submission. T-DNA derived sequences were
PUBMED     removed"
BASE COUNT      24 a      19 c      24 g      9 t
ORIGIN

Query Match      71.2%; Score 11.4; DB 29; Length 76;
Best Local Similarity 80.0%; Pred. No. 4.4e+04;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 RGCTAGCTACAAG 15
 Db 75 AGCTAGCTGACGCG 61

RESULT 13
 LOCUS A1461140 95 bp mRNA linear EST 28-NOV-2001
 DEFINITION B8475f01.y1 Gm-cl004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
 Gm-cl004-5138 5', mRNA sequence.
 A1461140
 VERSION A1461140.1 GI:4314021
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 95)
 Shoemaker, R., Keim, P., Vodkin, L., Expelding, J., Coryell, V., Khanna
 , A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
 Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers
 , Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
 , R., Ritter, E., Kohn, S., Shin, T., Jackson, T., Cardenas, M., McCann
 , R., Waterston, R. and Wilson, R.
 Public Soybean EST Project
 Unpublished
 Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: east@watson.wustl.edu
 This clone is available through: Reagen, Invitrogen Corp. 2130
 South Memorial Parkway Huntville, AL 35801 For further information
 call: (800) 533-4363 or contact via email: ccu@reagen.com
 Insert Length: 369 Std Error: 0.00
 Seq primer: -40RP from Gldco
 POLYA=No.

FEATURES
 source
 1..95
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl004-5138"
 /issue_type="root"
 /lab_host="XL10-Gold"
 /clone_lib="Gm-cl004"
 /note="Vector: pBluescript II Xr; Site 1: EcoRI; Site 2:
 XhoI; Root cDNA. The mRNA was isolated from entire roots
 of 8 day old 'Williams' seedlings which were propagated on
 paper towels with distilled water. StrataGene's cDNA
 Synthesis Kit (catalog #200401) was used to synthesize the
 cDNA. First-strand synthesis was performed with 5-methyl
 dCTP, hence the ligated cDNA is hemimethylated.
 StrataGene's first-strand synthesis primer was used
 (GAGAGAGAGAGAGAGAGACTGCTGAG(T)-18). After
 second-strand synthesis, the cDNA ends were 'polished',
 with clone Pfu DNA polymerase, ligated to EcoRI adapters,
 and phosphorylated. The XhoI site within the first-strand
 synthesis primer was restricted by digestion with XhoI;
 all XhoI sites in the cDNA would be protected by their
 hemimethylated status. The cDNA constructs were
 size-fractionated with a 500bp cutoff, using GbhcoBRL Life
 Technologies' cDNA Size Fractionation column. The column
 eluent was then ligated into StrataGene's pBluescript II
 XR Predigested vector (pBluescript II SK(+)) that had been
 digested with EcoRI and XhoI, and phosphorylated). Both
 the white and blue colonies appear to contain recombinant
 plasmids with cDNA inserts. Blue colonies 9n=15) have been

BASE COUNT
 ORIGIN 25 a 25 c 18 g 27 t

Query Match 71.2%; Score 11.4; DB 9; Length 95;
 Best Local Similarity 80.0%; Pred. No. 4.8e+04;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGCTAGCTACAAG 15
 Db 52 GGTCCTGCTACAAG 66

RESULT 14
 LOCUS B0823860/c 95 bp mRNA linear EST 01-AUG-2002
 DEFINITION 1030113D08.x1 C. reinhardtii CC-1690, Deflagellation (normalized),
 Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
 B0823860
 VERSION B0823860.1 GI:22075084
 KEYWORDS EST.
 SOURCE Chlamydomonas reinhardtii
 ORGANISM Chlamydomonas reinhardtii
 Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 Chlamydomonadales; Chlamydomonas.
 1 (bases 1 to 95)
 Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebvre
 , P., McDermott, J.P., Shrago, J., Sillflow, C. and Stern, D.
 Analyses of the Chlamydomonas reinhardtii Genome: A Model,
 Unicellular System for Analyzing Gene Function and Regulation in
 Vascular Plants. Project: 1030
 Unpublished
 Contact: Charles Hauser
 DCMB Box 91000
 Duke University
 Durham, NC 27708-1000
 Tel: 919 613 8159
 Fax: 919 613 8177
 Email: chauser@duke.edu.

FEATURES
 source
 1..95
 /organism="Chlamydomonas reinhardtii"
 /mol_type="mRNA"
 /strain="CC-1690 wild type mt+ 21gr"
 /db_xref="taxon:3055"
 /clone_lib="C. reinhardtii CC-1690, Deflagellation
 (normalized), Lambda Zap II"
 /note="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2:
 XhoI; Deflagellation library, constructed by John Davies
 and Jeffrey McDermott, combines cDNAs from CC-1690 cells
 which had been re-synthesizing flagella for 15, 30 and 60
 min after being deflagellated by pH shock. PolyA mRNA was
 purified from each sample, pooled and cDNA synthesized.
 The cDNA was directionally cloned into lambda Zap II
 (Stratagene) in the EcoRI (5') and XhoI (3') sites.
 pBluescript II SK- plasmids were excised from the lambda
 Zap clones by superinfection with ExA851st (Stratagene)
 phage. The library was normalized using method 4 described
 in Bonaldo et al., (1996) Genome Research 6: 791-806."

BASE COUNT
 ORIGIN 21 a 30 c 14 g 30 t

Query Match 71.2%; Score 11.4; DB 13; Length 95;
 Best Local Similarity 92.3%; Pred. No. 4.8e+04;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCTAGCTACAAG 15

sequenced, and possess putative cDNA inserts. This library
 was constructed by Dr. Paul Keim & Virginia H. Coryell,
 Department of Biology, Box5640, Northern Arizona
 University, Flagstaff, AZ 86011, Phone: 520-523-1078 (Dr.
 Paul Keim), 520-523-1372 (Virginia H. Coryell), Fax:
 520-523-7500, email: Paul.Keim@nau.edu,
 Virginia.coryell@nau.edu"

Db 66 GGTAAGCTACAAACG 54

RESULT 15

LOCUS AZ916132 96 bp DNA linear GSS 15-MAR-2001

DEFINITION Pct1.3-a8-c-1.0 Maize Pct1 B73 leaf Zea mays genomic, genomic

ACCESSION AZ916132

VERSION AZ916132.1 GI:13347408

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE

AUTHORS Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weishaar, B.

TITLE A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics

COMMENT Unpublished

3 (bases 1 to 58)

Strizhov, N., Rosso, M., Li, Y. and Weishaar, B.

Direct Submission

Submitted (07-MAR-2003) Weishaar, B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence is recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At3g53810. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>

FEATURES

source

Location/Qualifiers

1..96

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="B73"

/db_xref="taxon:4577"

/tissue_type="leaf"

/lab_host="DHS alpha"

/clone_lib="Maize Pct1 B73 leaf"

/note="Organ: Leaf; Vector: PUC19; Pct1 digested B73 genomic sucrose gradient size fractionated fragment sizes of 0.5kb to 2kb ligated to PUC19 transformed in DHS alpha"

BASE COUNT 22 a 29 c 27 g 18 t

ORIGIN

Query Match 71.2%; Score 11.4; DB 28; Length 96;

Best Local Similarity 80.0%; Pred. No. 4.8e+04;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGCTAGCTACAAACG 15

Db 80 AGCTAGCTACAAATG 94

RESULT 16

LOCUS BX288422 58 bp DNA linear GSS 07-MAR-2003

DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-414B10-018037,

ACCESSION BX288422

VERSION BX288422.1 GI:28887418

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE

AUTHORS Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Sedler, H. and Weishaar, B.

TITLE A pipeline for automated high-throughput generation of ESTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines

COMMENT Unpublished

REFERENCE

AUTHORS Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weishaar, B.

TITLE A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics

COMMENT Unpublished

3 (bases 1 to 58)

Strizhov, N., Rosso, M., Li, Y. and Weishaar, B.

Direct Submission

Submitted (07-MAR-2003) Weishaar, B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence is recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At3g53810. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>

FEATURES

source

Location/Qualifiers

1..58

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="GK-414B10-018037"

/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

BASE COUNT 15 a 17 c 11 g 15 t

ORIGIN

Query Match 68.8%; Score 11; DB 29; Length 58;

Best Local Similarity 100.0%; Pred. No. 6.6e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGCTACAAACG 16

Db 49 AGCTACAAACG 39

RESULT 17

LOCUS H62825 73 bp mRNA linear EST 10-OCT-1995

DEFINITION y746e04.s1 Soares fetal liver spleen INFIS Homo sapiens cDNA clone IMAGE:208350 3' similar to gb:M22918 MYOSIN LIGHT CHAIN ALKALI, SMOOTH-MUSCLE ISOFORM (HUMAN);, mRNA sequence.

ACCESSION H62825

VERSION H62825.1 GI:1017171

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, D., Rifkin, B., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project

COMMENT Unpublished

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

Insert Size: 705

altered);

ulus genomic

uteleostomi;

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 20 a 21 c 21 g 22 t
ORIGIN

Query Match 68.8%; Score 11; DB 28; Length 84;
Best Local Similarity 84.6%; Pred. No. 7.6e+04;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RGCGTACTACAA 13
:|||||
Db 59 AGGCTGCTACAA 71

RESULT 20 90 bp mRNA linear EST 08-MAR-2000
AI937714/c wp8a12.x1 NCI CGAP Brn25 Homo sapiens CDNA clone IMAGE:2468350 3'
LOCUS similar to gb:K63563 DNA-DIRECTED RNA POLYMERASE II 140 KD
DEFINITION POLYPEPTIDE (HUMAN); mRNA sequence.
ACCESSION AI937714
VERSION AI937714
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 90)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BRGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/btrp/image/image.html

Trace considered overall poor quality
Insert Length: 764 Std Error: 0.00
Seq primer: 40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. .90
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="2468350"
/tissue="anaplastic oligodendroglioma"
/lab_host="DH10B"
/clone_id="NCI CGAP Brn25"
/note="Organ: brain; Vector: pRTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTAGAGGAGCGCCGCAATGTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRTT3 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 25 a 10 c 16 g 39 t
ORIGIN

Qy 1 RGCGTACTACAA 13
:|||||
Db 81 AGGCTACTACAA 69

Query Match 68.8%; Score 11; DB 9; Length 90;
Best Local Similarity 84.6%; Pred. No. 7.8e+04;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 21 90 bp DNA linear GSS 05-AUG-2002
BH861753 SALK_087935 Arabidopsis thaliana TDNA insertion lines Arabidopsis
LOCUS thaliana genomic clone SALK_087935, genomic survey sequence.
DEFINITION BH861753
ACCESSION BH861753
VERSION BH861753.1 GI:22097079
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
REFERENCE 1 (bases 1 to 90)
AUTHORS Alonso,J.M., Leisbe,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished
COMMENT Contact: Joseph R. Ecker
The Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel.: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At2g27170.
Class: TDNA tagged.
Location/Qualifiers
1. .90
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_image="SALK_087935"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/cdna_protocols.html"

FEATURES
SOURCE
BASE COUNT 34 a 17 c 14 g 25 t
ORIGIN

Query Match 68.8%; Score 11; DB 28; Length 90;
Best Local Similarity 84.6%; Pred. No. 7.8e+04;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RGCGTACTACAA 13
:|||||
Db 41 AGGCTACTACAA 53

RESULT 22
AG224693 91 bp DNA linear GSS 12-DEC-2002
LOCUS Locust japonicus DNA, clone: LjB1a20_f, genomic survey sequence.
DEFINITION AG224693
ACCESSION AG224693.1 GI:26534755
VERSION
KEYWORDS
SOURCE
ORGANISM
Locust japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteeae;
Locust.

REFERENCE
1 Sato, S., Nakamura, Y. and Tabata, S.
TITLE Locust japonicus BAC End sequences
JOURNAL Published Only in Database (2002)
REFERENCE
2 (bases 1 to 91)
AUTHORS Sato, S.
TITLE Direct Submission
JOURNAL Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute,
The First Laboratory for Plant Gene Research; 2-6-7
Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail: sato@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/,
Tel: 81-438-52-3935 (ex.2336), Fax: 81-438-52-3934)
LOCATION/Qualifiers

FEATURES
source
1..91
/organism="Locust japonicus"
/mol_type="genomic DNA"
/strain="Miyakojima MG-20"
/db_xref="taxon:34305"
/clone="LjB1a20_f"
/clone_1ib="genomic BAC library"
/note="VECTOR: pBE10BAC11"

BASE COUNT 26 a 23 c 18 g 24 t
ORIGIN

Query Match 68.8%; Score 11; DB 29; Length 91;
Best Local Similarity 100.0%; Pred. No. 7.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 4 CTAGCTACAC 14
|||||
62 CTAGCTACAC 72

Db

RESULT 23
AZ431360 96 bp DNA linear GSS 03-OCT-2000
LOCUS 1M021614F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M021614 F, genomic survey sequence.
DEFINITION AZ431360
ACCESSION AZ431360.1 GI:10555373
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 96)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished
CONTACT Contact: Robert B. Weiss
UNIVERSITY University of Utah Genome Center
ADDRESS Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA

RESULT 24
A1681141 49 bp mRNA linear EST 26-MAY-1999
LOCUS tx4407.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:227429.3
DEFINITION similar to SW:R33A HUMAN P54725 UV EXCISION REPAIR PROTEIN
RAD23 HOMOLOG A, mRNA sequence.
ACCESSION A1681141
VERSION A1681141.1 GI:4891323
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 49)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
CONTACT Contact: Robert Strauberg, Ph.D.
EMAIL Email: cgaps-rc@mail.nih.gov
TISSUE Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA LIBRARY Preparation: M. Bento Soares, Ph.D.
CDNA LIBRARY Arrayed by: Greg Lennon, Ph.D.

FEATURES
source
1..96
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M021614"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (GI4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 31 a 32 c 12 g 21 t
ORIGIN

Query Match 68.8%; Score 11; DB 28; Length 96;
Best Local Similarity 84.6%; Pred. No. 8e+04;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY 1 RGCTAGCTACAA 13
:|||||
4 GGCTAGCTACCAA 16

Db

DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNLI at:
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Seq primer: -40up from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES
 source
 1.49
 /organism="Homo sapiens"
 /mol_type="RNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2272429"
 /issue_type="Carcinoid"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Lu24"
 /note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
 modified polylinker; Plasmid DNA from the normalized
 library NCI_CGAP_Lu2 was prepared, and as circles were
 made in vitro. Following HAP purification, this DNA was
 used as tracer in a subtractive hybridization reaction.
 The driver was PCR-amplified cDNAs from a pool of 5,000
 clones made from the same library (clones15
 1414920-1417991 and 1520904-1522439). Subtraction by Bento
 Soares and M. Fatima Bonaldo."

BASE COUNT
 ORIGIN
 16 a 19 c 13 g 1 t

Query Match 67.5%; Score 10.8; DB 9; Length 49;
 Best Local Similarity 85.7%; Pred. No. 8e+04; 2; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 GCTAGCTACACGA 16
 |||||
 29 GCGAGCTACACAA 42

RESULT 25
 AUI06358/c 50 bp mRNA linear EST 30-AUG-2001
 LOCUS AUI06358 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 DEFINITION HEPO2980, mRNA sequence.
 AUI06358
 ACCESSION AUI06358.1 GI:13555879
 VERSION EST.
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
 'H., Oka, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
 'Y., Nakamura, Y., Suyama, A. and Sugano, S.
 1 (bases 1 to 50)
 'H., Oka, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
 'Y., Nakamura, Y., Suyama, A. and Sugano, S.
 Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites
 EMBO Rep. 2 (5), 388-393 (2001)

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 11375929
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
 'S. Construction and characterization of a full length-enriched and
 a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
 source
 1.50
 /organism="Homo sapiens"
 /mol_type="RNA"
 /db_xref="taxon:9606"
 /clone="HEPO2980"

BASE COUNT
 ORIGIN
 3 a 20 c 12 g 15 t
 /clone_lib="Sugano Homo sapiens cDNA library"

Query Match 67.5%; Score 10.8; DB 9; Length 50;
 Best Local Similarity 85.7%; Pred. No. 8e+04; 2; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 3 GCTAGCTACACGA 16
 |||||
 Db 31 GCGAGCTACACGA 18

RESULT 26
 AA425092 52 bp mRNA linear EST 16-OCT-1997
 LOCUS AA425092
 DEFINITION zwilfl.r1 Soares NHPu.S1 Homo sapiens cDNA clone IMAGE:769005.5,
 similar to SW.HESI_MOUSE P35428 TRANSCRIPTION FACTOR HES-1., mRNA
 sequence.

ACCESSION AA425092 GI:2107543
 VERSION AA425092.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
 Kucaba, T., Lacy, M., Le, N., Lemon, G., Marra, M., Martin, J., Moore, B.,
 Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie
 'T., Waterston, R. and Wilson, R.
 Washu-Merck EST Project 1997
 Unpublished

TITLE
 JOURNAL
 COMMENT
 Contact: Wilson R.
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: est@watson.wustl.edu
 This clone is available royalty-free through ILNLI; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Seq primer: -28ml3 revz ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES
 source
 1.52
 /organism="Homo sapiens"
 /mol_type="RNA"
 /db_xref="GDB:5975323"
 /db_xref="taxon:9606"
 /clone="IMAGE:769005"
 /issue_type="Pooled human melanocyte, fetal heart, and
 pregnant uterus"
 /lab_host="DH10B"
 /clone_lib="Soares NHPu.S1"
 /note="Organ: mixed (see below); Vector: pT73D-Pac
 (Pharmacia) with a modified polylinker; Site 1: Not I;
 Site 2: Eco RI; Equal amounts of plasmid DNA from three
 normalized libraries (melanocyte 2NBH, pregnant uterus
 NHPu, and fetal heart NBH19W) were mixed, and as circles
 were made in vitro. Following HAP purification, this DNA
 was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from pools of
 5,000 clones made from the same 3 libraries. The pools
 consisted of I.M.A.G.E. clones 260232-265223,
 340488-345479, and 484488-489479."

BASE COUNT
 ORIGIN
 15 a 14 c 16 g 7 t
 Query Match 67.5%; Score 10.8; DB 9; Length 52;
 Best Local Similarity 85.7%; Pred. No. 8.2e+04; 2; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.	
REFERENCE	1 (bases 1 to 58)
AUTHORS	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Stepcoe,M., Tan,F., Underwood,K., Moore,B., Theisinger,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE	The WashU-HHMI Mouse EST Project
JOURNAL	Unpublished
COMMENT	Contact: Marra M/Mouse Est Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. MGI:484606
FEATURES	Trace considered overall poor quality Possible reversed clone: similarity on wrong strand Seq primer: -28ml3 rev2 EF from Amersham High quality sequence stop: 1. Location/Qualifiers 1..58 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="IMAGE:808262" /sex="male" /tissue_type="heart" /dev_stage="4 weeks" /lab_host="DH10B" /clone_lib="Soares mouse NBMH" /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCATCTGTGAAGCGGCGCGCAAGAATTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
BASE COUNT	16 a 18 c 4 g 20 t
ORIGIN	
Query Match	67.5%; Score 10.8; DB 9; Length 58;
Best Local Similarity	85.7%; Pred. No. 8.5e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Dy	3 GCTAGCTACAACGA 16 Db 16 GATGGCTACAACGA 3
RESULT 29	
AZ342599/c	AZ342599 59 bp DNA linear GSS 29-SEP-2000
LOCUS	1M0075C1R Mouse 10kb plamid UFGCM library Mus musculus genomic
DEFINITION	clone UFGCM0075C18 R, genomic survey sequence.
ACCESSION	AZ342599
VERSION	AZ342599.1 GI:10419997
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.
REFERENCE	1 (bases 1 to 59) Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C.,
AUTHORS	

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

'B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaak, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Maitra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

Contact: Wilson R.
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewartson.wustl.edu

WARNING: There is evidence that suggests that the 384-well parent plate of this clone contains both human and mouse derived clones. Thus, the origin of this clone is uncertain. This caution should be kept in mind should you use this clone.

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Possible reversed clone: similarity on wrong strand
Insert Length: 3173 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.

FEATURES
SOURCE

Location/Qualifiers
1..61
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3920316"
/db_xref="taxon:9606"
/clone="IMAGE:530804"
/dev_stage="Ntera-2/RA neuroepithelial cells"
/lab_host="SOLR (kanamycin resistant)"
/clone_id="Stratagene neuroepithelium (#937231)"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. NT2 cells (Ntera-2/cl.D) induced with Retinoic Acid for 24 hours. Average insert size: 1.5 kb, Uni-AP XR Vector; -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3' adaptor sequence: 5' CTCGAGTCTTTTCTTTTCTT 3'

BASE COUNT 18 a 15 c 7 g 15 t 6 others
ORIGIN
Query Match 67.5%; Score 10.8; DB 9; Length 61;
Best Local Similarity 85.7%; Pred. No. 8.7e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 GCTAGCTCAACGA 16
|||
40 GATGCTCAACGA 27

RESULT 32
D12015/c 62 bp mRNA linear EST 02-DEC-1992
LOCUS
DEFINITION
HMM0008149 Liver HepG2 cell line. Homo sapiens cDNA clone s149,
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

D12015
D12015.1 GI:2148294
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE

1 (bases 1 to 62)
Okubo, K., Horii, N., Matoba, R., Niiyama, T., Fukushima, A., Kojima, Y.
and Matsubara, K.
Large scale cDNA sequencing for analysis of quantitative and
qualitative aspects of gene expression

JOURNAL
MEDLINE
PUBMED
COMMENT

Nat. Genet. 2, 173-179 (1992)
1345164
Contact: Kouzaku Okubo, Naohiro Horii, Ryo Matoba, Tooshiyuki Niiyama

FEATURES
SOURCE

Atsushi Fukushima, Yoko Kojima & Kenichi Matsubara
Institute for Molecular and Cellular Biology
Osaka University
1-3 Yamada-Oka, Suita, Osaka 565, Japan.
Location/Qualifiers
1..62
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:D087595E"
/db_xref="taxon:9606"
/clone="s149"
/lab_host="E. coli"
/clone_id="Liver HepG2 cell line."
/note="3'-directed regional cDNA library. Cleaved by MboI
and transformed into E.coli."

BASE COUNT 15 a 13 c 10 g 24 t
ORIGIN

Query Match 67.5%; Score 10.8; DB 14; Length 62;
Best Local Similarity 75.0%; Pred. No. 8.7e+04;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GCGTACTCAACGA 16
|||
33 AGCGACTCAACGA 18

RESULT 33
AA499456 65 bp mRNA linear EST 01-JUL-1997
LOCUS
DEFINITION
v185904.c1 Stratagene mouse skin (#93713) Mus musculus cDNA clone
IMAGE:919062 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AA499456
AA499456.1 GI:2234423
EST.
Mus musculus (house mouse)
Mus musculus

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 65)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Stepec, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

The WashU-HHMI Mouse EST Project
Unpublished
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouse@wustl.edu

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:531278
Seq primer: -28m13 rev1 ET from Amersham.

FEATURES
SOURCE

Location/Qualifiers
1..65
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:919062"
/sex="females"
/tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/clone_id="Stratagene mouse skin (#93713)"
/note="Organ: skin; Vector: pBluescript SK-; Site 1: EcoRI
; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo
dt. Whole skin from 11 week old C57BL/6 female mice.

Average insert size: 1.0 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGGCAG 3' -3' adaptor sequence: 5' CTCGAGTTTATTTTATTTT 3' "

BASE COUNT

22 a 5 c 18 g 20 t

ORIGIN

Query Match 67.5%; Score 10.8; DB 9; Length 65;
Best Local Similarity 85.7%; Pred. No. 8.9e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCTAGCTACACGA 16

Db 19 GATGCTACACGA 32

RESULT 34
BH414369/c 65 bp DNA linear GSS 12-DEC-2001
LOCUS 1007037G02.2EL x1 1007 - Rescuemu Grid H Zea mays genomic, genomic
DEFINITION survey sequence.
ACCESSION BH414369.1 GI:17592332
VERSION BH414369.1
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 65)
Walbot, V.
Maize genomic sequences found using engineered Rescuemu transposon

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1007037 column: 16
Class: transposon-tagged.
Location/Qualifiers

FEATURES

source

1.65
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_11b="1007 - Rescuemu Grid H"
/note="Organ: leaf; Vector: Rescuemu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; Rescuemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription web sites. For more information on Rescuemu, go to the web site 'www.zmh.baker.edu' and follow the links for 'Rescuemu'. Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT

11 a 15 c 26 g 13 t

ORIGIN

Query Match 67.5%; Score 10.8; DB 28; Length 65;
Best Local Similarity 75.0%; Pred. No. 8.9e+04;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16

Db

17 GGCCAGCTACACGA 2

RESULT 35
TA184A08Q/c 65 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 184a08, reverse sequence,
DEFINITION genomic survey sequence.
ACCESSION AL473539
VERSION AL473539.1 GI:11840567
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euzoenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 65)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREP927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

1.65
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREP927"
/db_xref="taxon:5691"
/clone="184a08"
Location/Qualifiers

BASE COUNT

15 a 11 c 11 g 28 t

ORIGIN

Query Match 67.5%; Score 10.8; DB 29; Length 65;
Best Local Similarity 75.0%; Pred. No. 8.9e+04;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16

Db 63 GGCCAGCTACACGA 48

RESULT 36
BG447495 66 bp mRNA linear EST 15-MAR-2001
LOCUS EST0000018 Rat Liver Express Library Rattus norvegicus cDNA clone
DEFINITION liver000018, mRNA sequence.
ACCESSION BG447495
VERSION BG447495.1 GI:13357147
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE
AUTHORS
TITLE
COMMENT
1 (bases 1 to 66)
Li, Y.C., Xu, C.S. and Zh, Y.H.
Cloning the specific expressed genes in partial hepatectomy rat liver by suppression subtractive hybridization

JOURNAL
COMMENT

Unpublished
Contact: YC Li
Department of Biology
Henan Normal University
Jianshe road, Xinxiang, China
Email: lychang@mail.hennanu.edu.cn.
Location/Qualifiers

FEATURES

SOURCE

1.66
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="liver000018"
/sex="male"
/tissue_type="liver"
/dev_stage="embryonic day 17 post-fertilization"
/clone_lib="Rat Liver Express Library"
BASE COUNT 18 a 17 c 15 g 16 t
ORIGIN

Query Match 67.5%; Score 10.8; DB 10; Length 66;
Best Local Similarity 75.0%; Pred. No. 8.9e+04;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16
Db 61 AGGCTGCTTCAAGA 46

RESULT 37
AA771119/c 67 bp mRNA linear EST 29-JAN-1998
LOCUS vt16h01.r1 Barstead mouse myotubes MRLB5 Mus musculus cDNA clone
DEFINITION IMAGE:1163281 5' similar to SW:ATP6_MOUSE P00848 ATP SYNTHASE A
CHAIN ; mRNA sequence.

AA771119
AA771119.1 GI:2822930
EST.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
MUS musculus

REFERENCE
AUTHORS
1 (bases 1 to 67)
Matra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Stepcoe, M., Tan, F., Underwood, K., Moore, B.,
Theisinger, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

TITLE
JOURNAL
COMMENT
The WashU-HMI Mouse EST Project
Unpublished
Contact: Maira W/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu

This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:629193
Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

SOURCE

1.67
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C3H"
/db_xref="taxon:10090"
/clone="IMAGE:1163281"
/cell_line="C2C12"
/lab_host="DH10B"

BASE COUNT

21 a 18 c 9 g 19 t
ORIGIN

OY 3 GCTAGCTTACACGA 16
Db 67 GATGCTACACGA 54

RESULT 38
CB366166
LOCUS

DEFINITION ZF001-P00049-DPE-F2-D.P10 G1S2F001 Danio rerio cDNA clone
IMAGE:6910149 5' similar to fp15a03.y1 zebrafish gridded kidney
Danio rerio cDNA clone IMAGE:472612 5' similar to WP:CR25522
Y61A91A.E. mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CB366166.1 GI:29016477
EST.
Danio rerio (zebrafish)

REFERENCE
AUTHORS
1 (bases 1 to 67)
Mathavan, S., Wei, C., Thoreau, H., Chia, J.M. and Ruan, Y.
Genome Institute of Singapore
1 Science Park Road, The Capricorn #05-01, Singapore 117528
Tel: +65 6827 5200
Fax: +65 6827 5201
Email: g1s2f@nus.edu.sg

TITLE
JOURNAL
COMMENT
Unpublished
Contact: Ruan Y
Laboratory of Molecular Biotechnology
Genome Institute of Singapore
1 Science Park Road, The Capricorn #05-01, Singapore 117528
Tel: +65 6827 5200
Fax: +65 6827 5201
Email: g1s2f@nus.edu.sg

GIS Clone ID: ZF001-P00049-PP_L20
PCR Primers
FORWARD: M13
BACKWARD: M13
Plate: ZF001-P00049-DPE-F2-D
Seq primer: CGGATTAAGTGTATACGA
High quality sequence stop: 67.
Location/Qualifiers

FEATURES

SOURCE

1.67
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:6910149"
/tissue_type="Embryo"
/dev_stage="7 Different embryonic Stages (From just
fertilized Embryos to 72 hours just hatched baby fish)"
/lab_host="DH10B"
/clone_lib="G1S2F001"
/note="Vector: pDNR-LIB, Site 1: Sfi A (GGCCATTACGCC);
Site 2: Sfi B (GGCGGCTTGGCC); Priming method: Sfi-1 (dT)30
primed; Priming sequence: 5'ATTCAGA GGCGGAGGCGGC
GACATG(T)30VN; Directionally cloned; 5' cloning site:
Sfi A site GGCCATTACGCC; 5' linker/adaptor sequence:

5. AACGACTGATACACGCGAGTGGCC ; 3' cloning site: Sfi B site GGCCGCTCGGCC ; 3' linker/adaptor sequence: same as the priming sequence ; Average insert size: 2kb ; For PCR insert analysis: Use M13 Forward and reverse primers ; Library Amplified Recombinants (inserts): 98% ; Library complexity: 5x10⁶ ; Full-length construction (method): SMART, a Clontech method ; Library constructed by: S. Mathavan, Chla-Lin Wei, and Yijun Ruan Genome Institute of Singapore"

BASE COUNT 19 a 19 c 14 g 15 t

ORIGIN

Query Match 67.5% ; Score 10.8 ; DB 14 ; Length 67 ; Best Local Similarity 75.0% ; Pred. No. 9e+04 ; Mismatches 1 ; Indels 0 ; Gaps 0 ;

Matches 12 ; Conservative 1 ; Mismatches 3 ; Indels 0 ; Gaps 0 ;

QY 1 RGGCTAGCTACAACA 16
: |||||
33 GGCTTACCAACAACA 48

RESULT 39
D11778 69 bp mRNA linear EST 02-DEC-1992
LOCUS HUMH01E11 Liver HepG2 cell line. Homo sapiens CDNA clone hm01e11,
DEFINITION mRNA sequence.
ACCESSION D11778
VERSION D11778.1 GI:2155059
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 69) Okubo, K., Hori, N., Matoba, R., Miyama, T., Fukushima, A., Kojima, Y. and Matsubara, K.
TITLE Large scale CDNA sequencing for analysis of quantitative and qualitative aspects of gene expression
JOURNAL Nat. Genet. 2, 173-179 (1992)
MEDLINE 94258199
PUBMED
COMMENT Contact: Kousaku Okubo, Naohiro Hori, Ryo Matoba, Toshiyuki Miyama, Atsushi Fukushima, Yoko Kojima & Kenichi Matsubara
Institute for Molecular and Cellular Biology
Osaka University
1-3 Yamada-oka, Suita, Osaka 565, Japan.
FEATURES
source
1..69
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:D088324E"
/db_xref="taxon:9606"
/clone="hm01e11"
/lab_host="E.coli"
/clone_lib="Liver HepG2 cell line."
/note="3'-directed regional cDNA library. Cleaved by MboI and transformed into E.coli." 23 t

BASE COUNT 24 a 14 c 8 g 23 t

ORIGIN

Query Match 67.5% ; Score 10.8 ; DB 14 ; Length 69 ; Best Local Similarity 75.0% ; Pred. No. 9.1e+04 ; Mismatches 1 ; Indels 0 ; Gaps 0 ;

Matches 12 ; Conservative 1 ; Mismatches 3 ; Indels 0 ; Gaps 0 ;

QY 1 RGGCTAGCTACAACA 16
: |||||
20 AGGATGGCTACAACA 5

RESULT 40
AM104004 71 bp mRNA linear EST 20-OCT-1999
LOCUS AM104004
DEFINITION x63h05.x1 NCI_CGAP_Ov23 Homo sapiens CDNA clone IMAGE:2598489.3',

mRNA sequence.
AM104004
VERSION AM104004.1 GI:6074739
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 71) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps@email.nih.gov
Tissue Procurement: Christopher Morkaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/dbp/image/image.html
Seq primer: -40UP from Gibco.
FEATURES
source
1..71
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2598489"
/issue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
/clone_lib="NCI CGAP Ov23"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI. Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.35 kb. Tumor types include: mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Life Technologies catalog #: 11534-013"
BASE COUNT 24 a 8 c 14 g 25 t

ORIGIN

Query Match 67.5% ; Score 10.8 ; DB 9 ; Length 71 ; Best Local Similarity 75.0% ; Pred. No. 9.2e+04 ; Mismatches 1 ; Indels 0 ; Gaps 0 ;

Matches 12 ; Conservative 1 ; Mismatches 3 ; Indels 0 ; Gaps 0 ;

QY 1 RGGCTAGCTACAACA 16
: |||||
47 AGGATGGCTACAACA 62

Search completed: January 21, 2004, 08:16:07
Job time : 148 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 06:45:02 ; Search time 38 Seconds

(without alignments)
185.846 Million cell updates/sec

Title: US-09-423-035B-122

Perfect score: 16

Sequence: 1 rgsctacgacaaga 16

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 830498

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PCITUS.COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.8	92.5	16	4	US-09-536-393-19
2	14.8	92.5	16	4	US-09-536-393-20
3	14.8	92.5	29	4	US-09-270-140A-23
4	14.8	92.5	29	4	US-09-270-140A-25
5	14.8	92.5	30	4	US-09-270-140A-55
6	14.8	92.5	31	3	US-09-253-955-5
7	14.8	92.5	31	3	US-09-637-405-5
8	14.8	92.5	31	4	US-09-270-140A-42
9	14.8	92.5	31	4	US-09-270-140A-45
10	14.8	92.5	31	4	US-09-270-140A-48
11	14.8	92.5	31	4	US-09-270-140A-51
12	14.8	92.5	31	4	US-09-746-985B-5
13	14.8	92.5	32	4	US-09-270-140A-12
14	14.8	92.5	32	4	US-09-270-140A-15
15	14.8	92.5	32	4	US-09-270-140A-19
16	14.8	92.5	32	4	US-09-270-140A-28
17	14.8	92.5	32	4	US-09-270-140A-58
18	14.8	92.5	34	4	US-09-270-140A-9
19	14.8	92.5	34	4	US-09-270-140A-53
20	14.8	92.5	35	4	US-09-270-140A-3
21	14.8	92.5	35	4	US-09-270-140A-6
22	14.8	92.5	35	4	US-09-270-140A-31
23	14.8	92.5	35	4	US-09-270-140A-39
24	14.8	92.5	38	4	US-09-270-140A-34
25	14.8	92.5	38	4	US-09-270-140A-36
26	14.8	92.5	39	4	US-09-270-140A-91
27	14.8	92.5	39	4	US-09-270-140A-94

28	14.8	92.5	47	4	US-08-849-567A-85	Sequence 85, Appl
29	14.8	92.5	48	4	US-08-849-567A-87	Sequence 87, Appl
30	14.8	92.5	49	4	US-08-849-567A-81	Sequence 81, Appl
31	14.8	92.5	50	3	US-09-253-955-8	Sequence 8, Appl
32	14.8	92.5	50	3	US-09-637-405-8	Sequence 8, Appl
33	14.8	92.5	50	3	US-09-746-985B-8	Sequence 8, Appl
34	14.8	92.5	51	4	US-08-849-567A-86	Sequence 86, Appl
35	14.8	92.5	59	3	US-09-253-955-2	Sequence 2, Appl
36	14.8	92.5	59	3	US-09-637-405-2	Sequence 2, Appl
37	14.8	92.5	59	3	US-09-746-985B-2	Sequence 2, Appl
38	14.8	92.5	60	3	US-09-253-955-10	Sequence 10, Appl
39	14.8	92.5	60	3	US-09-637-405-10	Sequence 10, Appl
40	14.8	92.5	60	3	US-09-270-140A-95	Sequence 95, Appl
41	14.8	92.5	60	4	US-09-746-985B-10	Sequence 10, Appl
42	14.8	92.5	98	3	US-09-253-955-11	Sequence 11, Appl
43	14.8	92.5	98	3	US-09-637-405-11	Sequence 11, Appl
44	14.8	92.5	98	4	US-09-270-140A-96	Sequence 96, Appl
45	14.8	92.5	98	4	US-09-746-985B-11	Sequence 11, Appl
46	12.2	76.2	31	1	US-08-303-270-4	Sequence 4, Appl
47	11.6	72.5	30	3	US-09-242-797-5	Sequence 5, Appl
48	11.6	72.5	30	3	US-09-242-797-7	Sequence 7, Appl
49	11.6	72.5	48	3	US-09-997-918-43	Sequence 43, Appl
50	11.6	72.5	48	3	US-09-997-918-41	Sequence 41, Appl
51	11.6	72.5	50	3	US-09-292-071-3	Sequence 3, Appl
52	11.6	72.5	50	3	US-09-292-071-4	Sequence 4, Appl
53	11.6	72.5	50	3	US-09-292-069A-3	Sequence 3, Appl
54	11.6	72.5	50	3	US-09-292-069A-4	Sequence 4, Appl
55	11.6	72.5	50	3	US-09-418-721-3	Sequence 3, Appl
56	11.6	72.5	50	3	US-09-418-721-4	Sequence 4, Appl
57	11.6	72.5	50	4	US-09-767-013-3	Sequence 3, Appl
58	11.6	72.5	50	4	US-09-767-013-4	Sequence 4, Appl
59	11.6	72.5	50	4	US-09-292-072-3	Sequence 3, Appl
60	11.6	72.5	50	4	US-09-292-072-4	Sequence 4, Appl
61	11.6	72.5	50	4	US-09-170-456D-237	Sequence 237, App
62	11.6	72.5	50	4	US-09-170-456D-238	Sequence 238, App
63	11.6	72.5	55	3	US-08-997-918-48	Sequence 48, Appl
64	11.6	72.5	60	3	US-08-290-736C-37	Sequence 37, Appl
65	11.6	72.5	71	3	US-08-290-736C-46	Sequence 46, Appl
66	11.6	72.5	71	3	US-08-290-736C-47	Sequence 47, Appl
67	11.2	70.0	20	4	US-09-198-452A-4924	Sequence 4924, Ap
68	11.2	70.0	20	4	US-09-198-452A-6403	Sequence 6403, Ap
69	11.2	70.0	40	1	US-08-741-881-83	Sequence 83, Appl
70	11.2	70.0	40	1	US-08-739-158-83	Sequence 83, Appl
71	11.2	70.0	40	2	US-08-739-167-83	Sequence 83, Appl
72	11.2	70.0	40	2	US-08-404-786-83	Sequence 83, Appl
73	11.2	70.0	40	3	US-08-931-869-83	Sequence 83, Appl
74	11.2	70.0	40	4	US-09-350-399-83	Sequence 83, Appl
75	11.2	70.0	48	2	US-09-236-140A-83	Sequence 83, Appl
76	11.2	70.0	55	1	US-08-811-492-124	Sequence 124, App
77	11.2	70.0	55	1	US-08-180-195-10	Sequence 10, Appl
78	11.2	70.0	55	1	US-08-180-135-11	Sequence 11, Appl
79	11.2	70.0	55	1	US-08-477-329-10	Sequence 10, Appl
80	11.2	70.0	55	1	US-08-477-329-11	Sequence 11, Appl
81	11.2	70.0	55	2	US-08-811-492-125	Sequence 125, App
82	11.2	70.0	55	2	US-08-475-458-10	Sequence 10, Appl
83	11.2	70.0	55	2	US-08-475-458-11	Sequence 11, Appl
84	11.2	70.0	55	3	US-08-980-400-10	Sequence 10, Appl
85	11.2	70.0	55	3	US-08-980-400-11	Sequence 11, Appl
86	11.2	70.0	55	3	US-09-583-459A-10	Sequence 10, Appl
87	11.2	70.0	55	3	US-09-583-459A-11	Sequence 11, Appl
88	11.2	70.0	55	3	US-09-583-459A-11	Sequence 11, Appl
89	11.2	70.0	55	3	US-09-583-210-11	Sequence 11, Appl
90	11.2	70.0	55	4	US-09-583-459A-10	Sequence 10, Appl
91	11.2	70.0	55	4	US-09-583-459A-11	Sequence 11, Appl
92	11.2	70.0	55	4	US-09-435-059-11	Sequence 11, Appl
93	11.2	70.0	55	4	US-09-435-059-11	Sequence 11, Appl
94	11.2	70.0	75	4	US-09-702-705-242	Sequence 242, App
95	11.2	68.8	75	4	US-09-736-457-242	Sequence 242, App
96	11.2	68.8	78	4	US-09-702-705-1277	Sequence 1277, Ap
97	11.2	68.8	78	4	US-09-736-457-1277	Sequence 1277, Ap
98	10.8	67.5	27	3	US-08-981-189B-18	Sequence 18, Appl
99	10.8	67.5	33	4	US-09-523-686-6	Sequence 6, Appl
100	10.8	67.5	42	3	US-09-079-994A-5	Sequence 5, Appl

C 101	10.8	67.5	42	4	US-09-390-729-5	Sequence 5, Appl	174	10.2	63.7	48	5	PCT-US96-07796-16	Sequence 16, Appl
C 102	10.8	67.5	44	4	US-09-360-337-25	Sequence 25, Appl	C 175	10.2	63.7	53	4	US-09-132-316-6	Sequence 6, Appl
C 103	10.6	66.2	20	4	US-09-060-299-378	Sequence 378, App	176	10.2	63.7	60	3	US-08-814-052-15	Sequence 35, Appl
C 104	10.6	66.2	20	4	US-09-402-923A-378	Sequence 378, App	177	10.2	63.7	60	3	US-08-812-829-27	Sequence 27, Appl
C 105	10.6	66.2	21	1	US-08-435-480-6	Sequence 6, Appl	C 178	10	62.5	17	1	US-08-180-209B-15	Sequence 15, Appl
C 106	10.6	66.2	21	2	US-08-946-241B-6	Sequence 6, Appl	C 179	10	62.5	17	1	US-08-385-745-15	Sequence 15, Appl
C 107	10.6	66.2	21	3	US-09-309-053-6	Sequence 6, Appl	C 180	10	62.5	17	1	US-08-485-388-15	Sequence 15, Appl
C 108	10.6	66.2	21	3	US-08-940-968-14	Sequence 14, Appl	C 181	10	62.5	17	3	US-08-474-853-15	Sequence 15, Appl
C 109	10.6	66.2	25	3	US-09-012-097A-15	Sequence 15, Appl	C 182	10	62.5	17	3	US-09-166-205B-15	Sequence 15, Appl
C 110	10.6	66.2	25	4	US-08-672-213-36	Sequence 36, Appl	C 183	10	62.5	17	5	US-09-166-205B-15	Sequence 15, Appl
C 111	10.6	66.2	25	4	US-09-538-709-301	Sequence 301, App	C 184	10	62.5	20	2	PCT-US94-02629-15	Sequence 15, Appl
C 112	10.6	66.2	25	4	US-09-481-620A-31	Sequence 31, App	C 185	10	62.5	20	3	US-08-975-211-14	Sequence 14, Appl
C 113	10.6	66.2	27	4	US-09-109-329-26	Sequence 26, Appl	C 186	10	62.5	20	3	US-09-282-736-14	Sequence 14, Appl
C 114	10.6	66.2	28	1	US-08-221-078A-1	Sequence 1, Appl	C 187	10	62.5	20	4	US-09-198-432A-5936	Sequence 5936, Ap
C 115	10.6	66.2	28	1	US-08-221-171A-1	Sequence 1, Appl	C 188	10	62.5	24	1	US-09-649-728-2	Sequence 2, Appl
C 116	10.6	66.2	29	4	US-08-054-970-4	Sequence 4, Appl	C 189	10	62.5	24	1	US-08-324-243-1	Sequence 1, Appl
C 117	10.6	66.2	30	1	US-08-322-677A-13	Sequence 13, Appl	C 190	10	62.5	24	1	US-08-532-390-1	Sequence 1, Appl
C 118	10.6	66.2	30	1	US-08-322-676-13	Sequence 13, Appl	C 191	10	62.5	24	3	US-08-526-136-6	Sequence 6, Appl
C 119	10.6	66.2	30	3	US-08-898-218-13	Sequence 13, Appl	C 192	10	62.5	24	3	US-08-717-294-1	Sequence 1, Appl
C 120	10.6	66.2	30	3	US-08-848-793-13	Sequence 13, Appl	C 193	10	62.5	24	3	US-08-948-113D-4	Sequence 4, Appl
C 121	10.6	66.2	30	4	US-08-322-678-13	Sequence 13, Appl	C 194	10	62.5	24	5	PCT-US95-11511-1	Sequence 1, Appl
C 122	10.6	66.2	31	3	US-08-732-218-10	Sequence 13, Appl	C 195	10	62.5	25	1	US-08-056-200-8	Sequence 8, Appl
C 123	10.6	66.2	31	3	US-08-732-218-10	Sequence 10, Appl	C 196	10	62.5	25	2	US-08-800-644-8	Sequence 8, Appl
C 124	10.6	66.2	35	3	US-09-439-000-3	Sequence 57, Appl	C 197	10	62.5	25	4	US-08-982-285-50	Sequence 50, Appl
C 125	10.6	66.2	36	3	US-08-746-883-9	Sequence 9, Appl	C 198	10	62.5	26	1	US-08-982-285-51	Sequence 51, Appl
C 126	10.6	66.2	41	3	US-08-813-507-135	Sequence 135, App	C 199	10	62.5	26	1	US-08-412-614-17	Sequence 17, Appl
C 127	10.6	66.2	41	4	US-09-464-453-135	Sequence 135, App	C 200	10	62.5	26	1	US-08-412-614-18	Sequence 18, Appl
C 128	10.6	66.2	47	4	US-09-422-978-3652	Sequence 135, App	C 201	10	62.5	26	1	US-08-412-614-19	Sequence 19, Appl
C 129	10.6	66.2	49	4	US-09-538-709-957	Sequence 957, App	C 202	10	62.5	26	1	US-08-412-614-20	Sequence 20, Appl
C 130	10.6	66.2	64	3	US-08-729-601A-18	Sequence 18, App	C 203	10	62.5	26	1	US-08-093-741-53	Sequence 53, Appl
C 131	10.2	63.7	19	1	US-08-379-081B-141	Sequence 141, App	C 204	10	62.5	26	1	US-08-720-012-53	Sequence 53, Appl
C 132	10.2	63.7	19	1	US-08-379-081B-142	Sequence 142, App	C 205	10	62.5	26	2	US-08-435-637A-2	Sequence 2, Appl
C 133	10.2	63.7	19	1	US-08-379-081B-143	Sequence 143, App	C 206	10	62.5	26	2	US-08-635-761-17	Sequence 17, Appl
C 134	10.2	63.7	19	1	US-08-379-078-141	Sequence 141, App	C 207	10	62.5	26	2	US-08-635-761-18	Sequence 18, Appl
C 135	10.2	63.7	19	1	US-08-379-078-142	Sequence 142, App	C 208	10	62.5	26	2	US-08-635-761-19	Sequence 19, Appl
C 136	10.2	63.7	19	1	US-08-379-078-143	Sequence 143, App	C 209	10	62.5	26	3	US-09-312-520-17	Sequence 17, Appl
C 137	10.2	63.7	25	2	US-08-303-270-9	Sequence 9, Appl	C 210	10	62.5	26	3	US-09-312-520-18	Sequence 18, Appl
C 138	10.2	63.7	26	1	US-08-094-128A-28	Sequence 13, Appl	C 211	10	62.5	26	3	US-09-312-520-19	Sequence 19, Appl
C 139	10.2	63.7	26	1	US-08-455-674-28	Sequence 28, Appl	C 212	10	62.5	26	3	US-09-312-520-20	Sequence 20, Appl
C 140	10.2	63.7	26	1	US-08-450-257-34	Sequence 34, Appl	C 213	10	62.5	28	4	US-09-438-268-37	Sequence 37, Appl
C 141	10.2	63.7	26	1	US-08-455-992-28	Sequence 28, Appl	C 214	10	62.5	30	4	US-08-948-113B-8	Sequence 8, Appl
C 142	10.2	63.7	26	1	US-08-455-992-28	Sequence 34, Appl	C 215	10	62.5	31	4	US-08-948-113B-8	Sequence 8, Appl
C 143	10.2	63.7	26	1	US-08-455-992-28	Sequence 34, Appl	C 216	10	62.5	32	1	US-07-977-696C-8	Sequence 8, Appl
C 144	10.2	63.7	26	1	US-08-450-246-34	Sequence 28, Appl	C 217	10	62.5	32	1	US-08-129-830B-8	Sequence 8, Appl
C 145	10.2	63.7	26	1	US-08-450-098-34	Sequence 34, Appl	C 218	10	62.5	32	2	US-07-673-661B-14	Sequence 14, Appl
C 146	10.2	63.7	26	1	US-08-451-233-34	Sequence 34, Appl	C 219	10	62.5	32	4	US-08-976-1288A-8	Sequence 8, Appl
C 147	10.2	63.7	26	1	US-08-451-233-34	Sequence 34, Appl	C 220	10	62.5	32	4	US-08-452-129A-14	Sequence 14, Appl
C 148	10.2	63.7	26	1	US-08-235-203-34	Sequence 34, Appl	C 221	10	62.5	34	4	US-09-842-164A-22	Sequence 22, Appl
C 149	10.2	63.7	26	5	PCT-US92-00652-28	Sequence 28, Appl	C 222	10	62.5	35	1	US-09-842-164A-22	Sequence 22, Appl
C 150	10.2	63.7	30	1	US-08-182-530-4	Sequence 4, Appl	C 223	10	62.5	35	1	US-08-551-459-8	Sequence 4, Appl
C 151	10.2	63.7	30	1	US-08-050-058B-4	Sequence 4, Appl	C 224	10	62.5	35	4	US-09-085-720-15	Sequence 15, Appl
C 152	10.2	63.7	30	1	US-08-463-587A-4	Sequence 4, Appl	C 225	10	62.5	36	1	US-08-688-609-12	Sequence 12, Appl
C 153	10.2	63.7	30	2	US-08-463-587A-4	Sequence 8, Appl	C 226	10	62.5	36	3	US-09-002-832-12	Sequence 12, Appl
C 154	10.2	63.7	30	2	US-08-463-587A-4	Sequence 8, Appl	C 227	10	62.5	37	1	US-08-261-670-13	Sequence 13, Appl
C 155	10.2	63.7	30	3	US-08-441-871-8	Sequence 4, Appl	C 228	10	62.5	37	4	US-09-842-164A-19	Sequence 19, Appl
C 156	10.2	63.7	30	3	US-08-923-854-4	Sequence 4, Appl	C 229	10	62.5	37	4	US-09-842-164A-19	Sequence 19, Appl
C 157	10.2	63.7	30	5	PCT-US91-09133-4	Sequence 4, Appl	C 230	10	62.5	37	5	PCT-US93-02115-13	Sequence 13, Appl
C 158	10.2	63.7	37	1	US-07-718-274A-44	Sequence 44, Appl	C 231	10	62.5	39	3	US-08-717-294-4-3	Sequence 47, Appl
C 159	10.2	63.7	37	1	US-07-718-274A-56	Sequence 56, Appl	C 232	10	62.5	39	3	US-09-381-847-7	Sequence 3, Appl
C 160	10.2	63.7	37	1	US-08-149-106-44	Sequence 56, Appl	C 233	10	62.5	39	6	5519127-31	Patent No. 5519127
C 161	10.2	63.7	37	1	US-08-149-106-56	Sequence 56, Appl	C 234	10	62.5	40	1	US-08-443-957-25	Sequence 25, Appl
C 162	10.2	63.7	37	1	US-08-149-106-62	Sequence 62, Appl	C 235	10	62.5	40	4	US-09-842-164A-20	Sequence 20, Appl
C 163	10.2	63.7	37	1	US-08-298-021-44	Sequence 44, Appl	C 236	10	62.5	41	3	US-08-997-918-36	Sequence 36, Appl
C 164	10.2	63.7	37	1	US-08-298-021-56	Sequence 56, Appl	C 237	10	62.5	41	3	US-07-667-106-8	Sequence 8, Appl
C 165	10.2	63.7	37	1	US-08-298-021-62	Sequence 62, Appl	C 238	10	62.5	42	1	US-08-468-036-24	Sequence 24, Appl
C 166	10.2	63.7	40	5	PCT-US96-07795-17	Sequence 17, Appl	C 239	10	62.5	42	1	US-08-468-036-24	Sequence 24, Appl
C 167	10.2	63.7	40	5	PCT-US96-07795-17	Sequence 17, Appl	C 240	10	62.5	42	2	US-08-376-843-39	Sequence 39, Appl
C 168	10.2	63.7	41	4	US-08-980-241-3	Sequence 3, Appl	C 241	10	62.5	42	2	US-08-376-843-39	Sequence 39, Appl
C 169	10.2	63.7	41	4	US-08-980-241-3	Sequence 3, Appl	C 242	10	62.5	44	3	US-09-254-023B-7	Sequence 7, Appl
C 170	10.2	63.7	43	4	US-09-713-678-38	Sequence 38, Appl	C 243	10	62.5	45	3	US-09-315-794-4	Sequence 4, Appl
C 171	10.2	63.7	44	4	US-09-132-316-4	Sequence 4, Appl	C 244	10	62.5	45	3	US-09-389-341-4	Sequence 4, Appl
C 172	10.2	63.7	48	1	US-08-458-067-16	Sequence 16, Appl	C 245	10	62.5	46	3	US-09-171-945-102	Sequence 102, App
C 173	10.2	63.7	48	5	PCT-US96-07795-16	Sequence 16, Appl	C 246	10	62.5	47	2	US-09-081-731-4	Sequence 4, Appl

247	10	62.5	47	4	US-09-361-727-4	Sequence 4, Appli	320	9.6	60.0	21	4	US-09-091-952A-80	Sequence 80, Appli
C 248	10	62.5	47	4	US-09-641-638-1061	Sequence 1061, Ap	321	9.6	60.0	21	4	US-09-422-978-10259	Sequence 10259, A
249	10	62.5	47	4	US-09-422-978-858	Sequence 858, App	C 322	9.6	60.0	23	1	US-08-244-269-3	Sequence 3, Appli
250	10	62.5	50	1	US-08-519-197-5	Sequence 5, Appli	C 323-	9.6	60.0	23	1	US-08-348-683-16	Sequence 1, Appli
251	10	62.5	50	4	US-09-554-929-69	Sequence 69, Appli	C 324	9.6	60.0	23	4	US-09-207-388-6	Sequence 66, Appli
C 252	10	62.5	50	5	PCT-US95-11405-17	Sequence 17, Appli	C 325	9.6	60.0	24	2	US-08-859-998-90	Sequence 90, Appli
253	10	62.5	51	1	US-08-688-609-13	Sequence 13, Appli	C 326	9.6	60.0	24	4	US-09-225-928-9	Sequence 90, Appli
254	10	62.5	51	3	US-09-002-832-13	Sequence 13, Appli	C 327	9.6	60.0	24	4	US-09-225-201B-90	Sequence 90, Appli
C 255	10	62.5	53	2	US-08-657-382-32	Sequence 32, Appli	328	9.6	60.0	25	1	US-08-244-269-4	Sequence 4, Appli
C 256	10	62.5	53	4	PCT-US94-02539-32	Sequence 32, Appli	329	9.6	60.0	25	1	US-08-244-269-6	Sequence 6, Appli
C 257	10	62.5	54	5	US-09-479-645A-218	Sequence 218, App	330	9.6	60.0	25	1	US-08-348-683-18	Sequence 18, Appli
258	10	62.5	61	1	US-09-549-848B-66	Sequence 66, Appli	331	9.6	60.0	25	1	US-08-348-683-19	Sequence 19, Appli
259	10	62.5	62	1	US-08-366-783-13	Sequence 13, Appli	332	9.6	60.0	26	1	US-08-093-741-38	Sequence 38, Appli
260	10	62.5	62	2	US-08-846-021A-17	Sequence 17, Appli	333	9.6	60.0	26	2	US-08-720-012-38	Sequence 38, Appli
261	10	62.5	63	1	US-07-807-529A-16	Sequence 16, Appli	334	9.6	60.0	26	2	US-08-560-098A-31	Sequence 31, Appli
262	10	62.5	63	3	US-08-300-928C-65	Sequence 65, Appli	335	9.6	60.0	26	3	US-08-967-024C-19	Sequence 19, Appli
263	10	62.5	63	3	US-08-430-944D-65	Sequence 65, Appli	336	9.6	60.0	26	3	US-09-306-005-13	Sequence 13, Appli
264	10	62.5	63	3	US-08-430-014-65	Sequence 65, Appli	337	9.6	60.0	27	4	US-09-253-116-34	Sequence 34, Appli
265	10	62.5	63	3	US-08-431-184-65	Sequence 65, Appli	338	9.6	60.0	27	4	US-09-457-066-33	Sequence 33, Appli
C 266	10	62.5	71	2	US-08-465-591A-67	Sequence 67, Appli	339	9.6	60.0	27	4	US-09-564-5950-31	Sequence 31, Appli
C 267	10	62.5	71	2	US-08-465-594A-67	Sequence 67, Appli	340	9.6	60.0	27	4	US-09-706-968-33	Sequence 33, Appli
C 268	10	62.5	71	3	US-08-973-124-252	Sequence 252, App	341	9.6	60.0	27	4	US-09-585-228-17	Sequence 17, Appli
C 269	10	62.5	71	5	PCT-US96-08014-252	Sequence 252, App	342	9.6	60.0	29	2	US-08-816-693A-42	Sequence 42, Appli
C 270	10	62.5	74	3	US-09-315-794-2	Sequence 2, Appli	343	9.6	60.0	29	3	US-08-885-291-42	Sequence 42, Appli
C 271	10	62.5	74	3	US-09-389-341-2	Sequence 2, Appli	344	9.6	60.0	29	3	US-09-496-672-42	Sequence 42, Appli
272	10	62.5	79	1	US-08-472-255A-139	Sequence 139, App	345	9.6	60.0	30	1	US-08-049-473-15	Sequence 15, Appli
273	10	62.5	79	1	US-08-472-255A-165	Sequence 165, App	C 346	9.6	60.0	30	1	US-08-049-473-16	Sequence 16, Appli
274	10	62.5	79	1	US-08-479-724A-139	Sequence 139, App	347	9.6	60.0	30	1	US-08-312-648-15	Sequence 15, Appli
275	10	62.5	79	1	US-08-479-724A-165	Sequence 165, App	C 348	9.6	60.0	30	1	US-08-312-648-16	Sequence 16, Appli
276	10	62.5	79	3	US-08-472-256B-139	Sequence 139, App	C 349	9.6	60.0	30	3	US-08-913-842-51	Sequence 51, Appli
277	10	62.5	79	3	US-08-472-256B-165	Sequence 165, App	350	9.6	60.0	30	3	US-09-176-862-7	Sequence 7, Appli
278	10	62.5	79	3	US-08-952-793-139	Sequence 139, App	351	9.6	60.0	30	3	US-09-202-316-43	Sequence 43, Appli
279	10	62.5	79	3	US-08-952-793-165	Sequence 165, App	352	9.6	60.0	30	5	PCT-US94-04190-15	Sequence 15, Appli
280	10	62.5	79	4	US-09-849-928-165	Sequence 139, App	C 353	9.6	60.0	30	5	PCT-US94-04190-16	Sequence 16, Appli
281	10	62.5	79	4	US-09-849-928-165	Sequence 139, App	C 354	9.6	60.0	31	4	US-09-206-898-22	Sequence 22, Appli
282	10	62.5	79	5	PCT-US96-09455A-139	Sequence 139, App	355	9.6	60.0	32	1	US-08-628-665-13	Sequence 13, Appli
283	10	62.5	79	5	PCT-US96-09455A-165	Sequence 165, App	C 356	9.6	60.0	33	1	US-08-309-560-24	Sequence 24, Appli
284	10	62.5	83	3	US-09-133-944-3	Sequence 3, Appli	C 357	9.6	60.0	33	1	US-07-977-696C-57	Sequence 57, Appli
285	10	62.5	83	4	US-09-208-827-3	Sequence 3, Appli	C 358	9.6	60.0	33	1	US-08-129-930B-57	Sequence 57, Appli
C 286	10	62.5	84	1	US-07-745-206A-10	Sequence 10, Appli	C 359	9.6	60.0	33	2	US-08-583-562B-22	Sequence 22, Appli
C 287	10	62.5	84	1	US-08-455-543A-6	Sequence 6, Appli	C 360	9.6	60.0	33	2	US-08-779-113-22	Sequence 22, Appli
C 288	10	62.5	84	2	US-08-193-078B-6	Sequence 6, Appli	C 361	9.6	60.0	33	2	US-08-930-605-8	Sequence 8, Appli
C 289	10	62.5	84	2	US-08-223-305C-6	Sequence 6, Appli	C 362	9.6	60.0	33	4	US-08-976-288A-57	Sequence 57, Appli
C 290	10	62.5	84	2	US-08-149-097D-6	Sequence 6, Appli	363	9.6	60.0	33	4	US-09-813-781-22	Sequence 22, Appli
C 291	10	62.5	84	2	US-08-311-363-10	Sequence 10, Appli	C 364	9.6	60.0	33	5	PCT-US94-05821A-24	Sequence 24, Appli
C 292	10	62.5	84	3	US-08-949-386-6	Sequence 6, Appli	C 365	9.6	60.0	34	1	US-08-434-503-13	Sequence 13, Appli
C 293	10	62.5	84	3	US-08-450-562-6	Sequence 6, Appli	C 366	9.6	60.0	34	1	US-08-628-665-15	Sequence 15, Appli
C 294	10	62.5	84	4	US-08-984-709A-6	Sequence 6, Appli	367	9.6	60.0	36	1	US-08-197-791-23	Sequence 23, Appli
C 295	10	62.5	84	4	US-08-450-272-6	Sequence 6, Appli	368	9.6	60.0	36	1	US-08-399-696-15	Sequence 15, Appli
C 296	10	62.5	88	4	US-09-351-814-6	Sequence 6, Appli	369	9.6	60.0	36	4	US-09-371-772B-12826	Sequence 12826, A
C 297	9.8	61.3	19	1	US-08-379-081B-140	Sequence 140, App	370	9.6	60.0	39	2	US-08-723-306-12	Sequence 12, Appli
C 298	9.8	61.3	19	1	US-08-379-078-140	Sequence 140, App	371	9.6	60.0	39	5	PCT-US96-10041-12	Sequence 12, Appli
C 299	9.8	61.3	76	3	US-09-390-867A-6	Sequence 6, Appli	372	9.6	60.0	40	2	US-08-882-108-4	Sequence 4, Appli
C 300	9.8	61.3	76	4	US-09-548-260-6	Sequence 6, Appli	373	9.6	60.0	40	2	US-08-558-107-4	Sequence 4, Appli
C 301	9.8	61.3	87	3	US-09-390-867A-1	Sequence 1, Appli	374	9.6	60.0	40	3	US-09-243-539-4	Sequence 4, Appli
C 302	9.8	61.3	87	4	US-09-548-260-1	Sequence 1, Appli	C 375	9.6	60.0	40	4	US-09-330-235-9	Sequence 9, Appli
C 303	9.8	61.3	100	4	US-08-706-945D-91	Sequence 91, Appli	C 376	9.6	60.0	42	3	US-08-897-527-1	Sequence 1, Appli
C 304	9.6	60.0	18	1	US-08-093-741-37	Sequence 37, Appli	377	9.6	60.0	42	3	US-09-072-508-1	Sequence 1, Appli
C 305	9.6	60.0	18	1	US-08-720-012-37	Sequence 37, Appli	C 378	9.6	60.0	44	1	US-08-399-696-65	Sequence 65, Appli
C 306	9.6	60.0	18	2	US-08-560-098A-30	Sequence 30, Appli	C 379	9.6	60.0	45	3	US-09-363-970-26	Sequence 26, Appli
C 307	9.6	60.0	18	3	US-08-967-024C-18	Sequence 18, Appli	C 380	9.6	60.0	46	1	US-07-994-659A-56	Sequence 56, Appli
308	9.6	60.0	19	2	US-08-596-607-4	Sequence 4, Appli	C 381	9.6	60.0	47	4	US-09-422-978-933	Sequence 933, App
C 309	9.6	60.0	20	1	US-07-922-733A-42	Sequence 42, Appli	382	9.6	60.0	47	4	US-09-422-978-959	Sequence 959, App
C 310	9.6	60.0	20	1	US-07-799-828C-42	Sequence 42, Appli	383	9.6	60.0	47	4	US-09-422-978-1217	Sequence 1217, Ap
C 311	9.6	60.0	20	2	US-07-953-277A-42	Sequence 42, Appli	384	9.6	60.0	47	4	US-09-422-978-3244	Sequence 3244, Ap
312	9.6	60.0	20	3	US-09-289-267-68	Sequence 68, Appli	C 385	9.6	60.0	48	1	US-07-609-716-37	Sequence 37, Appli
313	9.6	60.0	20	3	US-09-101-886B-88	Sequence 88, Appli	C 386	9.6	60.0	48	1	US-07-609-716-38	Sequence 38, Appli
314	9.6	60.0	21	2	US-08-946-241B-5	Sequence 5, Appli	C 387	9.6	60.0	48	2	US-08-882-083-3	Sequence 3, Appli
315	9.6	60.0	21	3	US-09-309-053-5	Sequence 5, Appli	C 388	9.6	60.0	48	2	US-08-558-107-3	Sequence 3, Appli
316	9.6	60.0	21	3	US-08-109-037-15	Sequence 15, Appli	C 389	9.6	60.0	48	3	US-09-243-539-3	Sequence 3, Appli
317	9.6	60.0	21	3	US-08-109-037-88	Sequence 88, Appli	C 390	9.6	60.0	48	3	US-08-475-111A-37	Sequence 37, Appli
C 318	9.6	60.0	21	3	US-08-109-037-89	Sequence 89, Appli	391	9.6	60.0	48	3	US-08-475-111A-38	Sequence 38, Appli
C 319	9.6	60.0	21	3	US-08-109-037-90	Sequence 90, Appli	C 392	9.6	60.0	48	3	US-08-478-029A-37	Sequence 37, Appli

393	9.6	60.0	48	3	US-08-478-029A-38	Sequence 38, Appl	465	9.4	58.8	30	4	US-09-004-422-45	Sequence 45, Appl
394	9.6	60.0	49	1	US-08-644-271-26	Sequence 26, Appl	467	9.4	58.8	30	4	US-09-004-422-53	Sequence 53, Appl
395	9.6	60.0	49	3	US-09-363-970-27	Sequence 27, Appl	468	9.4	58.8	33	1	US-07-979-966A-16	Sequence 16, Appl
396	9.6	60.0	49	4	US-09-077-955-23	Sequence 23, Appl	469	9.4	58.8	36	1	US-08-147-966A-14	Sequence 14, Appl
397	9.6	60.0	50	1	US-07-994-469A-25	Sequence 25, Appl	470	9.4	58.8	37	1	US-07-621-130B-12	Sequence 12, Appl
398	9.6	60.0	50	1	US-08-445-640-20	Sequence 20, Appl	471	9.4	58.8	37	1	US-08-018-489C-12	Sequence 12, Appl
399	9.6	60.0	50	1	US-08-170-558-20	Sequence 20, Appl	472	9.4	58.8	44	3	US-09-227-850-11	Sequence 11, Appl
400	9.6	60.0	50	3	US-08-447-314-20	Sequence 20, Appl	473	9.4	58.8	45	1	US-08-450-332-3	Sequence 3, Appl
401	9.6	60.0	50	3	US-08-445-461-20	Sequence 20, Appl	474	9.4	58.8	45	2	US-08-637-640-3	Sequence 3, Appl
402	9.6	60.0	52	1	US-07-994-469A-35	Sequence 35, Appl	475	9.4	58.8	46	2	US-09-004-406C-3	Sequence 3, Appl
403	9.6	60.0	58	3	US-08-833-167-22	Sequence 22, Appl	476	9.4	58.8	47	1	US-07-749-446-5	Sequence 5, Appl
404	9.6	60.0	63	3	US-09-344-837A-22	Sequence 22, Appl	477	9.4	58.8	47	1	US-09-432-978-77A	Sequence 277A, Ap
405	9.6	60.0	63	4	US-08-833-167-20	Sequence 20, Appl	478	9.4	58.8	48	1	US-07-959-284-17	Sequence 17, Appl
406	9.6	60.0	64	4	US-09-344-837A-20	Sequence 20, Appl	479	9.4	58.8	48	2	US-08-308-736A-17	Sequence 17, Appl
407	9.6	60.0	64	4	US-09-180-827-15	Sequence 15, Appl	480	9.4	58.8	48	4	US-08-645-107A-17	Sequence 17, Appl
408	9.6	60.0	69	4	US-09-011-336-65	Sequence 65, Appl	481	9.4	58.8	48	4	US-09-197-349-17	Sequence 17, Appl
409	9.6	60.0	73	1	US-08-208-886C-18	Sequence 18, Appl	482	9.4	58.8	48	4	US-09-031-693-17	Sequence 17, Appl
410	9.6	60.0	73	1	US-08-704-744-18	Sequence 18, Appl	483	9.4	58.8	48	5	PCT-US93-09649A-17	Sequence 17, Appl
411	9.6	60.0	73	1	US-08-469-557-18	Sequence 18, Appl	484	9.4	58.8	48	5	PCT-US93-09649A-17	Sequence 17, Appl
412	9.6	60.0	73	2	US-08-290-793B-18	Sequence 18, Appl	485	9.4	58.8	51	1	US-08-530-492-125	Sequence 125, App
413	9.6	60.0	75	1	US-08-219-012-87	Sequence 87, Appl	486	9.4	58.8	51	3	US-08-906-517-125	Sequence 6, Appl
414	9.6	60.0	75	3	US-08-687-421-275	Sequence 275, App	487	9.4	58.8	61	3	US-08-465-687A-6	Sequence 6, Appl
415	9.6	60.0	75	3	US-09-060-756-163	Sequence 163, App	488	9.4	58.8	61	3	US-09-520-210-6	Sequence 6, Appl
416	9.6	60.0	75	4	US-09-670-314-163	Sequence 163, App	489	9.4	58.8	61	3	US-09-520-210-6	Sequence 6, Appl
417	9.6	60.0	79	4	US-09-023-228B-14	Sequence 14, Appl	490	9.4	58.8	63	4	US-09-520-210-6	Sequence 6, Appl
418	9.6	60.0	79	4	US-09-163-025B-14	Sequence 14, Appl	491	9.4	58.8	71	1	US-08-400-440A-96	Sequence 96, Appl
419	9.6	60.0	79	4	US-10-037-882-14	Sequence 14, Appl	492	9.4	58.8	71	1	US-08-400-440A-101	Sequence 101, App
420	9.6	60.0	84	4	US-09-313-894A-3374	Sequence 3974, Ap	493	9.4	58.8	71	1	US-08-463-093A-96	Sequence 96, Appl
421	9.6	60.0	85	1	US-07-741-931-5	Sequence 5, Appl	494	9.4	58.8	71	1	US-08-460-888A-96	Sequence 96, Appl
422	9.6	60.0	85	1	US-07-937-132A-5	Sequence 5, Appl	495	9.4	58.8	71	1	US-08-460-888A-101	Sequence 101, App
423	9.6	60.0	85	1	US-07-937-132A-6	Sequence 6, Appl	496	9.4	58.8	71	2	US-08-894-578-96	Sequence 96, Appl
424	9.6	60.0	86	1	US-07-741-931-7	Sequence 7, Appl	497	9.4	58.8	71	2	US-08-894-578-96	Sequence 96, Appl
425	9.6	60.0	86	1	US-07-937-132A-7	Sequence 7, Appl	498	9.4	58.8	71	2	US-08-894-578-96	Sequence 96, Appl
426	9.6	60.0	87	1	US-08-433-126A-108	Sequence 108, App	499	9.4	58.8	71	2	US-08-894-578-96	Sequence 96, Appl
427	9.6	60.0	87	1	US-08-433-126A-108	Sequence 108, App	500	9.4	58.8	71	4	US-09-412-017-96	Sequence 96, Appl
428	9.6	60.0	87	5	US-08-976-413A-108	Sequence 108, App	501	9.4	58.8	71	4	US-09-412-017-96	Sequence 96, Appl
429	9.6	60.0	87	5	PCT-US96-06059-108	Sequence 108, App	502	9.4	58.8	79	3	US-08-687-421-399	Sequence 399, App
430	9.6	60.0	90	1	US-08-317-403A-18	Sequence 18, App	503	9.4	58.8	86	1	US-08-442-062-59	Sequence 59, Appl
431	9.6	60.0	90	1	US-08-471-985A-18	Sequence 18, App	504	9.4	58.8	86	1	US-08-442-062-59	Sequence 59, Appl
432	9.6	60.0	90	5	PCT-US95-12401A-18	Sequence 11, Appl	505	9.4	58.8	86	1	US-08-748-697A-59	Sequence 59, Appl
433	9.6	60.0	92	3	US-09-129-740-7	Sequence 7, Appl	506	9.4	58.8	86	4	US-09-165-616-59	Sequence 59, Appl
434	9.6	60.0	92	3	US-09-568-527-7	Sequence 7, Appl	507	9.4	58.8	90	3	US-08-483-511-33	Sequence 33, Appl
435	9.6	60.0	98	5	PCT-US94-06456-11	Sequence 34, Appl	508	9.4	58.8	93	3	PCT-US93-01009-33	Sequence 33, Appl
436	9.6	60.0	98	5	PCT-US94-06456-10	Sequence 34, Appl	509	9.4	58.8	100	1	US-08-976-413A-434	Sequence 434, App
437	9.6	60.0	100	3	US-08-145-705A-34	Sequence 34, Appl	510	9.4	58.8	100	1	US-08-976-413A-434	Sequence 434, App
438	9.6	58.8	18	3	US-09-197-380-37	Sequence 37, Appl	511	9.2	57.5	17	3	US-09-027-998A-41	Sequence 41, Appl
439	9.4	58.8	20	1	US-08-099-868-7	Sequence 7, Appl	512	9.2	57.5	19	3	US-09-058-488-57	Sequence 57, Appl
440	9.4	58.8	20	2	US-08-256-426B-78	Sequence 78, Appl	513	9.2	57.5	20	1	US-07-829-016-9	Sequence 16, Appl
441	9.4	58.8	21	2	US-08-600-999-7	Sequence 9, Appl	514	9.2	57.5	20	1	US-08-062-632-1	Sequence 2, Appl
442	9.4	58.8	21	2	US-08-600-999-9	Sequence 9, Appl	515	9.2	57.5	20	1	US-08-062-632-1	Sequence 2, Appl
443	9.4	58.8	21	2	US-09-082-762-11	Sequence 11, Appl	516	9.2	57.5	20	2	US-08-487-651-9	Sequence 9, Appl
444	9.4	58.8	21	4	US-08-448-256-21	Sequence 21, Appl	517	9.2	57.5	20	2	US-08-487-651-9	Sequence 9, Appl
445	9.4	58.8	22	1	US-08-599-252-36	Sequence 36, Appl	518	9.2	57.5	20	4	US-09-444-053-52	Sequence 52, Appl
446	9.4	58.8	22	1	US-08-182-172-17	Sequence 17, Appl	519	9.2	57.5	20	4	US-09-732-199A-51	Sequence 51, Appl
447	9.4	58.8	22	5	PCT-US96-06352-36	Sequence 36, Appl	520	9.2	57.5	21	3	US-09-253-025-32	Sequence 32, Appl
448	9.4	58.8	22	5	PCT-US96-06352-36	Sequence 36, Appl	521	9.2	57.5	21	3	US-09-253-025-32	Sequence 32, Appl
449	9.4	58.8	22	5	PCT-US96-06352-36	Sequence 36, Appl	522	9.2	57.5	21	3	US-08-335-844A-61	Sequence 61, Appl
450	9.4	58.8	24	2	US-08-202-033-10	Sequence 10, Appl	523	9.2	57.5	21	4	US-08-936-107A-26	Sequence 26, Appl
451	9.4	58.8	24	2	US-08-548-974-10	Sequence 10, Appl	524	9.2	57.5	21	4	US-08-936-107A-26	Sequence 26, Appl
452	9.4	58.8	24	4	US-08-637-823B-10	Sequence 10, Appl	525	9.2	57.5	21	4	US-08-936-107A-26	Sequence 26, Appl
453	9.4	58.8	24	4	US-09-614-957D-10	Sequence 10, Appl	526	9.2	57.5	22	1	US-08-129-366-61	Sequence 61, Appl
454	9.4	58.8	24	4	US-08-637-823B-10	Sequence 10, Appl	527	9.2	57.5	22	1	US-08-078-222B-6	Sequence 6, Appl
455	9.4	58.8	27	3	US-08-403-555-1	Sequence 1, Appl	528	9.2	57.5	23	1	US-08-078-222B-6	Sequence 6, Appl
456	9.4	58.8	27	3	US-09-331-581-12	Sequence 12, Appl	529	9.2	57.5	23	2	US-08-661-330A-6	Sequence 6, Appl
457	9.4	58.8	29	3	US-08-506-553C-10	Sequence 10, Appl	530	9.2	57.5	23	3	US-09-038-217A-6	Sequence 6, Appl
458	9.4	58.8	29	3	US-09-389-155-37	Sequence 37, Appl	531	9.2	57.5	23	3	US-09-038-217A-6	Sequence 6, Appl
459	9.4	58.8	30	1	US-08-361-920-17	Sequence 17, Appl	532	9.2	57.5	23	4	US-09-609-154-43	Sequence 43, Appl
460	9.4	58.8	30	1	US-08-229-781-45	Sequence 45, Appl	533	9.2	57.5	23	4	US-09-609-154-43	Sequence 43, Appl
461	9.4	58.8	30	1	US-08-229-781-53	Sequence 53, Appl	534	9.2	57.5	23	4	US-09-609-154-43	Sequence 43, Appl
462	9.4	58.8	30	1	US-08-630-918-45	Sequence 45, Appl	535	9.2	57.5	24	1	US-08-447-034-6	Sequence 6, Appl
463	9.4	58.8	30	1	US-08-630-918-53	Sequence 53, Appl	536	9.2	57.5	24	1	US-08-520-928-3	Sequence 3, Appl
464	9.4	58.8	30	1	US-08-479-939-77	Sequence 77, Appl	537	9.2	57.5	24	2	US-08-880-829-17	Sequence 17, Appl
465	9.4	58.8	30	1	US-08-483-432-77	Sequence 77, Appl	538	9.2	57.5	24	3	US-08-880-829-19	Sequence 19, Appl

539	9.2	57.5	24	4	US-09-006-755B-10	Sequence 10, Appl	C 612	9.2	57.5	50	4	US-08-961-309-34	Sequence 34, Appl
C 540	9.2	57.5	25	3	US-08-986-727-26	Sequence 26, Appl	C 613	9.2	57.5	51	3	US-08-889-502-30	Sequence 30, Appl
C 541	9.2	57.5	26	4	US-09-534-638-16	Sequence 16, Appl	C 614	9.2	57.5	51	4	US-08-403-416A-14	Sequence 14, Appl
C 542	9.2	57.5	26	4	US-09-733-199A-6	Sequence 6, Appl	C 615	9.2	57.5	52	3	US-08-889-502-29	Sequence 29, Appl
C 543	9.2	57.5	26	4	US-09-538-709-34	Sequence 34, Appl	C 616	9.2	57.5	52	3	US-09-027-998A-18	Sequence 18, Appl
C 544	9.2	57.5	27	1	US-08-678-304-7	Sequence 7, Appl	C 617	9.2	57.5	52	3	US-09-027-998A-19	Sequence 19, Appl
C 545	9.2	57.5	27	4	US-09-253-316-34	Sequence 34, Appl	618	9.2	57.5	54	2	US-08-832-535-8	Sequence 8, Appl
C 546	9.2	57.5	27	4	US-09-457-066-33	Sequence 33, Appl	619	9.2	57.5	54	3	US-09-019-485-15	Sequence 15, Appl
C 547	9.2	57.5	27	4	US-09-564-595D-31	Sequence 31, Appl	620	9.2	57.5	54	4	US-09-528-436B-14	Sequence 14, Appl
C 548	9.2	57.5	27	4	US-09-706-968-33	Sequence 33, Appl	C 621	9.2	57.5	55	3	US-08-362-525-9	Sequence 9, Appl
C 549	9.2	57.5	27	4	US-09-585-228-17	Sequence 17, Appl	622	9.2	57.5	59	3	US-08-362-525-10	Sequence 10, Appl
C 550	9.2	57.5	28	2	US-08-683-743-16	Sequence 16, Appl	623	9.2	57.5	59	4	US-08-891-292A-34	Sequence 34, Appl
C 551	9.2	57.5	28	2	US-08-600-999-10	Sequence 10, Appl	624	9.2	57.5	59	4	US-08-891-292A-32	Sequence 32, Appl
C 552	9.2	57.5	29	2	US-08-537-402-3	Sequence 3, Appl	625	9.2	57.5	60	4	US-09-927-737C-32	Sequence 32, Appl
C 553	9.2	57.5	29	2	US-08-233-016-13	Sequence 13, Appl	626	9.2	57.5	59	4	US-09-927-737C-34	Sequence 34, Appl
C 554	9.2	57.5	29	3	US-09-121-539-4	Sequence 4, Appl	627	9.2	57.5	60	2	US-08-667-916-26	Sequence 26, Appl
C 555	9.2	57.5	29	3	US-09-121-539-5	Sequence 5, Appl	628	9.2	57.5	60	3	US-09-128-614-26	Sequence 26, Appl
C 556	9.2	57.5	30	2	US-08-600-999-8	Sequence 8, Appl	629	9.2	57.5	62	3	US-08-956-182-25	Sequence 25, Appl
C 557	9.2	57.5	30	3	US-08-666-354A-8	Sequence 8, Appl	C 630	9.2	57.5	65	3	US-08-986-727-16	Sequence 16, Appl
C 558	9.2	57.5	30	4	US-09-374-038-9	Sequence 9, Appl	C 631	9.2	57.5	67	2	US-08-771-624B-18	Sequence 18, Appl
C 559	9.2	57.5	30	4	US-09-638-119-9	Sequence 9, Appl	C 632	9.2	57.5	69	2	US-08-184-009-101	Sequence 101, Appl
C 560	9.2	57.5	30	4	US-09-529-279-23	Sequence 23, Appl	C 633	9.2	57.5	69	2	US-08-458-356-101	Sequence 101, Appl
C 561	9.2	57.5	30	4	US-09-538-709-20	Sequence 20, Appl	C 634	9.2	57.5	69	3	US-08-460-736-101	Sequence 101, Appl
C 562	9.2	57.5	30	4	US-10-158-895-23	Sequence 23, Appl	C 635	9.2	57.5	69	4	US-09-535-370-101	Sequence 101, Appl
C 563	9.2	57.5	32	2	US-08-880-829-8	Sequence 8, Appl	636	9.2	57.5	70	1	US-08-277-547-2	Sequence 2, Appl
C 564	9.2	57.5	33	1	US-08-438-639-55	Sequence 55, Appl	637	9.2	57.5	70	2	US-08-880-829-13	Sequence 13, Appl
C 565	9.2	57.5	33	1	US-07-813-338A-55	Sequence 55, Appl	638	9.2	57.5	70	2	US-08-880-829-12	Sequence 12, Appl
C 566	9.2	57.5	34	3	US-08-956-182-37	Sequence 37, Appl	639	9.2	57.5	70	5	PCT-US95-08782-2	Sequence 2, Appl
C 567	9.2	57.5	36	2	US-08-585-585A-13	Sequence 13, Appl	640	9.2	57.5	71	3	US-08-584-760A-35	Sequence 35, Appl
C 568	9.2	57.5	36	2	US-08-687-916-27	Sequence 27, Appl	641	9.2	57.5	73	2	US-08-880-829-12	Sequence 12, Appl
C 569	9.2	57.5	36	3	US-08-685-808-12	Sequence 12, Appl	C 642	9.2	57.5	78	1	US-08-729-601A-20	Sequence 20, Appl
C 570	9.2	57.5	36	3	US-08-505-860C-12	Sequence 12, Appl	C 643	9.2	57.5	78	3	US-07-982-712-10	Sequence 10, Appl
C 571	9.2	57.5	36	3	US-09-138-614-27	Sequence 27, Appl	C 644	9.2	57.5	80	3	US-09-039-555B-4	Sequence 4, Appl
C 572	9.2	57.5	37	1	US-08-150-331-8	Sequence 8, Appl	C 645	9.2	57.5	83	4	US-08-977-378-30	Sequence 30, Appl
C 573	9.2	57.5	37	1	US-08-150-331-29	Sequence 29, Appl	646	9.2	57.5	86	3	US-08-976-413A-343	Sequence 343, Appl
C 574	9.2	57.5	37	4	US-08-569-284-8	Sequence 8, Appl	647	9.2	57.5	87	1	US-08-433-126A-226	Sequence 226, Appl
C 575	9.2	57.5	37	4	US-08-569-284-8	Sequence 8, Appl	648	9.2	57.5	87	1	US-08-433-126A-226	Sequence 226, Appl
C 576	9.2	57.5	39	1	US-08-464-531-105	Sequence 105, Appl	649	9.2	57.5	87	5	PCT-US96-06059-226	Sequence 226, Appl
C 577	9.2	57.5	39	2	US-08-461-598-105	Sequence 105, Appl	C 650	9.2	57.5	89	1	US-07-964-624D-31	Sequence 31, Appl
C 578	9.2	57.5	39	3	US-08-322-137-105	Sequence 105, Appl	C 651	9.2	57.5	89	1	US-07-964-624D-31	Sequence 31, Appl
C 579	9.2	57.5	39	3	US-08-582-333A-41	Sequence 41, Appl	C 652	9.2	57.5	89	1	US-08-442-062-31	Sequence 31, Appl
C 580	9.2	57.5	40	3	US-08-362-525-6	Sequence 6, Appl	C 653	9.2	57.5	89	1	US-08-748-697A-31	Sequence 31, Appl
C 581	9.2	57.5	42	2	US-08-466-860-41	Sequence 41, Appl	C 654	9.2	57.5	89	4	US-09-165-616-31	Sequence 31, Appl
C 582	9.2	57.5	42	3	US-08-472-040A-41	Sequence 41, Appl	C 655	9.2	57.5	95	3	US-08-789-333F-96	Sequence 96, Appl
C 583	9.2	57.5	42	3	US-08-276-776-41	Sequence 41, Appl	C 656	9.2	57.5	95	4	US-08-787-738B-96	Sequence 96, Appl
C 584	9.2	57.5	42	3	US-08-471-209-41	Sequence 41, Appl	657	9.2	57.5	99	3	US-09-035-820-2	Sequence 2, Appl
C 585	9.2	57.5	44	3	US-09-027-998A-12	Sequence 12, Appl	658	9.2	57.5	14	3	US-09-275-850-23	Sequence 23, Appl
C 586	9.2	57.5	44	3	US-09-027-998A-13	Sequence 13, Appl	C 659	9.2	56.2	15	1	US-08-311-486C-61	Sequence 61, Appl
C 587	9.2	57.5	45	3	US-09-027-998A-9	Sequence 9, Appl	660	9.2	56.2	15	3	US-09-275-850-17	Sequence 17, Appl
C 588	9.2	57.5	45	3	US-09-027-998A-10	Sequence 10, Appl	661	9.2	56.2	17	4	US-08-584-040-2622	Sequence 2622, Appl
C 589	9.2	57.5	45	3	US-09-027-998A-15	Sequence 15, Appl	662	9.2	56.2	17	4	US-08-584-040-2623	Sequence 2623, Appl
C 590	9.2	57.5	45	3	US-09-027-998A-16	Sequence 16, Appl	663	9.2	56.2	17	4	US-09-371-772B-1146	Sequence 1146, Appl
C 591	9.2	57.5	46	4	US-08-977-378-19	Sequence 19, Appl	664	9.2	56.2	17	4	US-09-371-772B-1147	Sequence 1147, Appl
C 592	9.2	57.5	47	4	US-09-671-317-574	Sequence 574, Appl	665	9.2	56.2	18	2	US-09-197-008-21	Sequence 21, Appl
C 593	9.2	57.5	47	4	US-09-422-978-583	Sequence 583, Appl	666	9.2	56.2	18	4	US-09-394-455-49	Sequence 49, Appl
C 594	9.2	57.5	47	4	US-09-422-978-586	Sequence 2566, Appl	667	9.2	56.2	18	4	US-08-422-978-7271	Sequence 7271, Appl
C 595	9.2	57.5	48	1	US-08-171-389-200	Sequence 200, Appl	668	9.2	56.2	19	1	US-08-433-783-36	Sequence 36, Appl
C 596	9.2	57.5	48	1	US-08-123-936-200	Sequence 200, Appl	669	9.2	56.2	19	2	US-08-337-358-36	Sequence 36, Appl
C 597	9.2	57.5	48	1	US-08-475-228A-200	Sequence 200, Appl	670	9.2	56.2	19	5	PCT-US93-12144-36	Sequence 36, Appl
C 598	9.2	57.5	48	3	US-08-483-080A-200	Sequence 200, Appl	671	9.2	56.2	19	5	PCT-US95-07537A-36	Sequence 36, Appl
C 599	9.2	57.5	48	4	US-09-354-947-200	Sequence 200, Appl	672	9.2	56.2	19	5	PCT-US95-07537B-36	Sequence 36, Appl
C 600	9.2	57.5	48	5	PCT-US93-12388-200	Sequence 200, Appl	C 673	9.2	56.2	20	1	US-07-743-518-4	Sequence 4, Appl
C 601	9.2	57.5	50	1	US-08-530-492-55	Sequence 55, Appl	C 674	9.2	56.2	20	1	US-07-743-518-9	Sequence 9, Appl
C 602	9.2	57.5	50	1	US-08-472-194A-19	Sequence 19, Appl	C 675	9.2	56.2	20	1	US-07-977-484A-39	Sequence 39, Appl
C 603	9.2	57.5	50	3	US-08-463-903-64	Sequence 64, Appl	676	9.2	56.2	20	1	US-08-580-401-4	Sequence 4, Appl
C 604	9.2	57.5	50	3	US-08-463-903-65	Sequence 65, Appl	677	9.2	56.2	20	1	US-08-294-424-8	Sequence 8, Appl
C 605	9.2	57.5	50	3	US-09-262-142-19	Sequence 19, Appl	C 678	9.2	56.2	20	2	US-08-468-551-1	Sequence 1, Appl
C 606	9.2	57.5	50	3	US-08-906-517-55	Sequence 55, Appl	C 679	9.2	56.2	20	2	US-08-256-426B-39	Sequence 39, Appl
C 607	9.2	57.5	50	3	US-09-282-147-43	Sequence 43, Appl	C 680	9.2	56.2	20	2	US-09-166-203-44	Sequence 44, Appl
C 608	9.2	57.5	50	4	US-08-849-567A-19	Sequence 19, Appl	C 681	9.2	56.2	20	3	US-09-166-203-51	Sequence 51, Appl
C 609	9.2	57.5	50	4	US-07-935-695-64	Sequence 64, Appl	682	9.2	56.2	20	3	US-09-280-799-63	Sequence 83, Appl
C 610	9.2	57.5	50	4	US-07-935-695-65	Sequence 65, Appl	683	9.2	56.2	20	3	US-09-488-671-47	Sequence 47, Appl
C 611	9.2	57.5	50	4	US-08-961-309-33	Sequence 33, Appl	684	9.2	56.2	20	3	US-09-560-594-49	Sequence 49, Appl

C 685	9	56.2	20	3	US-09-377-309-44	Sequence 44, Appl	C 758	9	56.2	27	2	US-08-634-224-6	Sequence 6, Appl
C 686	9	56.2	20	3	US-09-377-309-51	Sequence 51, Appl	C 759	9	56.2	27	2	US-08-232-081B-32	Sequence 32, Appl
C 687	9	56.2	20	4	US-09-398-179-18	Sequence 18, Appl	C 760	9	56.2	27	2	US-08-634-400-6	Sequence 6, Appl
C 688	9	56.2	20	4	US-09-488-074-13	Sequence 13, Appl	C 761	9	56.2	27	2	US-08-635-878-6	Sequence 6, Appl
C 689	9	56.2	20	4	US-09-417-822-11	Sequence 11, Appl	C 762	9	56.2	27	2	US-08-770-057-6	Sequence 6, Appl
C 690	9	56.2	20	4	US-09-657-346A-33	Sequence 33, Appl	C 763	9	56.2	27	3	US-08-803-085-33	Sequence 33, Appl
C 691	9	56.2	20	4	US-09-422-978-3992	Sequence 3992, Ap	C 764	9	56.2	27	3	US-08-354-679C-7	Sequence 7, Appl
C 692	9	56.2	20	4	US-09-920-759-87	Sequence 87, Appl	C 765	9	56.2	27	3	US-08-523-894-59	Sequence 59, Appl
C 693	9	56.2	20	4	US-09-198-452A-574	Sequence 2574, Ap	C 766	9	56.2	27	3	US-09-335-697B-6	Sequence 6, Appl
C 694	9	56.2	20	4	US-09-198-452A-6492	Sequence 6492, Ap	C 767	9	56.2	27	3	US-08-393-272B-7	Sequence 7, Appl
C 695	9	56.2	20	4	US-09-198-452A-6635	Sequence 6635, Ap	C 768	9	56.2	27	4	US-08-443-580F-7	Sequence 7, Appl
C 696	9	56.2	21	1	US-07-725-076B-2	Sequence 2, Appl	C 769	9	56.2	27	4	US-09-335-697B-6	Sequence 6, Appl
C 697	9	56.2	21	1	US-08-271-874-2	Sequence 20, Appl	C 770	9	56.2	27	4	US-08-571-263-7	Sequence 7, Appl
C 698	9	56.2	21	2	US-08-809-267-20	Sequence 20, Appl	C 771	9	56.2	27	4	US-09-142-593-35	Sequence 35, Appl
C 699	9	56.2	21	2	US-08-809-267-21	Sequence 21, Appl	C 772	9	56.2	27	5	PCT-US93-08157-7	Sequence 7, Appl
C 700	9	56.2	21	2	US-08-557-614-8	Sequence 9, Appl	C 773	9	56.2	28	1	US-08-495-743-36	Sequence 36, Appl
C 701	9	56.2	21	4	US-09-101-307D-9	Sequence 41, Appl	C 774	9	56.2	28	1	US-08-495-739-36	Sequence 36, Appl
C 702	9	56.2	21	5	US-09-394-455-41	Sequence 20, Appl	C 775	9	56.2	28	1	US-08-495-741-36	Sequence 36, Appl
C 703	9	56.2	21	5	PCT-US95-13662A-20	Sequence 20, Appl	C 776	9	56.2	28	2	US-08-911-434A-9	Sequence 9, Appl
C 704	9	56.2	21	5	PCT-US95-13662A-21	Sequence 21, Appl	C 777	9	56.2	28	3	US-08-062-023-36	Sequence 36, Appl
C 705	9	56.2	22	2	US-08-564-090A-17	Sequence 17, Appl	C 778	9	56.2	28	4	US-09-020-846-20	Sequence 20, Appl
C 706	9	56.2	22	2	US-09-103-875-101	Sequence 101, App	C 779	9	56.2	28	4	US-09-537-168-40	Sequence 40, Appl
C 707	9	56.2	22	3	US-09-302-681-78	Sequence 78, Appl	C 780	9	56.2	28	4	US-09-438-954-21	Sequence 21, Appl
C 708	9	56.2	22	3	PCT-US94-06698-17	Sequence 17, Appl	C 781	9	56.2	29	1	US-08-217-210B-26	Sequence 26, Appl
C 709	9	56.2	22	5	US-08-839-306-5	Sequence 5, Appl	C 782	9	56.2	29	3	US-08-933-983-46	Sequence 2, Appl
C 710	9	56.2	23	2	US-08-978-454-5	Sequence 5, Appl	C 783	9	56.2	29	4	US-09-304-232-853	Sequence 2, Appl
C 711	9	56.2	23	3	US-09-385-288-5	Sequence 5, Appl	C 784	9	56.2	30	1	US-08-160-670A-39	Sequence 39, Appl
C 712	9	56.2	23	3	US-09-527-030C-39	Sequence 39, App	C 785	9	56.2	30	1	US-08-057-167-19	Sequence 19, Appl
C 713	9	56.2	23	4	US-09-513-458-42	Sequence 42, Appl	C 786	9	56.2	30	1	US-08-229-781-43	Sequence 43, Appl
C 714	9	56.2	23	4	US-07-994-469A-46	Sequence 46, Appl	C 787	9	56.2	30	1	US-08-384-708A-9	Sequence 9, Appl
C 715	9	56.2	24	3	US-08-933-983-33	Sequence 33, Appl	C 788	9	56.2	30	1	US-08-630-918-43	Sequence 43, Appl
C 716	9	56.2	24	4	US-09-670-075A-11	Sequence 11, Appl	C 789	9	56.2	30	1	US-08-352-179-3	Sequence 2, Appl
C 717	9	56.2	25	1	US-08-336-132-8	Sequence 8, Appl	C 790	9	56.2	30	1	US-08-352-179-3	Sequence 3, Appl
C 718	9	56.2	25	1	US-08-664-449-60	Sequence 60, Appl	C 791	9	56.2	30	2	US-08-356-361-17	Sequence 17, Appl
C 719	9	56.2	25	1	US-08-743-130A-19	Sequence 19, Appl	C 792	9	56.2	30	2	US-08-769-667A-17	Sequence 17, Appl
C 720	9	56.2	25	2	US-08-192-946-22	Sequence 22, Appl	C 793	9	56.2	30	2	US-08-600-999-3	Sequence 3, Appl
C 721	9	56.2	25	3	US-09-417-822-16	Sequence 16, Appl	C 794	9	56.2	30	3	US-08-913-842-55	Sequence 55, Appl
C 722	9	56.2	25	4	US-08-982-285-50	Sequence 50, Appl	C 795	9	56.2	30	3	US-09-242-797-4	Sequence 4, Appl
C 723	9	56.2	25	4	US-08-982-285-51	Sequence 51, Appl	C 796	9	56.2	30	3	US-08-687-421-9	Sequence 9, Appl
C 724	9	56.2	25	4	US-09-358-856C-39	Sequence 39, Appl	C 797	9	56.2	30	3	US-09-494-252-1	Sequence 1, Appl
C 725	9	56.2	25	4	US-08-467-420A-43	Sequence 43, Appl	C 798	9	56.2	30	4	US-09-004-422-13	Sequence 13, Appl
C 726	9	56.2	26	1	US-08-470-110A-43	Sequence 43, Appl	C 800	9	56.2	30	4	US-09-052-919-53	Sequence 53, Appl
C 727	9	56.2	26	1	US-08-667-769A-43	Sequence 43, Appl	C 801	9	56.2	30	4	US-09-101-272G-85	Sequence 85, Appl
C 728	9	56.2	26	2	US-08-940-371-43	Sequence 23, Appl	C 802	9	56.2	30	4	US-09-765-873A-22	Sequence 22, Appl
C 729	9	56.2	26	2	US-08-463-081B-23	Sequence 23, Appl	C 803	9	56.2	30	4	US-09-231-899-14	Sequence 74, Appl
C 730	9	56.2	26	2	US-08-463-081B-24	Sequence 24, Appl	C 804	9	56.2	30	4	US-09-937-832-2	Sequence 2, Appl
C 731	9	56.2	26	2	US-08-461-379A-23	Sequence 23, Appl	C 805	9	56.2	30	5	PCT-US93-05412-19	Sequence 19, Appl
C 732	9	56.2	26	2	US-08-461-379A-24	Sequence 24, Appl	C 806	9	56.2	31	2	US-08-466-120-3	Sequence 3, Appl
C 733	9	56.2	26	2	US-08-462-390B-23	Sequence 23, Appl	C 807	9	56.2	31	2	US-08-483-636-50	Sequence 50, Appl
C 734	9	56.2	26	2	US-08-462-390B-24	Sequence 24, Appl	C 808	9	56.2	31	2	US-08-600-999-11	Sequence 11, Appl
C 735	9	56.2	26	2	US-08-859-998-1122	Sequence 1122, Ap	C 809	9	56.2	31	2	US-08-483-632-80	Sequence 80, Appl
C 736	9	56.2	26	3	US-08-463-074B-23	Sequence 23, Appl	C 810	9	56.2	31	3	US-08-803-085-20	Sequence 20, Appl
C 737	9	56.2	26	3	US-08-463-074B-24	Sequence 24, Appl	C 811	9	56.2	31	3	US-08-688-034-6	Sequence 6, Appl
C 738	9	56.2	26	3	US-08-465-585C-23	Sequence 23, Appl	C 812	9	56.2	32	2	US-08-356-361-19	Sequence 19, Appl
C 739	9	56.2	26	3	US-08-465-585C-24	Sequence 24, Appl	C 813	9	56.2	32	2	US-08-769-967A-19	Sequence 19, Appl
C 740	9	56.2	26	3	US-08-652-446-23	Sequence 23, Appl	C 814	9	56.2	32	2	US-08-859-968A-1208	Sequence 1208, Ap
C 741	9	56.2	26	3	US-08-652-446-24	Sequence 24, Appl	C 815	9	56.2	32	3	US-09-394-268-4	Sequence 4, Appl
C 742	9	56.2	26	3	US-08-637-647-43	Sequence 43, Appl	C 816	9	56.2	32	4	US-09-225-928B-1208	Sequence 1208, Ap
C 743	9	56.2	26	3	US-09-334-489-7	Sequence 7, Appl	C 817	9	56.2	32	4	US-09-687-748-4	Sequence 4, Appl
C 744	9	56.2	26	3	US-09-225-928-1122	Sequence 1122, Ap	C 818	9	56.2	32	4	US-09-225-201B-1208	Sequence 1208, Ap
C 745	9	56.2	26	4	US-09-225-201B-1122	Sequence 1122, Ap	C 819	9	56.2	32	4	US-09-420-819-8	Sequence 8, Appl
C 746	9	56.2	26	5	PCT-US95-17082A-43	Sequence 43, Appl	C 820	9	56.2	33	1	US-08-253-877C-41	Sequence 41, Appl
C 747	9	56.2	27	1	US-07-601-094-12	Sequence 12, Appl	C 821	9	56.2	33	2	US-08-452-164A-11	Sequence 11, Appl
C 748	9	56.2	27	1	US-07-601-094-13	Sequence 13, Appl	C 822	9	56.2	34	2	US-09-101-272G-86	Sequence 86, Appl
C 749	9	56.2	27	1	US-07-725-076B-3	Sequence 3, Appl	C 823	9	56.2	35	3	US-08-328-592-9	Sequence 9, Appl
C 750	9	56.2	27	1	US-08-012-735-13	Sequence 12, Appl	C 824	9	56.2	35	5	PCT-US95-11955A-40	Sequence 40, Appl
C 751	9	56.2	27	1	US-08-012-735-13	Sequence 13, Appl	C 825	9	56.2	36	1	US-08-612-895A-9	Sequence 9, Appl
C 752	9	56.2	27	1	US-08-073-103A-7	Sequence 7, Appl	C 826	9	56.2	36	2	US-09-211-930-13	Sequence 13, Appl
C 753	9	56.2	27	1	US-08-271-874-3	Sequence 3, Appl	C 827	9	56.2	36	2	US-09-211-930-14	Sequence 14, Appl
C 754	9	56.2	27	1	US-08-443-341-7	Sequence 7, Appl	C 828	9	56.2	36	3	US-09-093-293-9	Sequence 9, Appl
C 755	9	56.2	27	1	US-08-488-376-6	Sequence 6, Appl	C 829	9	56.2	36	3	US-09-340-993-13	Sequence 13, Appl
C 756	9	56.2	27	1	US-08-634-223-6	Sequence 6, Appl	C 830	9	56.2	36	3	US-09-340-993-14	Sequence 14, Appl
C 757	9	56.2	27	2	US-08-634-223-6	Sequence 6, Appl	C 831	9	56.2	36	3	US-09-340-993-14	Sequence 14, Appl

831	9	56.2	36	3	US-09-459-553-9	Sequence 9, Appli	904	9	56.2	54	4	US-09-887-586A-17	Sequence 17, Appli
C 832	9	56.2	36	4	US-09-468-442-13	Sequence 13, Appli	C 905	9	56.2	54	4	US-09-887-586A-18	Sequence 18, Appli
C 833	9	56.2	36	5	US-09-468-442-14	Sequence 14, Appli	C 906	9	56.2	54	4	US-09-885-752-17	Sequence 17, Appli
C 834	9	56.2	36	6	US-09-882-246-9	Sequence 9, Appli	C 907	9	56.2	54	4	US-09-895-752-18	Sequence 18, Appli
C 835	9	56.2	36	4	US-09-101-272G-10	Sequence 10, Appli	C 908	9	56.2	54	4	US-09-903-012B-11	Sequence 11, Appli
C 836	9	56.2	36	5	PCT-US94-10562A-9	Sequence 9, Appli	C 909	9	56.2	54	4	US-09-903-012B-18	Sequence 18, Appli
837	9	56.2	37	3	US-08-850-961-39	Sequence 39, Appli	C 910	9	56.2	55	5	PCT-US93-01901-17	Sequence 29, Appli
C 838	9	56.2	37	4	US-09-479-776-39	Sequence 39, Appli	C 911	9	56.2	56	6	US-08-821-827C-26	Sequence 26, Appli
C 839	9	56.2	37	4	US-09-366-009-18	Sequence 18, Appli	C 912	9	56.2	56	6	US-09-220-202B-26	Sequence 26, Appli
C 840	9	56.2	37	4	US-08-809-156B-18	Sequence 18, Appli	C 913	9	56.2	59	4	US-08-160-670A-35	Sequence 35, Appli
C 841	9	56.2	38	1	US-08-094-534-21	Sequence 21, Appli	C 914	9	56.2	59	5	PCT-US96-11985A-6	Sequence 6, Appli
C 842	9	56.2	38	1	US-08-581-543-21	Sequence 21, Appli	C 915	9	56.2	60	1	US-08-219-012-57	Sequence 57, Appli
C 843	9	56.2	38	5	PCT-US94-08000-21	Sequence 21, Appli	C 916	9	56.2	60	3	US-08-687-421-27	Sequence 27, Appli
C 844	9	56.2	38	6	5519127-43	Patent No. 5519127	C 917	9	56.2	60	3	US-08-290-736C-23	Sequence 23, Appli
C 845	9	56.2	39	1	US-08-253-155A-83	Sequence 83, Appli	C 918	9	56.2	60	4	US-09-626-929-14	Sequence 14, Appli
C 846	9	56.2	39	1	US-08-625-209A-12	Sequence 12, Appli	C 919	9	56.2	60	4	US-09-484-950-14	Sequence 14, Appli
C 847	9	56.2	39	3	US-08-853-733B-12	Sequence 12, Appli	C 920	9	56.2	60	4	US-09-408-392-14	Sequence 14, Appli
C 848	9	56.2	39	3	US-07-987-264-33	Sequence 33, Appli	C 921	9	56.2	60	4	US-09-626-930-14	Sequence 14, Appli
C 849	9	56.2	39	3	US-07-987-264-37	Sequence 37, Appli	C 922	9	56.2	60	4	US-09-626-528-14	Sequence 14, Appli
C 850	9	56.2	40	3	US-08-589-939-58	Sequence 58, Appli	C 923	9	56.2	60	4	US-09-626-595-14	Sequence 14, Appli
C 851	9	56.2	40	3	US-09-234-332-16	Sequence 16, Appli	C 924	9	56.2	60	4	US-09-694-863-14	Sequence 14, Appli
C 852	9	56.2	40	3	US-08-746-883-7	Sequence 7, Appli	C 925	9	56.2	65	4	US-09-527-030G-292	Sequence 292, App
C 853	9	56.2	40	3	US-08-974-691-11	Sequence 11, Appli	C 926	9	56.2	65	4	US-09-527-030G-293	Sequence 293, App
C 854	9	56.2	40	4	US-09-538-709-1193	Sequence 1193, Ap	C 927	9	56.2	65	4	US-09-527-030G-465	Sequence 465, App
C 855	9	56.2	41	1	US-08-294-424-6	Sequence 6, Appli	C 928	9	56.2	68	1	US-07-744-382C-33	Sequence 33, Appli
856	9	56.2	41	1	US-08-813-940-18	Sequence 18, Appli	C 929	9	56.2	68	5	PCT-US91-03540A-1	Sequence 1, Appli
C 857	9	56.2	41	5	PCT-US93-01901-25	Sequence 25, Appli	C 930	9	56.2	68	5	PCT-US92-06821A-39	Sequence 39, Appli
C 858	9	56.2	42	1	US-08-271-880A-52	Sequence 52, Appli	C 931	9	56.2	68	6	5168050-10	Patent No. 5168050
C 859	9	56.2	42	2	US-08-910-408-52	Sequence 52, Appli	C 932	9	56.2	71	1	US-08-472-255A-112	Sequence 112, App
C 860	9	56.2	42	2	US-09-249-215-52	Sequence 52, Appli	C 933	9	56.2	71	1	US-08-479-724A-112	Sequence 112, App
861	9	56.2	42	3	US-08-952-793-226	Sequence 226, App	C 934	9	56.2	71	2	US-08-488-402A-26	Sequence 26, Appli
C 862	9	56.2	42	3	US-09-849-928-226	Sequence 226, App	C 935	9	56.2	71	2	US-08-484-552A-26	Sequence 26, Appli
C 863	9	56.2	42	5	PCT-US96-09455A-226	Sequence 226, App	C 936	9	56.2	71	2	US-08-839-581A-9	Sequence 9, Appli
C 864	9	56.2	43	3	US-08-874-825-45	Sequence 45, Appli	C 937	9	56.2	71	3	US-08-472-256B-112	Sequence 112, App
865	9	56.2	43	3	US-08-663-824-45	Sequence 45, Appli	C 938	9	56.2	71	3	US-09-023-591A-9	Sequence 9, Appli
C 866	9	56.2	43	4	US-09-231-303-45	Sequence 45, Appli	C 939	9	56.2	71	3	US-08-952-793-151	Sequence 151, App
C 867	9	56.2	44	6	5252466-21	Patent No. 5252466	C 940	9	56.2	71	3	US-08-952-793-151	Sequence 151, App
868	9	56.2	45	1	US-07-921-796-2	Sequence 2, Appli	C 941	9	56.2	71	3	US-08-220-736C-25	Sequence 25, Appli
C 869	9	56.2	45	3	US-08-889-502-9	Sequence 9, Appli	C 942	9	56.2	71	3	US-08-230-736C-26	Sequence 26, Appli
C 870	9	56.2	45	4	US-08-406-824A-10	Sequence 10, Appli	C 943	9	56.2	71	3	US-08-230-736C-40	Sequence 40, Appli
C 871	9	56.2	45	6	5395760-9	Patent No. 5395760	C 944	9	56.2	71	4	US-08-290-736C-42	Sequence 42, Appli
C 872	9	56.2	46	3	US-08-803-085-19	Sequence 19, Appli	C 945	9	56.2	71	4	US-09-625-188-25	Sequence 25, Appli
C 873	9	56.2	46	4	US-09-740-002-6	Sequence 6, Appli	C 946	9	56.2	71	4	US-09-301-593-87	Sequence 87, Appli
C 874	9	56.2	47	1	US-08-530-492-144	Sequence 144, App	C 947	9	56.2	71	4	US-09-849-928-112	Sequence 112, App
C 875	9	56.2	47	1	US-08-530-492-144	Sequence 144, App	C 948	9	56.2	71	4	US-09-849-928-351	Sequence 351, App
C 876	9	56.2	47	2	US-08-811-492-126	Sequence 126, App	C 949	9	56.2	71	5	PCT-US96-09455A-112	Sequence 112, App
C 877	9	56.2	47	3	US-08-906-517-144	Sequence 144, App	C 950	9	56.2	71	5	PCT-US96-09455A-351	Sequence 351, App
C 878	9	56.2	47	3	US-08-906-517-144	Sequence 144, App	C 951	9	56.2	71	5	PCT-US96-09472-26	Sequence 26, Appli
C 879	9	56.2	47	4	US-09-671-317-942	Sequence 942, App	C 952	9	56.2	72	1	US-08-105-483-211	Sequence 211, App
C 880	9	56.2	47	4	US-09-422-978-2566	Sequence 2566, App	C 953	9	56.2	72	1	US-08-105-483-212	Sequence 212, App
C 881	9	56.2	47	4	US-09-422-978-2591	Sequence 2591, App	C 954	9	56.2	72	1	US-08-303-124-10	Sequence 10, Appli
C 882	9	56.2	47	4	US-09-422-978-3622	Sequence 3622, App	C 955	9	56.2	72	1	US-08-303-124-11	Sequence 11, Appli
C 883	9	56.2	48	3	US-09-063-893A-18	Sequence 18, Appli	C 956	9	56.2	72	1	US-08-204-729-11	Sequence 11, Appli
C 884	9	56.2	48	3	US-09-306-405-55	Sequence 55, Appli	C 957	9	56.2	72	1	US-08-204-729-11	Sequence 11, Appli
C 885	9	56.2	48	4	US-09-302-620B-68	Sequence 68, Appli	C 958	9	56.2	72	1	US-08-475-063-28	Sequence 28, Appli
C 886	9	56.2	49	3	US-08-889-502-10	Sequence 10, Appli	C 959	9	56.2	72	1	US-08-207-792-28	Sequence 28, Appli
C 887	9	56.2	49	4	US-09-061-154-8	Sequence 8, Appli	C 960	9	56.2	72	1	US-08-709-209-211	Sequence 211, App
C 888	9	56.2	50	2	US-08-833-468-6	Sequence 6, Appli	C 961	9	56.2	72	1	US-08-709-209-212	Sequence 212, App
C 889	9	56.2	50	2	US-08-628-747-24	Sequence 24, Appli	C 962	9	56.2	72	1	US-08-458-101-211	Sequence 211, App
C 890	9	56.2	51	2	US-08-116-778E-42	Sequence 42, Appli	C 963	9	56.2	72	1	US-08-458-101-212	Sequence 212, App
C 891	9	56.2	51	2	US-08-438-562-42	Sequence 42, Appli	C 964	9	56.2	72	2	US-08-480-697B-10	Sequence 10, Appli
C 892	9	56.2	51	2	US-08-483-528B-7	Sequence 7, Appli	C 965	9	56.2	72	2	US-08-480-697B-11	Sequence 11, Appli
C 893	9	56.2	51	3	US-08-673-799C-7	Sequence 7, Appli	C 966	9	56.2	73	1	US-08-475-063-29	Sequence 29, Appli
C 894	9	56.2	51	3	US-07-987-264-8	Sequence 8, Appli	C 967	9	56.2	73	1	US-08-207-792-29	Sequence 29, Appli
C 895	9	56.2	51	3	US-09-151-189-3	Sequence 3, Appli	C 968	9	56.2	73	3	US-08-102-005-1	Sequence 1, Appli
C 896	9	56.2	51	4	US-09-393-385B-7	Sequence 7, Appli	C 969	9	56.2	75	1	US-08-219-012-85	Sequence 85, Appli
C 897	9	56.2	51	4	US-09-394-455-55	Sequence 55, Appli	C 970	9	56.2	75	1	US-08-219-012-88	Sequence 88, Appli
C 898	9	56.2	54	1	US-08-353-400-11	Sequence 11, Appli	C 971	9	56.2	75	3	US-08-687-421-273	Sequence 273, App
C 899	9	56.2	54	1	US-08-353-400-12	Sequence 12, Appli	C 972	9	56.2	75	3	US-08-687-421-276	Sequence 276, App
C 900	9	56.2	54	4	US-09-398-395A-17	Sequence 17, Appli	C 973	9	56.2	76	1	US-08-657-012-6	Sequence 6, Appli
C 901	9	56.2	54	4	US-09-398-395A-18	Sequence 18, Appli	C 974	9	56.2	76	3	US-09-013-872-6	Sequence 6, Appli
C 902	9	56.2	54	4	US-09-479-645A-169	Sequence 169, App	C 975	9	56.2	76	3	US-09-184-198-6	Sequence 6, Appli
C 903	9	56.2	54	4	US-09-479-645A-175	Sequence 175, App	C 976	9	56.2	76	4	US-09-633-653-6	Sequence 6, Appli

```

C 977 9 56.2 77 1 US-08-384-708A-190 Sequence 190, App
C 978 9 56.2 77 3 US-08-687-421-282 Sequence 282, App
C 979 9 56.2 78 4 US-08-653-648A-47 Sequence 47, App1
C 980 9 56.2 79 1 US-08-471-985A-75 Sequence 75, App1
C 981 9 56.2 79 1 US-08-471-985A-99 Sequence 99, App1
C 982 9 56.2 79 1 US-08-472-255A-140 Sequence 140, App
C 983 9 56.2 79 1 US-08-472-255A-146 Sequence 146, App
C 984 9 56.2 79 1 US-08-472-255A-160 Sequence 160, App
C 985 9 56.2 79 1 US-08-472-255A-161 Sequence 161, App
C 986 9 56.2 79 1 US-08-479-724A-146 Sequence 146, App
C 987 9 56.2 79 1 US-08-479-724A-140 Sequence 140, App
C 988 9 56.2 79 1 US-08-479-724A-160 Sequence 160, App
C 989 9 56.2 79 1 US-08-479-724A-161 Sequence 161, App
C 990 9 56.2 79 3 US-08-472-256B-140 Sequence 140, App
C 991 9 56.2 79 3 US-08-472-256B-146 Sequence 146, App
C 992 9 56.2 79 3 US-08-472-256B-160 Sequence 160, App
C 993 9 56.2 79 3 US-08-472-256B-161 Sequence 161, App
C 994 9 56.2 79 3 US-08-952-793-146 Sequence 146, App
C 995 9 56.2 79 3 US-08-952-793-160 Sequence 160, App
C 996 9 56.2 79 3 US-08-952-793-161 Sequence 161, App
C 997 9 56.2 79 4 US-08-952-793-160 Sequence 160, App
C 998 9 56.2 79 4 US-09-849-928-140 Sequence 140, App
C 999 9 56.2 79 4 US-09-849-928-146 Sequence 146, App
C1000 9 56.2 79 4 US-09-849-928-160 Sequence 160, App

```

ALIGNMENTS

```

RESULT 1
US-09-536-393-19
; Sequence 19, Application US/09536393
; Patent No. 6562570

```

```

; GENERAL INFORMATION:
; APPLICANT: Rossi, John J.
; APPLICANT: Scherr, Michaela
; APPLICANT: R1998, Arthur D.
; TITLE OF INVENTION: Method for Identifying Accessible Binding Sites on RNA
; FILE REFERENCE: 1954-285
; CURRENT APPLICATION NUMBER: US/09/536,393
; CURRENT FILING DATE: 2000-03-28
; EARLIER APPLICATION NUMBER: 60/127,529
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 19
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNazyme core
US-09-536-393-19

```

```

Query Match 92.5%; Score 14.8; DB 4; Length 16;
Best Local Similarity 87.5%; Pred. No. 7.4;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 RGCTAGCHACACGA 16
Db 1 AGGCTAGCTACACGA 16

```

```

RESULT 2
US-09-536-393-20
; Sequence 20, Application US/09536393
; Patent No. 6562570

```

```

; GENERAL INFORMATION:
; APPLICANT: Rossi, John J.
; APPLICANT: Scherr, Michaela
; APPLICANT: R1998, Arthur D.
; TITLE OF INVENTION: Method for Identifying Accessible Binding Sites on RNA
; FILE REFERENCE: 1954-285
; CURRENT APPLICATION NUMBER: US/09/536,393

```

```

; CURRENT FILING DATE: 2000-03-28
; EARLIER APPLICATION NUMBER: 60/127,529
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 20
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNazyme core
US-09-536-393-20

```

```

Query Match 92.5%; Score 14.8; DB 4; Length 16;
Best Local Similarity 87.5%; Pred. No. 7.4;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 RGCTAGCHACACGA 16
Db 1 AGGCTAGCTACACGA 16

```

```

RESULT 3
US-09-270-140A-23
; Sequence 23, Application US/09270140A
; Patent No. 6361941

```

```

; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: UK91799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 23
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNazyme for
; OTHER INFORMATION: N-ras codon 61 position 1 - mutant (C to A, G or
; OTHER INFORMATION: U)
US-09-270-140A-23

```

```

Query Match 92.5%; Score 14.8; DB 4; Length 29;
Best Local Similarity 87.5%; Pred. No. 7.9;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 RGCTAGCHACACGA 16
Db 8 AGGCTAGCTACACGA 23

```

```

RESULT 4
US-09-270-140A-25
; Sequence 25, Application US/09270140A
; Patent No. 6361941

```

```

; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J631799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1

```



```
; SEQ ID NO 25
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for
; OTHER INFORMATION: N-ras codon 61, position 1
US-09-270-140A-25
```

```
Query Match          92.5%; Score 14.8; DB 4; Length 29;
Best Local Similarity 87.5%; Pred. No. 7.9;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 RGGCTAGCHACACGA 16
         :|||||:|||||
Db      9 AGGCTAGCTACACGA 24
```

```
RESULT 5
US-09-270-140A-55
; Sequence 55, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray J
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J61799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
```

```
SEQ ID NO 55
```

```
LENGTH: 30
```

```
TYPE: DNA
```

```
ORGANISM: Artificial Sequence
```

```
FEATURE:
```

```
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for
```

```
; OTHER INFORMATION: codon 508 - mutant (CTT deletion) for Cystic
```

```
; OTHER INFORMATION: fibrosis
```

```
US-09-270-140A-55
```

```
Query Match          92.5%; Score 14.8; DB 4; Length 30;
Best Local Similarity 87.5%; Pred. No. 7.9;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 RGGCTAGCHACACGA 16
         :|||||:|||||
Db      8 AGGCTAGCTACACGA 23
```

```
RESULT 6
US-09-253-955-5
; Sequence 5, Application US/09253955
; Patent No. 6140055
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison V
; APPLICANT: Fuery, Caroline J
; APPLICANT: Cairns, Murray J
; TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
```

```
; TITLE OF INVENTION: Molecules And Kits
```

```
; FILE REFERENCE: J1770SequenceListing
```

```
; CURRENT APPLICATION NUMBER: US/09/253,955
```

```
; CURRENT FILING DATE: 1999-02-22
```

```
; EARLIER APPLICATION NUMBER: 60/076,899
```

```
; EARLIER FILING DATE: 1998-03-05
```

```
; NUMBER OF SEQ ID NOS: 11
```

```
; SOFTWARE: PatentIn Ver. 2.0
```

```
SEQ ID NO 5
```

```
LENGTH: 31
```

```
TYPE: DNA
```

```
; ORGANISM: synthetic construct
US-09-253-955-5
```

```
Query Match          92.5%; Score 14.8; DB 3; Length 31;
Best Local Similarity 87.5%; Pred. No. 7.9;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 RGGCTAGCHACACGA 16
         :|||||:|||||
Db      8 AGGCTAGCTACACGA 23
```

```
RESULT 7
US-09-637-405-5
; Sequence 5, Application US/09637405
; Patent No. 620113
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison V
; APPLICANT: Fuery, Caroline J
; APPLICANT: Cairns, Murray J
; TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
```

```
; TITLE OF INVENTION: Molecules And Kits
```

```
; FILE REFERENCE: J1770SequenceListing
```

```
; CURRENT APPLICATION NUMBER: US/09/637,405
```

```
; CURRENT FILING DATE: 2000-08-11
```

```
; EARLIER APPLICATION NUMBER: 09/253,955
```

```
; EARLIER FILING DATE: 1999-02-22
```

```
; NUMBER OF SEQ ID NOS: 11
```

```
; SOFTWARE: PatentIn Ver. 2.0
```

```
SEQ ID NO 5
```

```
LENGTH: 31
```

```
TYPE: DNA
```

```
ORGANISM: synthetic construct
```

```
US-09-637-405-5
```

```
Query Match          92.5%; Score 14.8; DB 3; Length 31;
Best Local Similarity 87.5%; Pred. No. 7.9;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 RGGCTAGCHACACGA 16
         :|||||:|||||
Db      8 AGGCTAGCTACACGA 23
```

```
RESULT 8
```

```
US-09-270-140A-42
```

```
; Sequence 42, Application US/09270140A
```

```
; Patent No. 6361941
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Todd, Alison
```

```
; APPLICANT: Fuery, Caroline
```

```
; APPLICANT: Cairns, Murray
```

```
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
```

```
; FILE REFERENCE: J61799
```

```
; CURRENT APPLICATION NUMBER: US/09/270,140A
```

```
; CURRENT FILING DATE: 1999-03-16
```

```
; PRIOR APPLICATION NUMBER: 60/079,651
```

```
; PRIOR FILING DATE: 1998-03-27
```

```
; NUMBER OF SEQ ID NOS: 96
```

```
; SOFTWARE: PatentIn Ver. 2.1
```

```
SEQ ID NO 42
```

```
LENGTH: 31
```

```
TYPE: DNA
```

```
ORGANISM: Artificial Sequence
```

```
FEATURE:
```

```
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for
```

```
; OTHER INFORMATION: codon 542 - Cystic fibrosis
```

```
US-09-270-140A-42
```

```
Query Match          92.5%; Score 14.8; DB 4; Length 31;
Best Local Similarity 87.5%; Pred. No. 7.9;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 RGGCTAGCHACACGA 16
:|||||:|||||
DB 10 AGGCTAGCTACACGA 25

RESULT 9

US-09-270-140A-45
; Sequence 45, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jk11799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for
; OTHER INFORMATION: cystic fibrosis Codon 542 - mutant (G to U)
US-09-270-140A-45

Query Match 92.5%; Score 14.8; DB 4; Length 31;
Best Local Similarity 87.5%; Pred. No. 7.9;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16
:|||||:|||||
DB 10 AGGCTAGCTACACGA 25

RESULT 10

US-09-270-140A-48
; Sequence 48, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jk11799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for
; OTHER INFORMATION: Codon 551 - wildtype
US-09-270-140A-48

Query Match 92.5%; Score 14.8; DB 4; Length 31;
Best Local Similarity 87.5%; Pred. No. 7.9;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16
:|||||:|||||
DB 9 GGGCTAGCTACACGA 24

RESULT 11
US-09-270-140A-51
; Sequence 51, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jk11799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for
; OTHER INFORMATION: Codon 51 - mutant (G to A)
US-09-270-140A-51

Query Match 92.5%; Score 14.8; DB 4; Length 31;
Best Local Similarity 87.5%; Pred. No. 7.9;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16
:|||||:|||||
DB 9 AGGCTAGCTACACGA 24

RESULT 12

US-09-746-985B-5
; Sequence 5, Application US/09746985B
; Patent No. 6365724
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison V
; APPLICANT: Fuery, Caroline J
; APPLICANT: Cairns, Murray J
; TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
; TITLE OF INVENTION: Molecules And Kits
; FILE REFERENCE: SequenceListing
; CURRENT APPLICATION NUMBER: US/09/746,985B
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/076,899
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-746-985B-5

Query Match 92.5%; Score 14.8; DB 4; Length 31;
Best Local Similarity 87.5%; Pred. No. 7.9;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16
:|||||:|||||
DB 8 AGGCTAGCTACACGA 23

RESULT 13

US-09-270-140A-12
; Sequence 12, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:

APPLICANT: Todd, Alison
APPLICANT: Fuery, Caroline
TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
FILE REFERENCE: J6J1799
CURRENT APPLICATION NUMBER: US/09/270,140A
CURRENT FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 60/079,651
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNazyme for
OTHER INFORMATION: H-ras codon 61, position 1-mutant
US-09-270-140A-12

Query Match 92.5%; Score 14.8; DB 4; Length 32;
Best Local Similarity 87.5%; Pred. No. 8;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAAGA 16
DB 10 GGGCTAGCTACAAGA 25

RESULT 14
US-09-270-140A-15
Sequence 15, Application US/09270140A
Patent No. 6361941
GENERAL INFORMATION:
APPLICANT: Todd, Alison
APPLICANT: Fuery, Caroline
APPLICANT: Cairns, Murray
TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
FILE REFERENCE: J6J1799
CURRENT APPLICATION NUMBER: US/09/270,140A
CURRENT FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 60/079,651
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNazyme for
OTHER INFORMATION: H-ras codon 61
US-09-270-140A-15

Query Match 92.5%; Score 14.8; DB 4; Length 32;
Best Local Similarity 87.5%; Pred. No. 8;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAAGA 16
DB 12 GGGCTAGCTACAAGA 27

RESULT 15
US-09-270-140A-19
Sequence 19, Application US/09270140A
Patent No. 6361941
GENERAL INFORMATION:
APPLICANT: Todd, Alison
APPLICANT: Fuery, Caroline
APPLICANT: Cairns, Murray
TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
FILE REFERENCE: J6J1799

CURRENT APPLICATION NUMBER: US/09/270,140A
CURRENT FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 60/079,651
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNazyme for
OTHER INFORMATION: H-ras codon 61, position 3
US-09-270-140A-19

Query Match 92.5%; Score 14.8; DB 4; Length 32;
Best Local Similarity 87.5%; Pred. No. 8;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAAGA 16
DB 11 AGGCTAGCTACAAGA 26

RESULT 16
US-09-270-140A-28
Sequence 28, Application US/09270140A
Patent No. 6361941
GENERAL INFORMATION:
APPLICANT: Todd, Alison
APPLICANT: Fuery, Caroline
APPLICANT: Cairns, Murray
TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
FILE REFERENCE: J6J1799
CURRENT APPLICATION NUMBER: US/09/270,140A
CURRENT FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 60/079,651
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNazyme
US-09-270-140A-28

Query Match 92.5%; Score 14.8; DB 4; Length 32;
Best Local Similarity 93.8%; Pred. No. 8;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAAGA 16
DB 9 RGGCTAGCTACAAGA 24

RESULT 17
US-09-270-140A-58
Sequence 58, Application US/09270140A
Patent No. 6361941
GENERAL INFORMATION:
APPLICANT: Todd, Alison
APPLICANT: Fuery, Caroline
APPLICANT: Cairns, Murray
TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
FILE REFERENCE: J6J1799
CURRENT APPLICATION NUMBER: US/09/270,140A
CURRENT FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 60/079,651
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.1

```

; SEQ ID NO 58
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:DNAzyme for
; OTHER INFORMATION: codon 342 - mutant (G to A)
US-09-270-140A-58

Query Match          92.5%; Score 14.8; DB 4; Length 32;
Best Local Similarity 87.5%; Pred. No. 8;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACACGA 16
   :|||||:|||||
Db 9 GGGCTAGCTACACGA 24

RESULT 18
US-09-270-140A-9
; Sequence 9, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jc41799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for
; OTHER INFORMATION: k-ras codon 13 mutant RNA
US-09-270-140A-9

Query Match          92.5%; Score 14.8; DB 4; Length 34;
Best Local Similarity 87.5%; Pred. No. 8;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACACGA 16
   :|||||:|||||
Db 13 AGGCTAGCTACACGA 28

RESULT 19
US-09-270-140A-53
; Sequence 53, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jc41799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 53
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```

; OTHER INFORMATION: Description of Artificial Sequence:DNAzyme for
; OTHER INFORMATION: codon 08 - wildtype
US-09-270-140A-53

Query Match          92.5%; Score 14.8; DB 4; Length 34;
Best Local Similarity 87.5%; Pred. No. 8;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACACGA 16
   :|||||:|||||
Db 11 AGGCTAGCTACACGA 26

RESULT 20
US-09-270-140A-3
; Sequence 3, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jc41799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:DNAzyme for
; OTHER INFORMATION: k-ras codon 12
US-09-270-140A-3

Query Match          92.5%; Score 14.8; DB 4; Length 35;
Best Local Similarity 93.8%; Pred. No. 8;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACACGA 16
   :|||||:|||||
Db 11 RGCTAGCTACACGA 26

RESULT 21
US-09-270-140A-6
; Sequence 6, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jc41799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:DNAzyme for
US-09-270-140A-6

Query Match          92.5%; Score 14.8; DB 4; Length 35;
Best Local Similarity 87.5%; Pred. No. 8;
```

Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16

Db 11 AGGCTAGCTACACGA 26

RESULT 22

US-09-270-140A-31

; Sequence 31, Application US/09270140A

; Patent No. 6361941

; GENERAL INFORMATION:

; APPLICANT: Todd, Alison

; APPLICANT: Puery, Caroline

; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods

; FILE REFERENCE: Jc11799

; CURRENT APPLICATION NUMBER: US/09/270,140A

; PRIOR FILING DATE: 1999-03-16

; PRIOR APPLICATION NUMBER: 60/079,651

; NUMBER OF SEQ ID NOS: 96

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 31

; LENGTH: 35

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for

; OTHER INFORMATION: Codon 70 HIV-1 AZT resistant mutant

US-09-270-140A-31

Query Match 92.5%; Score 14.8; DB 4; Length 35;

Best Local Similarity 87.5%; Pred. No. 8;

Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16

Db 9 AGGCTAGCTACACGA 24

RESULT 23

US-09-270-140A-39

; Sequence 39, Application US/09270140A

; Patent No. 6361941

; GENERAL INFORMATION:

; APPLICANT: Todd, Alison

; APPLICANT: Puery, Caroline

; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods

; FILE REFERENCE: Jc11799

; CURRENT APPLICATION NUMBER: US/09/270,140A

; PRIOR FILING DATE: 1999-03-16

; PRIOR APPLICATION NUMBER: 60/079,651

; PRIOR FILING DATE: 1998-03-27

; NUMBER OF SEQ ID NOS: 96

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 39

; LENGTH: 35

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for

; OTHER INFORMATION: codon 74

US-09-270-140A-39

Query Match 92.5%; Score 14.8; DB 4; Length 35;

Best Local Similarity 87.5%; Pred. No. 8;

Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16

Db 8 AGGCTAGCTACACGA 23

RESULT 24

US-09-270-140A-34

; Sequence 34, Application US/09270140A

; Patent No. 6361941

; GENERAL INFORMATION:

; APPLICANT: Todd, Alison

; APPLICANT: Puery, Caroline

; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods

; FILE REFERENCE: Jc11799

; CURRENT APPLICATION NUMBER: US/09/270,140A

; PRIOR FILING DATE: 1999-03-16

; PRIOR APPLICATION NUMBER: 60/079,651

; NUMBER OF SEQ ID NOS: 96

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 34

; LENGTH: 38

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for

; OTHER INFORMATION: codon 215 - mutant (C to U or A)

US-09-270-140A-34

Query Match 92.5%; Score 14.8; DB 4; Length 38;

Best Local Similarity 87.5%; Pred. No. 8.1;

Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16

Db 11 AGGCTAGCTACACGA 26

RESULT 25

US-09-270-140A-36

; Sequence 36, Application US/09270140A

; Patent No. 6361941

; GENERAL INFORMATION:

; APPLICANT: Todd, Alison

; APPLICANT: Puery, Caroline

; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods

; FILE REFERENCE: Jc11799

; CURRENT APPLICATION NUMBER: US/09/270,140A

; PRIOR FILING DATE: 1999-03-16

; PRIOR APPLICATION NUMBER: 60/079,651

; PRIOR FILING DATE: 1998-03-27

; NUMBER OF SEQ ID NOS: 96

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 36

; LENGTH: 38

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for

; OTHER INFORMATION: codon 215 - mutant

US-09-270-140A-36

Query Match 92.5%; Score 14.8; DB 4; Length 38;

Best Local Similarity 87.5%; Pred. No. 8.1;

Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16

Db 10 GGGCTAGCTACACGA 25

RESULT 26

US-09-270-140A-91

; Sequence 91, Application US/09270140A

```
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jk1799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 91
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Dz1 DNazyme
US-09-270-140A-91
```

```
Query Match          92.5%; Score 14.8; DB 4; Length 39;
Best Local Similarity 87.5%; Pred. No. 8.1;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 RGCTAGCHACAACGA 16
        :|||||:|||||
Db       8 GGGCTAGCTACAACGA 23
```

```
RESULT 27
US-09-270-140A-94
; Sequence 94, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jk1799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 94
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Dz3 DNazyme
US-09-270-140A-94
```

```
Query Match          92.5%; Score 14.8; DB 4; Length 39;
Best Local Similarity 87.5%; Pred. No. 8.1;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 RGCTAGCHACAACGA 16
        :|||||:|||||
Db       8 AGGCTAGCTACAACGA 23
```

```
RESULT 28
US-08-849-567A-85
; Sequence 85, Application US/08849567A
; Patent No. 6326174
; GENERAL INFORMATION:
; APPLICANT: Joyce, Gerald F.
; APPLICANT: Breaker, Ronald R.
; TITLE OF INVENTION: ENZYMATIC DNA MOLECULES
; FILE REFERENCE: SCR1943S
; CURRENT APPLICATION NUMBER: US/08/849,567A
```

```
; CURRENT FILING DATE: 1997-08-25
; PRIOR APPLICATION NUMBER: PCT/US95/15580
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 08/472,194
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/349,023
; PRIOR FILING DATE: 1994-12-02
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 85
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA enzyme
US-08-849-567A-85
```

```
Query Match          92.5%; Score 14.8; DB 4; Length 47;
Best Local Similarity 87.5%; Pred. No. 8.3;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 RGCTAGCHACAACGA 16
        :|||||:|||||
Db       11 AGGCTAGCTACAACGA 26
```

```
RESULT 29
US-08-849-567A-87
; Sequence 87, Application US/08849567A
; Patent No. 6326174
; GENERAL INFORMATION:
; APPLICANT: Joyce, Gerald F.
; APPLICANT: Breaker, Ronald R.
; TITLE OF INVENTION: ENZYMATIC DNA MOLECULES
; FILE REFERENCE: SCR1943S
; CURRENT APPLICATION NUMBER: US/08/849,567A
; PRIOR FILING DATE: 1997-08-25
; PRIOR APPLICATION NUMBER: PCT/US95/15580
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 08/472,194
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/349,023
; PRIOR FILING DATE: 1994-12-02
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 87
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA enzyme
US-08-849-567A-87
```

```
Query Match          92.5%; Score 14.8; DB 4; Length 48;
Best Local Similarity 87.5%; Pred. No. 8.3;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 RGCTAGCHACAACGA 16
        :|||||:|||||
Db       10 AGGCTAGCTACAACGA 25
```

```
RESULT 30
US-08-849-567A-81
; Sequence 81, Application US/08849567A
; Patent No. 6326174
; GENERAL INFORMATION:
; APPLICANT: Joyce, Gerald F.
; APPLICANT: Breaker, Ronald R.
; TITLE OF INVENTION: ENZYMATIC DNA MOLECULES
; FILE REFERENCE: SCR1943S
; CURRENT APPLICATION NUMBER: US/08/849,567A
; CURRENT FILING DATE: 1997-08-25
```

PRIOR APPLICATION NUMBER: PCT/US95/15580
PRIOR FILING DATE: 1995-12-01
PRIOR APPLICATION NUMBER: 08/472,194
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/349,023
PRIOR FILING DATE: 1994-12-02
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 81
LENGTH: 49
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNA enzyme
US-08-849-567A-81

Query Match 92.5%; Score 14.8; DB 4; Length 49;
Best Local Similarity 87.5%; Pred. No. 8.3;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACAAGA 16
:|||||:|||||
Db 10 AGCTAGCTACAAGA 25

RESULT 31
US-09-253-955-8/c
Sequence 8, Application US/09253955
Patent No. 6140055
GENERAL INFORMATION:
APPLICANT: Todd, Alison V
APPLICANT: Fuery, Caroline J
TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
FILE REFERENCE: J11770SequenceListing
CURRENT APPLICATION NUMBER: US/09/253,955
CURRENT FILING DATE: 1999-02-22
EARLIER APPLICATION NUMBER: 60/076,899
EARLIER FILING DATE: 1998-03-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 50
TYPE: DNA
ORGANISM: Synthetic construct
US-09-253-955-8

Query Match 92.5%; Score 14.8; DB 3; Length 50;
Best Local Similarity 87.5%; Pred. No. 8.3;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACAAGA 16
:|||||:|||||
Db 22 AGCTAGCTACAAGA 7

RESULT 32
US-09-637-405-8/c
Sequence 8, Application US/09637405
Patent No. 6201113
GENERAL INFORMATION:
APPLICANT: Todd, Alison V
APPLICANT: Fuery, Caroline J
APPLICANT: Cairns, Murray J
TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
FILE REFERENCE: J11770SequenceListing
CURRENT APPLICATION NUMBER: US/09/637,405
CURRENT FILING DATE: 2000-08-11
EARLIER APPLICATION NUMBER: 09/253,955
EARLIER FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 50
TYPE: DNA
ORGANISM: synthetic construct
US-09-637-405-8

Query Match 92.5%; Score 14.8; DB 3; Length 50;
Best Local Similarity 87.5%; Pred. No. 8.3;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACAAGA 16
:|||||:|||||
Db 22 AGCTAGCTACAAGA 7

RESULT 33
US-09-746-985B-8/c
Sequence 8, Application US/09746985B
Patent No. 6365724
GENERAL INFORMATION:
APPLICANT: Todd, Alison V
APPLICANT: Fuery, Caroline J
APPLICANT: Cairns, Murray J
TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
FILE REFERENCE: SequenceListing
CURRENT APPLICATION NUMBER: US/09/746,985B
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/076,899
PRIOR FILING DATE: 1998-03-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR primer
US-09-746-985B-8

Query Match 92.5%; Score 14.8; DB 4; Length 50;
Best Local Similarity 87.5%; Pred. No. 8.3;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACAAGA 16
:|||||:|||||
Db 22 AGCTAGCTACAAGA 7

RESULT 34
US-08-849-567A-86
Sequence 86, Application US/08849567A
Patent No. 6326174
GENERAL INFORMATION:
APPLICANT: Joyce, Gerald R.
APPLICANT: Breaker, Ronald R.
TITLE OF INVENTION: ENZYMAIC DNA MOLECULES
FILE REFERENCE: SCR19435
CURRENT APPLICATION NUMBER: US/08/849,567A
CURRENT FILING DATE: 1997-08-25
PRIOR APPLICATION NUMBER: PCT/US95/15580
PRIOR FILING DATE: 1995-12-01
PRIOR APPLICATION NUMBER: 08/472,194
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/349,023
PRIOR FILING DATE: 1994-12-02
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 86
LENGTH: 51
TYPE: DNA
ORGANISM: Artificial Sequence


```
; Patent No. 620113
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison V
; APPLICANT: Fuery, Caroline J
; APPLICANT: Cairns, Murray J
; TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
; TITLE OF INVENTION: Molecules And Kits
; FILE REFERENCE: J1170SequencesListig
; CURRENT APPLICATION NUMBER: US/09/637,405
; CURRENT FILING DATE: 2000-08-11
; EARLIER APPLICATION NUMBER: 09/253,955
; EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 10
; LENGTH: 60
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-637-405-10
```

```
Query Match          92.5%; Score 14.8; DB 3; Length 60;
Best Local Similarity 87.5%; Pred.No. 8.5;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 RGGCTAGCHACACGA 16
        :|||||:|||||
Db      32 GGGCTAGCTACACGA 17
```

```
RESULT 40
US-09-270-140A-95/C
; Sequence 95, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J601799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 95
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:3" zymogene
; OTHER INFORMATION: primer ek42Dz2
US-09-270-140A-95
```

```
Query Match          92.5%; Score 14.8; DB 4; Length 60;
Best Local Similarity 87.5%; Pred.No. 8.5;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 RGGCTAGCHACACGA 16
        :|||||:|||||
Db      32 GGGCTAGCTACACGA 17
```

Search completed: January 21, 2004, 08:17:14
Job time : 47 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 06:47:52 ; Search time 154 Seconds
(without alignments)
366.209 Million cell updates/sec

Title: US-09-423-035B-122
Perfect score: 16
Sequence: 1 rggctagchacaacga 16

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2324096 seqs, 1762381658 residues

Total number of hits satisfying chosen parameters: 1462038

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_NEW_PUB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	14.8 92.5	16 10	US-09-877-526A-21	Sequence 21, Appl
2	14.8 92.5	16 10	US-09-866-316B-15	Sequence 15, Appl
3	14.8 92.5	16 10	US-09-864-785-3928	Sequence 3928, Ap
4	14.8 92.5	16 11	US-09-992-160-21	Sequence 21, Appl
5	14.8 92.5	16 11	US-09-730-289B-3896	Sequence 3896, Ap
6	14.8 92.5	16 11	US-09-780-533A-6679	Sequence 6679, Ap
7	14.8 92.5	16 11	US-09-877-478-6585	Sequence 6585, Ap
8	14.8 92.5	16 11	US-09-848-754A-9645	Sequence 9645, Ap
9	14.8 92.5	16 11	US-09-776-474-2991	Sequence 2991, Ap
10	14.8 92.5	16 11	US-09-930-423-4549	Sequence 4549, Ap
11	14.8 92.5	16 11	US-09-780-164-2602	Sequence 2602, Ap
12	14.8 92.5	16 11	US-09-827-395A-2617	Sequence 2617, Appl
13	14.8 92.5	16 12	US-10-366-191-14	Sequence 14, Appl
14	14.8 92.5	16 12	US-10-435-044A-19	Sequence 19, Appl
15	14.8 92.5	16 12	US-10-435-044A-20	Sequence 20, Appl

16	14.8 92.5	16 13	US-09-745-237A-4549	Sequence 4549, Ap
17	14.8 92.5	16 13	US-09-792-818-2304	Sequence 2304, Ap
18	14.8 92.5	16 13	US-10-279-401-11	Sequence 11, Appl
19	14.8 92.5	16 13	US-10-201-389A-13	Sequence 13, Appl
20	14.8 92.5	16 13	US-10-238-700-4666	Sequence 4666, Ap
21	14.8 92.5	16 13	US-10-277-494-445	Sequence 445, Appl
22	14.8 92.5	16 13	US-10-230-006-2677	Sequence 2677, Ap
23	14.8 92.5	16 13	US-10-306-477A-11	Sequence 11, Appl
24	14.8 92.5	16 15	US-10-151-116-12	Sequence 12, Appl
25	14.8 92.5	16 15	US-10-163-552-1997	Sequence 1997, Ap
26	14.8 92.5	16 15	US-10-156-306-8013	Sequence 8013, Ap
27	14.8 92.5	16 16	US-10-157-580A-170	Sequence 170, Appl
28	14.8 92.5	16 16	US-10-201-394A-13	Sequence 13, Appl
29	14.8 92.5	23 13	US-10-277-494-334	Sequence 334, Appl
30	14.8 92.5	23 13	US-10-277-494-335	Sequence 335, Appl
31	14.8 92.5	23 13	US-10-277-494-336	Sequence 336, Appl
32	14.8 92.5	23 13	US-10-277-494-337	Sequence 337, Appl
33	14.8 92.5	23 13	US-10-277-494-338	Sequence 338, Appl
34	14.8 92.5	23 13	US-10-277-494-339	Sequence 339, Appl
35	14.8 92.5	23 13	US-10-277-494-340	Sequence 340, Appl
36	14.8 92.5	23 13	US-10-277-494-341	Sequence 341, Appl
37	14.8 92.5	23 13	US-10-277-494-342	Sequence 342, Appl
38	14.8 92.5	23 13	US-10-277-494-343	Sequence 343, Appl
39	14.8 92.5	23 13	US-10-277-494-344	Sequence 344, Appl
40	14.8 92.5	23 13	US-10-277-494-345	Sequence 345, Appl
41	14.8 92.5	23 13	US-10-277-494-346	Sequence 346, Appl
42	14.8 92.5	23 13	US-10-277-494-347	Sequence 347, Appl
43	14.8 92.5	23 13	US-10-277-494-348	Sequence 348, Appl
44	14.8 92.5	23 13	US-10-277-494-349	Sequence 349, Appl
45	14.8 92.5	23 13	US-10-277-494-350	Sequence 350, Appl
46	14.8 92.5	23 13	US-10-277-494-351	Sequence 351, Appl
47	14.8 92.5	23 13	US-10-277-494-352	Sequence 352, Appl
48	14.8 92.5	23 13	US-10-277-494-353	Sequence 353, Appl
49	14.8 92.5	23 13	US-10-277-494-354	Sequence 354, Appl
50	14.8 92.5	23 13	US-10-277-494-355	Sequence 355, Appl
51	14.8 92.5	23 13	US-10-277-494-356	Sequence 356, Appl
52	14.8 92.5	24 13	US-10-277-494-357	Sequence 357, Appl
53	14.8 92.5	24 13	US-10-277-494-358	Sequence 358, Appl
54	14.8 92.5	25 13	US-10-277-494-359	Sequence 359, Appl
55	14.8 92.5	25 13	US-10-277-494-360	Sequence 360, Appl
56	14.8 92.5	26 13	US-10-277-494-361	Sequence 361, Appl
57	14.8 92.5	26 13	US-10-277-494-362	Sequence 362, Appl
58	14.8 92.5	27 13	US-10-277-494-363	Sequence 363, Appl
59	14.8 92.5	28 15	US-10-163-552-1982	Sequence 1982, Ap
60	14.8 92.5	28 15	US-10-163-552-1984	Sequence 1984, Ap
61	14.8 92.5	29 12	US-10-420-194-706	Sequence 706, Appl
62	14.8 92.5	29 12	US-10-420-194-710	Sequence 710, Appl
63	14.8 92.5	29 12	US-10-420-194-711	Sequence 711, Appl
64	14.8 92.5	29 12	US-10-420-194-712	Sequence 712, Appl
65	14.8 92.5	29 12	US-10-420-194-713	Sequence 713, Appl
66	14.8 92.5	29 12	US-10-420-194-715	Sequence 715, Appl
67	14.8 92.5	29 12	US-10-420-194-716	Sequence 716, Appl
68	14.8 92.5	29 12	US-10-420-194-717	Sequence 717, Appl
69	14.8 92.5	29 12	US-10-420-194-718	Sequence 718, Appl
70	14.8 92.5	29 12	US-10-420-194-719	Sequence 719, Appl
71	14.8 92.5	29 12	US-10-420-194-720	Sequence 720, Appl
72	14.8 92.5	29 12	US-10-420-194-721	Sequence 721, Appl
73	14.8 92.5	29 12	US-10-420-194-722	Sequence 722, Appl
74	14.8 92.5	29 12	US-10-420-194-723	Sequence 723, Appl
75	14.8 92.5	29 12	US-10-420-194-724	Sequence 724, Appl
76	14.8 92.5	29 12	US-10-420-194-725	Sequence 725, Appl
77	14.8 92.5	29 12	US-10-420-194-726	Sequence 726, Appl
78	14.8 92.5	29 12	US-10-420-194-727	Sequence 727, Appl
79	14.8 92.5	29 12	US-10-420-194-728	Sequence 728, Appl
80	14.8 92.5	29 12	US-10-420-194-729	Sequence 729, Appl
81	14.8 92.5	29 12	US-10-420-194-730	Sequence 730, Appl
82	14.8 92.5	29 12	US-10-420-194-731	Sequence 731, Appl
83	14.8 92.5	29 12	US-10-420-194-732	Sequence 732, Appl
84	14.8 92.5	29 12	US-10-420-194-733	Sequence 733, Appl
85	14.8 92.5	29 12	US-10-420-194-734	Sequence 734, Appl
86	14.8 92.5	29 12	US-10-420-194-735	Sequence 735, Appl
87	14.8 92.5	29 12	US-10-420-194-736	Sequence 736, Appl
88	14.8 92.5	29 12	US-10-420-194-737	Sequence 737, Appl

89	14.8	92.5	29	12	US-10-420-194-774	Sequence 774, App	162	14.8	92.5	30	13	US-09-792-818-2291	Sequence 2291, App
90	14.8	92.5	29	12	US-10-420-194-777	Sequence 777, App	163	14.8	92.5	30	13	US-09-817-879-9597	Sequence 9597, App
91	14.8	92.5	29	12	US-10-420-194-779	Sequence 779, App	164	14.8	92.5	30	13	US-09-817-879-9598	Sequence 9598, App
92	14.8	92.5	29	12	US-10-420-194-781	Sequence 781, App	165	14.8	92.5	30	13	US-09-817-879-9599	Sequence 9599, App
93	14.8	92.5	29	12	US-10-420-194-786	Sequence 786, App	166	14.8	92.5	30	13	US-09-817-879-9600	Sequence 9600, App
94	14.8	92.5	29	12	US-10-420-194-788	Sequence 788, App	167	14.8	92.5	30	13	US-09-817-879-9601	Sequence 9601, App
95	14.8	92.5	29	12	US-10-420-194-792	Sequence 792, App	168	14.8	92.5	30	13	US-09-817-879-9602	Sequence 9602, App
96	14.8	92.5	29	12	US-10-420-194-795	Sequence 795, App	169	14.8	92.5	30	13	US-09-817-879-9603	Sequence 9603, App
97	14.8	92.5	29	12	US-10-420-194-799	Sequence 799, App	170	14.8	92.5	30	13	US-09-817-879-9604	Sequence 9604, App
98	14.8	92.5	29	12	US-10-420-194-804	Sequence 804, App	171	14.8	92.5	30	13	US-09-817-879-9605	Sequence 9605, App
99	14.8	92.5	29	13	US-10-277-494-302	Sequence 302, App	172	14.8	92.5	30	15	US-10-122-013-14	Sequence 9606, App
100	14.8	92.5	29	13	US-10-277-494-303	Sequence 303, App	173	14.8	92.5	30	15	US-10-163-552-1963	Sequence 14, Appl
101	14.8	92.5	29	13	US-10-277-494-304	Sequence 304, App	174	14.8	92.5	30	15	US-10-163-552-1968	Sequence 1983, App
102	14.8	92.5	29	13	US-10-277-494-305	Sequence 305, App	175	14.8	92.5	30	15	US-10-163-552-1966	Sequence 1986, App
103	14.8	92.5	29	13	US-10-277-494-306	Sequence 306, App	176	14.8	92.5	30	15	US-10-156-306-7919	Sequence 1987, App
104	14.8	92.5	29	13	US-10-277-494-307	Sequence 307, App	177	14.8	92.5	30	15	US-10-156-306-7920	Sequence 7919, App
105	14.8	92.5	29	13	US-10-277-494-308	Sequence 308, App	178	14.8	92.5	30	15	US-10-156-306-7921	Sequence 7920, App
106	14.8	92.5	29	13	US-10-277-494-309	Sequence 309, App	179	14.8	92.5	30	15	US-10-156-306-7922	Sequence 7921, App
107	14.8	92.5	29	13	US-10-277-494-310	Sequence 310, App	180	14.8	92.5	30	15	US-10-156-306-7923	Sequence 7922, App
108	14.8	92.5	29	13	US-10-277-494-311	Sequence 311, App	181	14.8	92.5	30	15	US-10-156-306-7924	Sequence 7923, App
109	14.8	92.5	29	13	US-10-277-494-312	Sequence 312, App	182	14.8	92.5	30	15	US-10-156-306-7925	Sequence 7924, App
110	14.8	92.5	29	13	US-10-277-494-313	Sequence 313, App	183	14.8	92.5	30	15	US-10-156-306-7926	Sequence 7925, App
111	14.8	92.5	29	13	US-10-277-494-314	Sequence 314, App	184	14.8	92.5	30	15	US-10-156-306-7927	Sequence 7926, App
112	14.8	92.5	29	13	US-10-277-494-315	Sequence 315, App	185	14.8	92.5	30	15	US-10-156-306-7928	Sequence 7927, App
113	14.8	92.5	29	13	US-10-277-494-316	Sequence 316, App	186	14.8	92.5	30	15	US-10-156-306-7929	Sequence 7928, App
114	14.8	92.5	29	13	US-10-277-494-317	Sequence 317, App	187	14.8	92.5	30	15	US-10-156-306-7930	Sequence 7929, App
115	14.8	92.5	29	13	US-10-277-494-318	Sequence 318, App	188	14.8	92.5	30	15	US-09-864-785-2151	Sequence 9, Appl
116	14.8	92.5	29	13	US-10-277-494-319	Sequence 319, App	189	14.8	92.5	30	15	US-09-864-785-2152	Sequence 2151, App
117	14.8	92.5	29	13	US-10-277-494-320	Sequence 320, App	190	14.8	92.5	30	15	US-09-864-785-2153	Sequence 2152, App
118	14.8	92.5	29	13	US-10-122-013-2	Sequence 2, Appl	191	14.8	92.5	30	15	US-09-864-785-2154	Sequence 2153, App
119	14.8	92.5	29	15	US-10-122-013-3	Sequence 3, Appl	192	14.8	92.5	30	15	US-09-864-785-2155	Sequence 2154, App
120	14.8	92.5	29	15	US-10-122-013-4	Sequence 4, Appl	193	14.8	92.5	30	15	US-09-864-785-2156	Sequence 2155, App
121	14.8	92.5	29	15	US-10-122-013-5	Sequence 5, Appl	194	14.8	92.5	30	15	US-09-864-785-2157	Sequence 2156, App
122	14.8	92.5	29	15	US-10-122-013-6	Sequence 6, Appl	195	14.8	92.5	30	15	US-09-864-785-2158	Sequence 2157, App
123	14.8	92.5	29	15	US-10-122-013-7	Sequence 7, Appl	196	14.8	92.5	30	15	US-09-864-785-2159	Sequence 2158, App
124	14.8	92.5	29	15	US-10-122-013-8	Sequence 8, Appl	197	14.8	92.5	30	15	US-09-864-785-2160	Sequence 2159, App
125	14.8	92.5	29	15	US-10-122-013-9	Sequence 9, Appl	198	14.8	92.5	30	15	US-09-864-785-2161	Sequence 2160, App
126	14.8	92.5	29	15	US-10-122-013-10	Sequence 10, Appl	199	14.8	92.5	30	15	US-09-864-785-2162	Sequence 2161, App
127	14.8	92.5	29	15	US-10-122-013-11	Sequence 11, Appl	200	14.8	92.5	30	15	US-09-864-785-2163	Sequence 2162, App
128	14.8	92.5	29	15	US-10-122-013-12	Sequence 12, Appl	201	14.8	92.5	30	15	US-09-864-785-2164	Sequence 2163, App
129	14.8	92.5	29	15	US-10-122-013-13	Sequence 13, Appl	202	14.8	92.5	30	15	US-09-864-785-2165	Sequence 2164, App
130	14.8	92.5	29	15	US-10-122-013-14	Sequence 14, Appl	203	14.8	92.5	30	15	US-09-864-785-2166	Sequence 2165, App
131	14.8	92.5	29	15	US-10-122-013-15	Sequence 15, Appl	204	14.8	92.5	30	15	US-09-864-785-2167	Sequence 2166, App
132	14.8	92.5	29	15	US-10-157-580A-149	Sequence 149, App	205	14.8	92.5	30	15	US-09-864-785-2168	Sequence 2167, App
133	14.8	92.5	29	15	US-10-157-580A-150	Sequence 150, App	206	14.8	92.5	30	15	US-09-864-785-2169	Sequence 2168, App
134	14.8	92.5	29	15	US-10-157-580A-151	Sequence 151, App	207	14.8	92.5	30	15	US-09-864-785-2170	Sequence 2169, App
135	14.8	92.5	29	15	US-10-157-580A-152	Sequence 152, App	208	14.8	92.5	30	15	US-09-864-785-2171	Sequence 2170, App
136	14.8	92.5	29	15	US-10-157-580A-153	Sequence 153, App	209	14.8	92.5	30	15	US-09-864-785-2172	Sequence 2171, App
137	14.8	92.5	30	10	US-09-864-785-3808	Sequence 3808, App	210	14.8	92.5	30	15	US-09-864-785-2173	Sequence 2172, App
138	14.8	92.5	30	10	US-09-864-785-3809	Sequence 3809, App	211	14.8	92.5	30	15	US-09-864-785-2174	Sequence 2173, App
139	14.8	92.5	30	10	US-09-864-785-3810	Sequence 3810, App	212	14.8	92.5	30	15	US-09-864-785-2175	Sequence 2174, App
140	14.8	92.5	30	10	US-09-864-785-3911	Sequence 3911, App	213	14.8	92.5	30	15	US-09-864-785-2176	Sequence 2175, App
141	14.8	92.5	30	10	US-09-864-785-3912	Sequence 3912, App	214	14.8	92.5	30	15	US-09-864-785-2177	Sequence 2176, App
142	14.8	92.5	30	11	US-09-725-926A-7	Sequence 7, Appl	215	14.8	92.5	30	15	US-09-864-785-2178	Sequence 2177, App
143	14.8	92.5	30	11	US-09-877-478-6567	Sequence 6567, App	216	14.8	92.5	30	15	US-09-864-785-2179	Sequence 2178, App
144	14.8	92.5	30	11	US-09-877-478-6568	Sequence 6568, App	217	14.8	92.5	30	15	US-09-864-785-2180	Sequence 2179, App
145	14.8	92.5	30	11	US-09-877-478-6569	Sequence 6569, App	218	14.8	92.5	30	15	US-09-864-785-2181	Sequence 2180, App
146	14.8	92.5	30	11	US-09-877-478-6570	Sequence 6570, App	219	14.8	92.5	30	15	US-09-864-785-2182	Sequence 2181, App
147	14.8	92.5	30	11	US-09-877-478-6571	Sequence 6571, App	220	14.8	92.5	30	15	US-09-864-785-2183	Sequence 2182, App
148	14.8	92.5	30	11	US-09-740-332-9597	Sequence 9597, App	221	14.8	92.5	30	15	US-09-864-785-2184	Sequence 2183, App
149	14.8	92.5	30	11	US-09-740-332-9598	Sequence 9598, App	222	14.8	92.5	30	15	US-09-864-785-2185	Sequence 2184, App
150	14.8	92.5	30	11	US-09-740-332-9599	Sequence 9599, App	223	14.8	92.5	30	15	US-09-864-785-2186	Sequence 2185, App
151	14.8	92.5	30	11	US-09-740-332-9600	Sequence 9600, App	224	14.8	92.5	30	15	US-09-864-785-2187	Sequence 2186, App
152	14.8	92.5	30	11	US-09-740-332-9601	Sequence 9601, App	225	14.8	92.5	30	15	US-09-864-785-2188	Sequence 2187, App
153	14.8	92.5	30	11	US-09-740-332-9602	Sequence 9602, App	226	14.8	92.5	30	15	US-09-864-785-2189	Sequence 2188, App
154	14.8	92.5	30	11	US-09-740-332-9603	Sequence 9603, App	227	14.8	92.5	30	15	US-09-864-785-2190	Sequence 2189, App
155	14.8	92.5	30	11	US-09-740-332-9604	Sequence 9604, App	228	14.8	92.5	30	15	US-09-864-785-2191	Sequence 2190, App
156	14.8	92.5	30	11	US-09-740-332-9605	Sequence 9605, App	229	14.8	92.5	30	15	US-09-864-785-2192	Sequence 2191, App
157	14.8	92.5	30	11	US-09-740-332-9606	Sequence 9606, App	230	14.8	92.5	30	15	US-09-864-785-2193	Sequence 2192, App
158	14.8	92.5	30	13	US-09-792-818-2287	Sequence 2287, App	231	14.8	92.5	30	15	US-09-864-785-2194	Sequence 2193, App
159	14.8	92.5	30	13	US-09-792-818-2288	Sequence 2288, App	232	14.8	92.5	30	15	US-09-864-785-2195	Sequence 2194, App
160	14.8	92.5	30	13	US-09-792-818-2289	Sequence 2289, App	233	14.8	92.5	30	15	US-09-864-785-2196	Sequence 2195, App
161	14.8	92.5	30	13	US-09-792-818-2290	Sequence 2290, App	234	14.8	92.5	30	15	US-09-864-785-2197	Sequence 2196, App

235	14.8	92.5	31	10	US-09-864-785-2198	Sequence	2198	Ap	308	14.8	92.5	31	10	US-09-864-785-2271	Sequence	2271	Ap
236	14.8	92.5	31	10	US-09-864-785-2199	Sequence	2199	Ap	309	14.8	92.5	31	10	US-09-864-785-2272	Sequence	2272	Ap
237	14.8	92.5	31	10	US-09-864-785-2200	Sequence	2200	Ap	310	14.8	92.5	31	10	US-09-864-785-2273	Sequence	2273	Ap
238	14.8	92.5	31	10	US-09-864-785-2201	Sequence	2201	Ap	311	14.8	92.5	31	10	US-09-864-785-2274	Sequence	2274	Ap
239	14.8	92.5	31	10	US-09-864-785-2202	Sequence	2202	Ap	312	14.8	92.5	31	10	US-09-864-785-2275	Sequence	2275	Ap
240	14.8	92.5	31	10	US-09-864-785-2203	Sequence	2203	Ap	313	14.8	92.5	31	10	US-09-864-785-2276	Sequence	2276	Ap
241	14.8	92.5	31	10	US-09-864-785-2204	Sequence	2204	Ap	314	14.8	92.5	31	10	US-09-864-785-2277	Sequence	2277	Ap
242	14.8	92.5	31	10	US-09-864-785-2205	Sequence	2205	Ap	315	14.8	92.5	31	10	US-09-864-785-2278	Sequence	2278	Ap
243	14.8	92.5	31	10	US-09-864-785-2206	Sequence	2206	Ap	316	14.8	92.5	31	10	US-09-864-785-2279	Sequence	2279	Ap
244	14.8	92.5	31	10	US-09-864-785-2207	Sequence	2207	Ap	317	14.8	92.5	31	10	US-09-864-785-2280	Sequence	2280	Ap
245	14.8	92.5	31	10	US-09-864-785-2208	Sequence	2208	Ap	318	14.8	92.5	31	10	US-09-864-785-2281	Sequence	2281	Ap
246	14.8	92.5	31	10	US-09-864-785-2209	Sequence	2209	Ap	319	14.8	92.5	31	10	US-09-864-785-2282	Sequence	2282	Ap
247	14.8	92.5	31	10	US-09-864-785-2210	Sequence	2210	Ap	320	14.8	92.5	31	10	US-09-864-785-2283	Sequence	2283	Ap
248	14.8	92.5	31	10	US-09-864-785-2211	Sequence	2211	Ap	321	14.8	92.5	31	10	US-09-864-785-2284	Sequence	2284	Ap
249	14.8	92.5	31	10	US-09-864-785-2212	Sequence	2212	Ap	322	14.8	92.5	31	10	US-09-864-785-2285	Sequence	2285	Ap
250	14.8	92.5	31	10	US-09-864-785-2213	Sequence	2213	Ap	323	14.8	92.5	31	10	US-09-864-785-2286	Sequence	2286	Ap
251	14.8	92.5	31	10	US-09-864-785-2214	Sequence	2214	Ap	324	14.8	92.5	31	10	US-09-864-785-2287	Sequence	2287	Ap
252	14.8	92.5	31	10	US-09-864-785-2215	Sequence	2215	Ap	325	14.8	92.5	31	10	US-09-864-785-2288	Sequence	2288	Ap
253	14.8	92.5	31	10	US-09-864-785-2216	Sequence	2216	Ap	326	14.8	92.5	31	10	US-09-864-785-2289	Sequence	2289	Ap
254	14.8	92.5	31	10	US-09-864-785-2217	Sequence	2217	Ap	327	14.8	92.5	31	10	US-09-864-785-2290	Sequence	2290	Ap
255	14.8	92.5	31	10	US-09-864-785-2218	Sequence	2218	Ap	328	14.8	92.5	31	10	US-09-864-785-2291	Sequence	2291	Ap
256	14.8	92.5	31	10	US-09-864-785-2219	Sequence	2219	Ap	329	14.8	92.5	31	10	US-09-864-785-2292	Sequence	2292	Ap
257	14.8	92.5	31	10	US-09-864-785-2220	Sequence	2220	Ap	330	14.8	92.5	31	10	US-09-864-785-2293	Sequence	2293	Ap
258	14.8	92.5	31	10	US-09-864-785-2221	Sequence	2221	Ap	331	14.8	92.5	31	10	US-09-864-785-2294	Sequence	2294	Ap
259	14.8	92.5	31	10	US-09-864-785-2222	Sequence	2222	Ap	332	14.8	92.5	31	10	US-09-864-785-2295	Sequence	2295	Ap
260	14.8	92.5	31	10	US-09-864-785-2223	Sequence	2223	Ap	333	14.8	92.5	31	10	US-09-864-785-2296	Sequence	2296	Ap
261	14.8	92.5	31	10	US-09-864-785-2224	Sequence	2224	Ap	334	14.8	92.5	31	10	US-09-864-785-2297	Sequence	2297	Ap
262	14.8	92.5	31	10	US-09-864-785-2225	Sequence	2225	Ap	335	14.8	92.5	31	10	US-09-864-785-2298	Sequence	2298	Ap
263	14.8	92.5	31	10	US-09-864-785-2226	Sequence	2226	Ap	336	14.8	92.5	31	10	US-09-864-785-2299	Sequence	2299	Ap
264	14.8	92.5	31	10	US-09-864-785-2227	Sequence	2227	Ap	337	14.8	92.5	31	10	US-09-864-785-2300	Sequence	2300	Ap
265	14.8	92.5	31	10	US-09-864-785-2228	Sequence	2228	Ap	338	14.8	92.5	31	10	US-09-864-785-2301	Sequence	2301	Ap
266	14.8	92.5	31	10	US-09-864-785-2229	Sequence	2229	Ap	339	14.8	92.5	31	10	US-09-864-785-2302	Sequence	2302	Ap
267	14.8	92.5	31	10	US-09-864-785-2230	Sequence	2230	Ap	340	14.8	92.5	31	10	US-09-864-785-2303	Sequence	2303	Ap
268	14.8	92.5	31	10	US-09-864-785-2231	Sequence	2231	Ap	341	14.8	92.5	31	10	US-09-864-785-2304	Sequence	2304	Ap
269	14.8	92.5	31	10	US-09-864-785-2232	Sequence	2232	Ap	342	14.8	92.5	31	10	US-09-864-785-2305	Sequence	2305	Ap
270	14.8	92.5	31	10	US-09-864-785-2233	Sequence	2233	Ap	343	14.8	92.5	31	10	US-09-864-785-2306	Sequence	2306	Ap
271	14.8	92.5	31	10	US-09-864-785-2234	Sequence	2234	Ap	344	14.8	92.5	31	10	US-09-864-785-2307	Sequence	2307	Ap
272	14.8	92.5	31	10	US-09-864-785-2235	Sequence	2235	Ap	345	14.8	92.5	31	10	US-09-864-785-2308	Sequence	2308	Ap
273	14.8	92.5	31	10	US-09-864-785-2236	Sequence	2236	Ap	346	14.8	92.5	31	10	US-09-864-785-2309	Sequence	2309	Ap
274	14.8	92.5	31	10	US-09-864-785-2237	Sequence	2237	Ap	347	14.8	92.5	31	10	US-09-864-785-2310	Sequence	2310	Ap
275	14.8	92.5	31	10	US-09-864-785-2238	Sequence	2238	Ap	348	14.8	92.5	31	10	US-09-864-785-2311	Sequence	2311	Ap
276	14.8	92.5	31	10	US-09-864-785-2239	Sequence	2239	Ap	349	14.8	92.5	31	10	US-09-864-785-2312	Sequence	2312	Ap
277	14.8	92.5	31	10	US-09-864-785-2240	Sequence	2240	Ap	350	14.8	92.5	31	10	US-09-864-785-2313	Sequence	2313	Ap
278	14.8	92.5	31	10	US-09-864-785-2241	Sequence	2241	Ap	351	14.8	92.5	31	10	US-09-864-785-2314	Sequence	2314	Ap
279	14.8	92.5	31	10	US-09-864-785-2242	Sequence	2242	Ap	352	14.8	92.5	31	10	US-09-864-785-2315	Sequence	2315	Ap
280	14.8	92.5	31	10	US-09-864-785-2243	Sequence	2243	Ap	353	14.8	92.5	31	10	US-09-864-785-2316	Sequence	2316	Ap
281	14.8	92.5	31	10	US-09-864-785-2244	Sequence	2244	Ap	354	14.8	92.5	31	10	US-09-864-785-2317	Sequence	2317	Ap
282	14.8	92.5	31	10	US-09-864-785-2245	Sequence	2245	Ap	355	14.8	92.5	31	10	US-09-864-785-2318	Sequence	2318	Ap
283	14.8	92.5	31	10	US-09-864-785-2246	Sequence	2246	Ap	356	14.8	92.5	31	10	US-09-864-785-2319	Sequence	2319	Ap
284	14.8	92.5	31	10	US-09-864-785-2247	Sequence	2247	Ap	357	14.8	92.5	31	10	US-09-864-785-2320	Sequence	2320	Ap
285	14.8	92.5	31	10	US-09-864-785-2248	Sequence	2248	Ap	358	14.8	92.5	31	10	US-09-864-785-2321	Sequence	2321	Ap
286	14.8	92.5	31	10	US-09-864-785-2249	Sequence	2249	Ap	359	14.8	92.5	31	10	US-09-864-785-2322	Sequence	2322	Ap
287	14.8	92.5	31	10	US-09-864-785-2250	Sequence	2250	Ap	360	14.8	92.5	31	10	US-09-864-785-2323	Sequence	2323	Ap
288	14.8	92.5	31	10	US-09-864-785-2251	Sequence	2251	Ap	361	14.8	92.5	31	10	US-09-864-785-2324	Sequence	2324	Ap
289	14.8	92.5	31	10	US-09-864-785-2252	Sequence	2252	Ap	362	14.8	92.5	31	10	US-09-864-785-2325	Sequence	2325	Ap
290	14.8	92.5	31	10	US-09-864-785-2253	Sequence	2253	Ap	363	14.8	92.5	31	10	US-09-864-785-2326	Sequence	2326	Ap
291	14.8	92.5	31	10	US-09-864-785-2254	Sequence	2254	Ap	364	14.8	92.5	31	10	US-09-864-785-2327	Sequence	2327	Ap
292	14.8	92.5	31	10	US-09-864-785-2255	Sequence	2255	Ap	365	14.8	92.5	31	10	US-09-864-785-2328	Sequence	2328	Ap
293	14.8	92.5	31	10	US-09-864-785-2256	Sequence	2256	Ap	366	14.8	92.5	31	10	US-09-864-785-2329	Sequence	2329	Ap
294	14.8	92.5	31	10	US-09-864-785-2257	Sequence	2257	Ap	367	14.8	92.5	31	10	US-09-864-785-2330	Sequence	2330	Ap
295	14.8	92.5	31	10	US-09-864-785-2258	Sequence	2258	Ap	368	14.8	92.5	31	10	US-09-864-785-2331	Sequence	2331	Ap
296	14.8	92.5	31	10	US-09-864-785-2259	Sequence	2259	Ap	369	14.8	92.5	31	10	US-09-864-785-2332	Sequence	2332	Ap
297	14.8	92.5	31	10	US-09-864-785-2260	Sequence	2260	Ap	370	14.8	92.5	31	10	US-09-864-785-2333	Sequence	2333	Ap
298	14.8	92.5	31	10	US-09-864-785-2261	Sequence	2261	Ap	371	14.8	92.5	31	10	US-09-864-785-2334	Sequence	2334	Ap
299	14.8	92.5	31	10	US-09-864-785-2262	Sequence	2262	Ap	372	14.8	92.5	31	10	US-09-864-785-2335	Sequence	2335	Ap
300	14.8	92.5	31	10	US-09-864-785-2263	Sequence	2263	Ap	373	14.8	92.5	31	10	US-09-864-785-2336	Sequence	2336	Ap
301	14.8	92.5	31	10	US-09-864-785-2264	Sequence	2264	Ap	374	14.8	92.5	31	10	US-09-864-785-2337	Sequence	2337	Ap
302	14.8	92.5	31	10	US-09-864-785-2265	Sequence	2265	Ap	375	14.8	92.5	31	10	US-09-864-785-2338	Sequence	2338	Ap
303	14.8	92.5	31	10	US-09-864-785-2266	Sequence	2266	Ap	376	14.8	92.5	31	10	US-09-864-785-2339	Sequence	2339	Ap
304	14.8	92.5	31	10	US-09-864-785-2267	Sequence	2267	Ap	377	14.8	92.5	31	10	US-09-864-785-2340	Sequence	2340	Ap
305	14.8	92.5	31	10	US-09-864-785-2268	Sequence	2268	Ap	378	14.8	92.5	31	10	US-09-864-785-2341	Sequence	2341	Ap
306	14.8	92.5	31	10	US-09-864-785-2269	Sequence	2269	Ap	379	14.8	92.5	31	10	US-09-864-785-2342	Sequence	2342	Ap
307	14.8	92.5	31	10	US-09-864-785-2270	Sequence	2270	Ap	380	14.8	92.5	31	10	US-09-864-785-23			

527	14.8	92.5	31	10	US-09-864-785-2490	Sequence 2490, Ap	600	14.8	92.5	31	10	US-09-864-785-2563	Sequence 2563, Ap
528	14.8	92.5	31	10	US-09-864-785-2491	Sequence 2491, Ap	601	14.8	92.5	31	10	US-09-864-785-2564	Sequence 2564, Ap
529	14.8	92.5	31	10	US-09-864-785-2492	Sequence 2492, Ap	602	14.8	92.5	31	10	US-09-864-785-2565	Sequence 2565, Ap
530	14.8	92.5	31	10	US-09-864-785-2493	Sequence 2493, Ap	603	14.8	92.5	31	10	US-09-864-785-2566	Sequence 2566, Ap
531	14.8	92.5	31	10	US-09-864-785-2494	Sequence 2494, Ap	604	14.8	92.5	31	10	US-09-864-785-2567	Sequence 2567, Ap
532	14.8	92.5	31	10	US-09-864-785-2495	Sequence 2495, Ap	605	14.8	92.5	31	10	US-09-864-785-2568	Sequence 2568, Ap
533	14.8	92.5	31	10	US-09-864-785-2496	Sequence 2496, Ap	606	14.8	92.5	31	10	US-09-864-785-2569	Sequence 2569, Ap
534	14.8	92.5	31	10	US-09-864-785-2497	Sequence 2497, Ap	607	14.8	92.5	31	10	US-09-864-785-2570	Sequence 2570, Ap
535	14.8	92.5	31	10	US-09-864-785-2498	Sequence 2498, Ap	608	14.8	92.5	31	10	US-09-864-785-2571	Sequence 2571, Ap
536	14.8	92.5	31	10	US-09-864-785-2499	Sequence 2499, Ap	609	14.8	92.5	31	10	US-09-864-785-2572	Sequence 2572, Ap
537	14.8	92.5	31	10	US-09-864-785-2500	Sequence 2500, Ap	610	14.8	92.5	31	10	US-09-864-785-2573	Sequence 2573, Ap
538	14.8	92.5	31	10	US-09-864-785-2501	Sequence 2501, Ap	611	14.8	92.5	31	10	US-09-864-785-2574	Sequence 2574, Ap
539	14.8	92.5	31	10	US-09-864-785-2502	Sequence 2502, Ap	612	14.8	92.5	31	10	US-09-864-785-2575	Sequence 2575, Ap
540	14.8	92.5	31	10	US-09-864-785-2503	Sequence 2503, Ap	613	14.8	92.5	31	10	US-09-864-785-2576	Sequence 2576, Ap
541	14.8	92.5	31	10	US-09-864-785-2504	Sequence 2504, Ap	614	14.8	92.5	31	10	US-09-864-785-2577	Sequence 2577, Ap
542	14.8	92.5	31	10	US-09-864-785-2505	Sequence 2505, Ap	615	14.8	92.5	31	10	US-09-864-785-2578	Sequence 2578, Ap
543	14.8	92.5	31	10	US-09-864-785-2506	Sequence 2506, Ap	616	14.8	92.5	31	10	US-09-864-785-2579	Sequence 2579, Ap
544	14.8	92.5	31	10	US-09-864-785-2507	Sequence 2507, Ap	617	14.8	92.5	31	10	US-09-864-785-2580	Sequence 2580, Ap
545	14.8	92.5	31	10	US-09-864-785-2508	Sequence 2508, Ap	618	14.8	92.5	31	10	US-09-864-785-2581	Sequence 2581, Ap
546	14.8	92.5	31	10	US-09-864-785-2509	Sequence 2509, Ap	619	14.8	92.5	31	10	US-09-864-785-2582	Sequence 2582, Ap
547	14.8	92.5	31	10	US-09-864-785-2510	Sequence 2510, Ap	620	14.8	92.5	31	10	US-09-864-785-2583	Sequence 2583, Ap
548	14.8	92.5	31	10	US-09-864-785-2511	Sequence 2511, Ap	621	14.8	92.5	31	10	US-09-864-785-2584	Sequence 2584, Ap
549	14.8	92.5	31	10	US-09-864-785-2512	Sequence 2512, Ap	622	14.8	92.5	31	10	US-09-864-785-2585	Sequence 2585, Ap
550	14.8	92.5	31	10	US-09-864-785-2513	Sequence 2513, Ap	623	14.8	92.5	31	10	US-09-864-785-2586	Sequence 2586, Ap
551	14.8	92.5	31	10	US-09-864-785-2514	Sequence 2514, Ap	624	14.8	92.5	31	10	US-09-864-785-2587	Sequence 2587, Ap
552	14.8	92.5	31	10	US-09-864-785-2515	Sequence 2515, Ap	625	14.8	92.5	31	10	US-09-864-785-2588	Sequence 2588, Ap
553	14.8	92.5	31	10	US-09-864-785-2516	Sequence 2516, Ap	626	14.8	92.5	31	10	US-09-864-785-2589	Sequence 2589, Ap
554	14.8	92.5	31	10	US-09-864-785-2517	Sequence 2517, Ap	627	14.8	92.5	31	10	US-09-864-785-2590	Sequence 2590, Ap
555	14.8	92.5	31	10	US-09-864-785-2518	Sequence 2518, Ap	628	14.8	92.5	31	10	US-09-864-785-2591	Sequence 2591, Ap
556	14.8	92.5	31	10	US-09-864-785-2519	Sequence 2519, Ap	629	14.8	92.5	31	10	US-09-864-785-2592	Sequence 2592, Ap
557	14.8	92.5	31	10	US-09-864-785-2520	Sequence 2520, Ap	630	14.8	92.5	31	10	US-09-864-785-2593	Sequence 2593, Ap
558	14.8	92.5	31	10	US-09-864-785-2521	Sequence 2521, Ap	631	14.8	92.5	31	10	US-09-864-785-2594	Sequence 2594, Ap
559	14.8	92.5	31	10	US-09-864-785-2522	Sequence 2522, Ap	632	14.8	92.5	31	10	US-09-864-785-2595	Sequence 2595, Ap
560	14.8	92.5	31	10	US-09-864-785-2523	Sequence 2523, Ap	633	14.8	92.5	31	10	US-09-864-785-2596	Sequence 2596, Ap
561	14.8	92.5	31	10	US-09-864-785-2524	Sequence 2524, Ap	634	14.8	92.5	31	10	US-09-864-785-2597	Sequence 2597, Ap
562	14.8	92.5	31	10	US-09-864-785-2525	Sequence 2525, Ap	635	14.8	92.5	31	10	US-09-864-785-2598	Sequence 2598, Ap
563	14.8	92.5	31	10	US-09-864-785-2526	Sequence 2526, Ap	636	14.8	92.5	31	10	US-09-864-785-2599	Sequence 2599, Ap
564	14.8	92.5	31	10	US-09-864-785-2527	Sequence 2527, Ap	637	14.8	92.5	31	10	US-09-864-785-2600	Sequence 2600, Ap
565	14.8	92.5	31	10	US-09-864-785-2528	Sequence 2528, Ap	638	14.8	92.5	31	10	US-09-864-785-2601	Sequence 2601, Ap
566	14.8	92.5	31	10	US-09-864-785-2529	Sequence 2529, Ap	639	14.8	92.5	31	10	US-09-864-785-2602	Sequence 2602, Ap
567	14.8	92.5	31	10	US-09-864-785-2530	Sequence 2530, Ap	640	14.8	92.5	31	10	US-09-864-785-2603	Sequence 2603, Ap
568	14.8	92.5	31	10	US-09-864-785-2531	Sequence 2531, Ap	641	14.8	92.5	31	10	US-09-864-785-2604	Sequence 2604, Ap
569	14.8	92.5	31	10	US-09-864-785-2532	Sequence 2532, Ap	642	14.8	92.5	31	10	US-09-864-785-2605	Sequence 2605, Ap
570	14.8	92.5	31	10	US-09-864-785-2533	Sequence 2533, Ap	643	14.8	92.5	31	10	US-09-864-785-2606	Sequence 2606, Ap
571	14.8	92.5	31	10	US-09-864-785-2534	Sequence 2534, Ap	644	14.8	92.5	31	10	US-09-864-785-2607	Sequence 2607, Ap
572	14.8	92.5	31	10	US-09-864-785-2535	Sequence 2535, Ap	645	14.8	92.5	31	10	US-09-864-785-2608	Sequence 2608, Ap
573	14.8	92.5	31	10	US-09-864-785-2536	Sequence 2536, Ap	646	14.8	92.5	31	10	US-09-864-785-2609	Sequence 2609, Ap
574	14.8	92.5	31	10	US-09-864-785-2537	Sequence 2537, Ap	647	14.8	92.5	31	10	US-09-864-785-2610	Sequence 2610, Ap
575	14.8	92.5	31	10	US-09-864-785-2538	Sequence 2538, Ap	648	14.8	92.5	31	10	US-09-864-785-2611	Sequence 2611, Ap
576	14.8	92.5	31	10	US-09-864-785-2539	Sequence 2539, Ap	649	14.8	92.5	31	10	US-09-864-785-2612	Sequence 2612, Ap
577	14.8	92.5	31	10	US-09-864-785-2540	Sequence 2540, Ap	650	14.8	92.5	31	10	US-09-864-785-2613	Sequence 2613, Ap
578	14.8	92.5	31	10	US-09-864-785-2541	Sequence 2541, Ap	651	14.8	92.5	31	10	US-09-864-785-2614	Sequence 2614, Ap
579	14.8	92.5	31	10	US-09-864-785-2542	Sequence 2542, Ap	652	14.8	92.5	31	10	US-09-864-785-2615	Sequence 2615, Ap
580	14.8	92.5	31	10	US-09-864-785-2543	Sequence 2543, Ap	653	14.8	92.5	31	10	US-09-864-785-2616	Sequence 2616, Ap
581	14.8	92.5	31	10	US-09-864-785-2544	Sequence 2544, Ap	654	14.8	92.5	31	10	US-09-864-785-2617	Sequence 2617, Ap
582	14.8	92.5	31	10	US-09-864-785-2545	Sequence 2545, Ap	655	14.8	92.5	31	10	US-09-864-785-2618	Sequence 2618, Ap
583	14.8	92.5	31	10	US-09-864-785-2546	Sequence 2546, Ap	656	14.8	92.5	31	10	US-09-864-785-2619	Sequence 2619, Ap
584	14.8	92.5	31	10	US-09-864-785-2547	Sequence 2547, Ap	657	14.8	92.5	31	10	US-09-864-785-2620	Sequence 2620, Ap
585	14.8	92.5	31	10	US-09-864-785-2548	Sequence 2548, Ap	658	14.8	92.5	31	10	US-09-864-785-2621	Sequence 2621, Ap
586	14.8	92.5	31	10	US-09-864-785-2549	Sequence 2549, Ap	659	14.8	92.5	31	10	US-09-864-785-2622	Sequence 2622, Ap
587	14.8	92.5	31	10	US-09-864-785-2550	Sequence 2550, Ap	660	14.8	92.5	31	10	US-09-864-785-2623	Sequence 2623, Ap
588	14.8	92.5	31	10	US-09-864-785-2551	Sequence 2551, Ap	661	14.8	92.5	31	10	US-09-864-785-2624	Sequence 2624, Ap
589	14.8	92.5	31	10	US-09-864-785-2552	Sequence 2552, Ap	662	14.8	92.5	31	10	US-09-864-785-2625	Sequence 2625, Ap
590	14.8	92.5	31	10	US-09-864-785-2553	Sequence 2553, Ap	663	14.8	92.5	31	10	US-09-864-785-2626	Sequence 2626, Ap
591	14.8	92.5	31	10	US-09-864-785-2554	Sequence 2554, Ap	664	14.8	92.5	31	10	US-09-864-785-2627	Sequence 2627, Ap
592	14.8	92.5	31	10	US-09-864-785-2555	Sequence 2555, Ap	665	14.8	92.5	31	10	US-09-864-785-2628	Sequence 2628, Ap
593	14.8	92.5	31	10	US-09-864-785-2556	Sequence 2556, Ap	666	14.8	92.5	31	10	US-09-864-785-2629	Sequence 2629, Ap
594	14.8	92.5	31	10	US-09-864-785-2557	Sequence 2557, Ap	667	14.8	92.5	31	10	US-09-864-785-2630	Sequence 2630, Ap
595	14.8	92.5	31	10	US-09-864-785-2558	Sequence 2558, Ap	668	14.8	92.5	31	10	US-09-864-785-2631	Sequence 2631, Ap
596	14.8	92.5	31	10	US-09-864-785-2559	Sequence 2559, Ap	669	14.8	92.5	31	10	US-09-864-785-2632	Sequence 2632, Ap
597	14.8	92.5	31	10	US-09-864-785-2560	Sequence 2560, Ap	670	14.8	92.5	31	10	US-09-864-785-2633	Sequence 2633, Ap
598	14.8	92.5	31	10	US-09-864-785-2561	Sequence 2561, Ap	671	14.8	92.5	31	10	US-09-864-785-2634	Sequence 2634, Ap
599	14.8	92.5	31	10	US-09-864-785-2562	Sequence 2562, Ap	672	14.8	92.5	31	10	US-09-864-785-2635	Sequence 2635, Ap

673	14.8	92.5	31	10	US-09-864-785-2636	Sequence 2636, Ap	746	14.8	92.5	31	11	US-09-730-289B-2952	Sequence 2952, Ap
674	14.8	92.5	31	10	US-09-864-785-2637	Sequence 2637, Ap	747	14.8	92.5	31	11	US-09-730-289B-2953	Sequence 2953, Ap
675	14.8	92.5	31	10	US-09-864-785-2638	Sequence 2638, Ap	748	14.8	92.5	31	11	US-09-730-289B-2954	Sequence 2954, Ap
676	14.8	92.5	31	10	US-09-864-785-2639	Sequence 2639, Ap	749	14.8	92.5	31	11	US-09-730-289B-2955	Sequence 2955, Ap
677	14.8	92.5	31	10	US-09-864-785-2640	Sequence 2640, Ap	750	14.8	92.5	31	11	US-09-730-289B-2956	Sequence 2956, Ap
678	14.8	92.5	31	10	US-09-864-785-2641	Sequence 2641, Ap	751	14.8	92.5	31	11	US-09-730-289B-2957	Sequence 2957, Ap
679	14.8	92.5	31	10	US-09-864-785-2642	Sequence 2642, Ap	752	14.8	92.5	31	11	US-09-730-289B-2958	Sequence 2958, Ap
680	14.8	92.5	31	10	US-09-864-785-2643	Sequence 2643, Ap	753	14.8	92.5	31	11	US-09-730-289B-2959	Sequence 2959, Ap
681	14.8	92.5	31	10	US-09-864-785-2644	Sequence 2644, Ap	754	14.8	92.5	31	11	US-09-730-289B-2960	Sequence 2960, Ap
682	14.8	92.5	31	10	US-09-864-785-2645	Sequence 2645, Ap	755	14.8	92.5	31	11	US-09-730-289B-2961	Sequence 2961, Ap
683	14.8	92.5	31	10	US-09-864-785-2646	Sequence 2646, Ap	756	14.8	92.5	31	11	US-09-730-289B-2962	Sequence 2962, Ap
684	14.8	92.5	31	10	US-09-864-785-2647	Sequence 2647, Ap	757	14.8	92.5	31	11	US-09-730-289B-2963	Sequence 2963, Ap
685	14.8	92.5	31	10	US-09-864-785-2648	Sequence 2648, Ap	758	14.8	92.5	31	11	US-09-730-289B-2964	Sequence 2964, Ap
686	14.8	92.5	31	10	US-09-864-785-2649	Sequence 2649, Ap	759	14.8	92.5	31	11	US-09-730-289B-2965	Sequence 2965, Ap
687	14.8	92.5	31	10	US-09-864-785-2650	Sequence 2650, Ap	760	14.8	92.5	31	11	US-09-730-289B-2966	Sequence 2966, Ap
688	14.8	92.5	31	10	US-09-864-785-2651	Sequence 2651, Ap	761	14.8	92.5	31	11	US-09-730-289B-2967	Sequence 2967, Ap
689	14.8	92.5	31	10	US-09-864-785-2652	Sequence 2652, Ap	762	14.8	92.5	31	11	US-09-730-289B-2968	Sequence 2968, Ap
690	14.8	92.5	31	10	US-09-864-785-2653	Sequence 2653, Ap	763	14.8	92.5	31	11	US-09-730-289B-2969	Sequence 2969, Ap
691	14.8	92.5	31	10	US-09-864-785-2654	Sequence 2654, Ap	764	14.8	92.5	31	11	US-09-730-289B-2970	Sequence 2970, Ap
692	14.8	92.5	31	10	US-09-864-785-2655	Sequence 2655, Ap	765	14.8	92.5	31	11	US-09-730-289B-2971	Sequence 2971, Ap
693	14.8	92.5	31	10	US-09-864-785-2656	Sequence 2656, Ap	766	14.8	92.5	31	11	US-09-730-289B-2972	Sequence 2972, Ap
694	14.8	92.5	31	10	US-09-864-785-2657	Sequence 2657, Ap	767	14.8	92.5	31	11	US-09-730-289B-2973	Sequence 2973, Ap
695	14.8	92.5	31	11	US-09-730-289B-2974	Sequence 2974, Ap	768	14.8	92.5	31	11	US-09-730-289B-2975	Sequence 2975, Ap
696	14.8	92.5	31	11	US-09-730-289B-2976	Sequence 2976, Ap	769	14.8	92.5	31	11	US-09-730-289B-2977	Sequence 2977, Ap
697	14.8	92.5	31	11	US-09-730-289B-2978	Sequence 2978, Ap	770	14.8	92.5	31	11	US-09-730-289B-2979	Sequence 2979, Ap
698	14.8	92.5	31	11	US-09-730-289B-2980	Sequence 2980, Ap	771	14.8	92.5	31	11	US-09-730-289B-2981	Sequence 2981, Ap
699	14.8	92.5	31	11	US-09-730-289B-2982	Sequence 2982, Ap	772	14.8	92.5	31	11	US-09-730-289B-2983	Sequence 2983, Ap
700	14.8	92.5	31	11	US-09-730-289B-2984	Sequence 2984, Ap	773	14.8	92.5	31	11	US-09-730-289B-2985	Sequence 2985, Ap
701	14.8	92.5	31	11	US-09-730-289B-2986	Sequence 2986, Ap	774	14.8	92.5	31	11	US-09-730-289B-2987	Sequence 2987, Ap
702	14.8	92.5	31	11	US-09-730-289B-2988	Sequence 2988, Ap	775	14.8	92.5	31	11	US-09-730-289B-2989	Sequence 2989, Ap
703	14.8	92.5	31	11	US-09-730-289B-2990	Sequence 2990, Ap	776	14.8	92.5	31	11	US-09-730-289B-2991	Sequence 2991, Ap
704	14.8	92.5	31	11	US-09-730-289B-2992	Sequence 2992, Ap	777	14.8	92.5	31	11	US-09-730-289B-2993	Sequence 2993, Ap
705	14.8	92.5	31	11	US-09-730-289B-2994	Sequence 2994, Ap	778	14.8	92.5	31	11	US-09-730-289B-2995	Sequence 2995, Ap
706	14.8	92.5	31	11	US-09-730-289B-2996	Sequence 2996, Ap	779	14.8	92.5	31	11	US-09-730-289B-2997	Sequence 2997, Ap
707	14.8	92.5	31	11	US-09-730-289B-2998	Sequence 2998, Ap	780	14.8	92.5	31	11	US-09-730-289B-2999	Sequence 2999, Ap
708	14.8	92.5	31	11	US-09-730-289B-3000	Sequence 3000, Ap	781	14.8	92.5	31	11	US-09-730-289B-3001	Sequence 3001, Ap
709	14.8	92.5	31	11	US-09-730-289B-3002	Sequence 3002, Ap	782	14.8	92.5	31	11	US-09-730-289B-3003	Sequence 3003, Ap
710	14.8	92.5	31	11	US-09-730-289B-3004	Sequence 3004, Ap	783	14.8	92.5	31	11	US-09-730-289B-3005	Sequence 3005, Ap
711	14.8	92.5	31	11	US-09-730-289B-3006	Sequence 3006, Ap	784	14.8	92.5	31	11	US-09-730-289B-3007	Sequence 3007, Ap
712	14.8	92.5	31	11	US-09-730-289B-3008	Sequence 3008, Ap	785	14.8	92.5	31	11	US-09-730-289B-3009	Sequence 3009, Ap
713	14.8	92.5	31	11	US-09-730-289B-3010	Sequence 3010, Ap	786	14.8	92.5	31	11	US-09-730-289B-3011	Sequence 3011, Ap
714	14.8	92.5	31	11	US-09-730-289B-3012	Sequence 3012, Ap	787	14.8	92.5	31	11	US-09-730-289B-3013	Sequence 3013, Ap
715	14.8	92.5	31	11	US-09-730-289B-3014	Sequence 3014, Ap	788	14.8	92.5	31	11	US-09-730-289B-3015	Sequence 3015, Ap
716	14.8	92.5	31	11	US-09-730-289B-3016	Sequence 3016, Ap	789	14.8	92.5	31	11	US-09-730-289B-3017	Sequence 3017, Ap
717	14.8	92.5	31	11	US-09-730-289B-3018	Sequence 3018, Ap	790	14.8	92.5	31	11	US-09-730-289B-3019	Sequence 3019, Ap
718	14.8	92.5	31	11	US-09-730-289B-3020	Sequence 3020, Ap	791	14.8	92.5	31	11	US-09-730-289B-3021	Sequence 3021, Ap
719	14.8	92.5	31	11	US-09-730-289B-3022	Sequence 3022, Ap	792	14.8	92.5	31	11	US-09-730-289B-3023	Sequence 3023, Ap
720	14.8	92.5	31	11	US-09-730-289B-3024	Sequence 3024, Ap	793	14.8	92.5	31	11	US-09-730-289B-3025	Sequence 3025, Ap
721	14.8	92.5	31	11	US-09-730-289B-3026	Sequence 3026, Ap	794	14.8	92.5	31	11	US-09-730-289B-3027	Sequence 3027, Ap
722	14.8	92.5	31	11	US-09-730-289B-3028	Sequence 3028, Ap	795	14.8	92.5	31	11	US-09-730-289B-3029	Sequence 3029, Ap
723	14.8	92.5	31	11	US-09-730-289B-3030	Sequence 3030, Ap	796	14.8	92.5	31	11	US-09-730-289B-3031	Sequence 3031, Ap
724	14.8	92.5	31	11	US-09-730-289B-3032	Sequence 3032, Ap	797	14.8	92.5	31	11	US-09-730-289B-3033	Sequence 3033, Ap
725	14.8	92.5	31	11	US-09-730-289B-3034	Sequence 3034, Ap	798	14.8	92.5	31	11	US-09-730-289B-3035	Sequence 3035, Ap
726	14.8	92.5	31	11	US-09-730-289B-3036	Sequence 3036, Ap	799	14.8	92.5	31	11	US-09-730-289B-3037	Sequence 3037, Ap
727	14.8	92.5	31	11	US-09-730-289B-3038	Sequence 3038, Ap	800	14.8	92.5	31	11	US-09-730-289B-3039	Sequence 3039, Ap
728	14.8	92.5	31	11	US-09-730-289B-3040	Sequence 3040, Ap	801	14.8	92.5	31	11	US-09-730-289B-3041	Sequence 3041, Ap
729	14.8	92.5	31	11	US-09-730-289B-3042	Sequence 3042, Ap	802	14.8	92.5	31	11	US-09-730-289B-3043	Sequence 3043, Ap
730	14.8	92.5	31	11	US-09-730-289B-3044	Sequence 3044, Ap	803	14.8	92.5	31	11	US-09-730-289B-3045	Sequence 3045, Ap
731	14.8	92.5	31	11	US-09-730-289B-3046	Sequence 3046, Ap	804	14.8	92.5	31	11	US-09-730-289B-3047	Sequence 3047, Ap
732	14.8	92.5	31	11	US-09-730-289B-3048	Sequence 3048, Ap	805	14.8	92.5	31	11	US-09-730-289B-3049	Sequence 3049, Ap
733	14.8	92.5	31	11	US-09-730-289B-3050	Sequence 3050, Ap	806	14.8	92.5	31	11	US-09-730-289B-3051	Sequence 3051, Ap
734	14.8	92.5	31	11	US-09-730-289B-3052	Sequence 3052, Ap	807	14.8	92.5	31	11	US-09-730-289B-3053	Sequence 3053, Ap
735	14.8	92.5	31	11	US-09-730-289B-3054	Sequence 3054, Ap	808	14.8	92.5	31	11	US-09-730-289B-3055	Sequence 3055, Ap
736	14.8	92.5	31	11	US-09-730-289B-3056	Sequence 3056, Ap	809	14.8	92.5	31	11	US-09-730-289B-3057	Sequence 3057, Ap
737	14.8	92.5	31	11	US-09-730-289B-3058	Sequence 3058, Ap	810	14.8	92.5	31	11	US-09-730-289B-3059	Sequence 3059, Ap
738	14.8	92.5	31	11	US-09-730-289B-3060	Sequence 3060, Ap	811	14.8	92.5	31	11	US-09-730-289B-3061	Sequence 3061, Ap
739	14.8	92.5	31	11	US-09-730-289B-3062	Sequence 3062, Ap	812	14.8	92.5	31	11	US-09-730-289B-3063	Sequence 3063, Ap
740	14.8	92.5	31	11	US-09-730-289B-3064	Sequence 3064, Ap	813	14.8	92.5	31	11	US-09-730-289B-3065	Sequence 3065, Ap
741	14.8	92.5	31	11	US-09-730-289B-3066	Sequence 3066, Ap	814	14.8	92.5	31	11	US-09-730-289B-3067	Sequence 3067, Ap
742	14.8	92.5	31	11	US-09-730-289B-3068	Sequence 3068, Ap	815	14.8	92.5	31	11	US-09-730-289B-3069	Sequence 3069, Ap
743	14.8	92.5	31	11	US-09-730-289B-3070	Sequence 3070, Ap	816	14.8	92.5	31	11	US-09-730-289B-3071	Sequence 3071, Ap
744	14.8	92.5	31	11	US-09-730-289B-3072	Sequence 3072, Ap	817	14.8	92.5	31	11	US-09-730-289B-3073	Sequence 3073, Ap
745	14.8	92.5	31	11	US-09-730-289B-3074	Sequence 3074, Ap	818	14.8	92.5	31	11	US-09-730-289B-3075	Sequence 3075, Ap

819	14.8	92.5	31	11	US-09-730-2898-3025	Sequence 3025, Ap	892	14.8	92.5	31	11	US-09-730-2898-3098	Sequence 3098, Ap
820	14.8	92.5	31	11	US-09-730-2898-3026	Sequence 3026, Ap	893	14.8	92.5	31	11	US-09-730-2898-3099	Sequence 3099, Ap
821	14.8	92.5	31	11	US-09-730-2898-3027	Sequence 3027, Ap	894	14.8	92.5	31	11	US-09-730-2898-3100	Sequence 3100, Ap
822	14.8	92.5	31	11	US-09-730-2898-3028	Sequence 3028, Ap	895	14.8	92.5	31	11	US-09-730-2898-3101	Sequence 3101, Ap
823	14.8	92.5	31	11	US-09-730-2898-3029	Sequence 3029, Ap	896	14.8	92.5	31	11	US-09-730-2898-3102	Sequence 3102, Ap
824	14.8	92.5	31	11	US-09-730-2898-3030	Sequence 3030, Ap	897	14.8	92.5	31	11	US-09-730-2898-3103	Sequence 3103, Ap
825	14.8	92.5	31	11	US-09-730-2898-3031	Sequence 3031, Ap	898	14.8	92.5	31	11	US-09-730-2898-3104	Sequence 3104, Ap
826	14.8	92.5	31	11	US-09-730-2898-3032	Sequence 3032, Ap	899	14.8	92.5	31	11	US-09-730-2898-3105	Sequence 3105, Ap
827	14.8	92.5	31	11	US-09-730-2898-3033	Sequence 3033, Ap	900	14.8	92.5	31	11	US-09-730-2898-3106	Sequence 3106, Ap
828	14.8	92.5	31	11	US-09-730-2898-3034	Sequence 3034, Ap	901	14.8	92.5	31	11	US-09-730-2898-3107	Sequence 3107, Ap
829	14.8	92.5	31	11	US-09-730-2898-3035	Sequence 3035, Ap	902	14.8	92.5	31	11	US-09-730-2898-3108	Sequence 3108, Ap
830	14.8	92.5	31	11	US-09-730-2898-3036	Sequence 3036, Ap	903	14.8	92.5	31	11	US-09-730-2898-3109	Sequence 3109, Ap
831	14.8	92.5	31	11	US-09-730-2898-3037	Sequence 3037, Ap	904	14.8	92.5	31	11	US-09-730-2898-3110	Sequence 3110, Ap
832	14.8	92.5	31	11	US-09-730-2898-3038	Sequence 3038, Ap	905	14.8	92.5	31	11	US-09-730-2898-3111	Sequence 3111, Ap
833	14.8	92.5	31	11	US-09-730-2898-3039	Sequence 3039, Ap	906	14.8	92.5	31	11	US-09-730-2898-3112	Sequence 3112, Ap
834	14.8	92.5	31	11	US-09-730-2898-3040	Sequence 3040, Ap	907	14.8	92.5	31	11	US-09-730-2898-3113	Sequence 3113, Ap
835	14.8	92.5	31	11	US-09-730-2898-3041	Sequence 3041, Ap	908	14.8	92.5	31	11	US-09-730-2898-3114	Sequence 3114, Ap
836	14.8	92.5	31	11	US-09-730-2898-3042	Sequence 3042, Ap	909	14.8	92.5	31	11	US-09-730-2898-3115	Sequence 3115, Ap
837	14.8	92.5	31	11	US-09-730-2898-3043	Sequence 3043, Ap	910	14.8	92.5	31	11	US-09-730-2898-3116	Sequence 3116, Ap
838	14.8	92.5	31	11	US-09-730-2898-3044	Sequence 3044, Ap	911	14.8	92.5	31	11	US-09-730-2898-3117	Sequence 3117, Ap
839	14.8	92.5	31	11	US-09-730-2898-3045	Sequence 3045, Ap	912	14.8	92.5	31	11	US-09-730-2898-3118	Sequence 3118, Ap
840	14.8	92.5	31	11	US-09-730-2898-3046	Sequence 3046, Ap	913	14.8	92.5	31	11	US-09-730-2898-3119	Sequence 3119, Ap
841	14.8	92.5	31	11	US-09-730-2898-3047	Sequence 3047, Ap	914	14.8	92.5	31	11	US-09-730-2898-3120	Sequence 3120, Ap
842	14.8	92.5	31	11	US-09-730-2898-3048	Sequence 3048, Ap	915	14.8	92.5	31	11	US-09-730-2898-3121	Sequence 3121, Ap
843	14.8	92.5	31	11	US-09-730-2898-3049	Sequence 3049, Ap	916	14.8	92.5	31	11	US-09-730-2898-3122	Sequence 3122, Ap
844	14.8	92.5	31	11	US-09-730-2898-3050	Sequence 3050, Ap	917	14.8	92.5	31	11	US-09-730-2898-3123	Sequence 3123, Ap
845	14.8	92.5	31	11	US-09-730-2898-3051	Sequence 3051, Ap	918	14.8	92.5	31	11	US-09-730-2898-3124	Sequence 3124, Ap
846	14.8	92.5	31	11	US-09-730-2898-3052	Sequence 3052, Ap	919	14.8	92.5	31	11	US-09-730-2898-3125	Sequence 3125, Ap
847	14.8	92.5	31	11	US-09-730-2898-3053	Sequence 3053, Ap	920	14.8	92.5	31	11	US-09-730-2898-3126	Sequence 3126, Ap
848	14.8	92.5	31	11	US-09-730-2898-3054	Sequence 3054, Ap	921	14.8	92.5	31	11	US-09-730-2898-3127	Sequence 3127, Ap
849	14.8	92.5	31	11	US-09-730-2898-3055	Sequence 3055, Ap	922	14.8	92.5	31	11	US-09-730-2898-3128	Sequence 3128, Ap
850	14.8	92.5	31	11	US-09-730-2898-3056	Sequence 3056, Ap	923	14.8	92.5	31	11	US-09-730-2898-3129	Sequence 3129, Ap
851	14.8	92.5	31	11	US-09-730-2898-3057	Sequence 3057, Ap	924	14.8	92.5	31	11	US-09-730-2898-3130	Sequence 3130, Ap
852	14.8	92.5	31	11	US-09-730-2898-3058	Sequence 3058, Ap	925	14.8	92.5	31	11	US-09-730-2898-3131	Sequence 3131, Ap
853	14.8	92.5	31	11	US-09-730-2898-3059	Sequence 3059, Ap	926	14.8	92.5	31	11	US-09-730-2898-3132	Sequence 3132, Ap
854	14.8	92.5	31	11	US-09-730-2898-3060	Sequence 3060, Ap	927	14.8	92.5	31	11	US-09-730-2898-3133	Sequence 3133, Ap
855	14.8	92.5	31	11	US-09-730-2898-3061	Sequence 3061, Ap	928	14.8	92.5	31	11	US-09-730-2898-3134	Sequence 3134, Ap
856	14.8	92.5	31	11	US-09-730-2898-3062	Sequence 3062, Ap	929	14.8	92.5	31	11	US-09-730-2898-3135	Sequence 3135, Ap
857	14.8	92.5	31	11	US-09-730-2898-3063	Sequence 3063, Ap	930	14.8	92.5	31	11	US-09-730-2898-3136	Sequence 3136, Ap
858	14.8	92.5	31	11	US-09-730-2898-3064	Sequence 3064, Ap	931	14.8	92.5	31	11	US-09-730-2898-3137	Sequence 3137, Ap
859	14.8	92.5	31	11	US-09-730-2898-3065	Sequence 3065, Ap	932	14.8	92.5	31	11	US-09-730-2898-3138	Sequence 3138, Ap
860	14.8	92.5	31	11	US-09-730-2898-3066	Sequence 3066, Ap	933	14.8	92.5	31	11	US-09-730-2898-3139	Sequence 3139, Ap
861	14.8	92.5	31	11	US-09-730-2898-3067	Sequence 3067, Ap	934	14.8	92.5	31	11	US-09-730-2898-3140	Sequence 3140, Ap
862	14.8	92.5	31	11	US-09-730-2898-3068	Sequence 3068, Ap	935	14.8	92.5	31	11	US-09-730-2898-3141	Sequence 3141, Ap
863	14.8	92.5	31	11	US-09-730-2898-3069	Sequence 3069, Ap	936	14.8	92.5	31	11	US-09-730-2898-3142	Sequence 3142, Ap
864	14.8	92.5	31	11	US-09-730-2898-3070	Sequence 3070, Ap	937	14.8	92.5	31	11	US-09-730-2898-3143	Sequence 3143, Ap
865	14.8	92.5	31	11	US-09-730-2898-3071	Sequence 3071, Ap	938	14.8	92.5	31	11	US-09-730-2898-3144	Sequence 3144, Ap
866	14.8	92.5	31	11	US-09-730-2898-3072	Sequence 3072, Ap	939	14.8	92.5	31	11	US-09-730-2898-3145	Sequence 3145, Ap
867	14.8	92.5	31	11	US-09-730-2898-3073	Sequence 3073, Ap	940	14.8	92.5	31	11	US-09-730-2898-3146	Sequence 3146, Ap
868	14.8	92.5	31	11	US-09-730-2898-3074	Sequence 3074, Ap	941	14.8	92.5	31	11	US-09-730-2898-3147	Sequence 3147, Ap
869	14.8	92.5	31	11	US-09-730-2898-3075	Sequence 3075, Ap	942	14.8	92.5	31	11	US-09-730-2898-3148	Sequence 3148, Ap
870	14.8	92.5	31	11	US-09-730-2898-3076	Sequence 3076, Ap	943	14.8	92.5	31	11	US-09-730-2898-3149	Sequence 3149, Ap
871	14.8	92.5	31	11	US-09-730-2898-3077	Sequence 3077, Ap	944	14.8	92.5	31	11	US-09-730-2898-3150	Sequence 3150, Ap
872	14.8	92.5	31	11	US-09-730-2898-3078	Sequence 3078, Ap	945	14.8	92.5	31	11	US-09-730-2898-3151	Sequence 3151, Ap
873	14.8	92.5	31	11	US-09-730-2898-3079	Sequence 3079, Ap	946	14.8	92.5	31	11	US-09-730-2898-3152	Sequence 3152, Ap
874	14.8	92.5	31	11	US-09-730-2898-3080	Sequence 3080, Ap	947	14.8	92.5	31	11	US-09-730-2898-3153	Sequence 3153, Ap
875	14.8	92.5	31	11	US-09-730-2898-3081	Sequence 3081, Ap	948	14.8	92.5	31	11	US-09-730-2898-3154	Sequence 3154, Ap
876	14.8	92.5	31	11	US-09-730-2898-3082	Sequence 3082, Ap	949	14.8	92.5	31	11	US-09-730-2898-3155	Sequence 3155, Ap
877	14.8	92.5	31	11	US-09-730-2898-3083	Sequence 3083, Ap	950	14.8	92.5	31	11	US-09-730-2898-3156	Sequence 3156, Ap
878	14.8	92.5	31	11	US-09-730-2898-3084	Sequence 3084, Ap	951	14.8	92.5	31	11	US-09-730-2898-3157	Sequence 3157, Ap
879	14.8	92.5	31	11	US-09-730-2898-3085	Sequence 3085, Ap	952	14.8	92.5	31	11	US-09-730-2898-3158	Sequence 3158, Ap
880	14.8	92.5	31	11	US-09-730-2898-3086	Sequence 3086, Ap	953	14.8	92.5	31	11	US-09-730-2898-3159	Sequence 3159, Ap
881	14.8	92.5	31	11	US-09-730-2898-3087	Sequence 3087, Ap	954	14.8	92.5	31	11	US-09-730-2898-3160	Sequence 3160, Ap
882	14.8	92.5	31	11	US-09-730-2898-3088	Sequence 3088, Ap	955	14.8	92.5	31	11	US-09-730-2898-3161	Sequence 3161, Ap
883	14.8	92.5	31	11	US-09-730-2898-3089	Sequence 3089, Ap	956	14.8	92.5	31	11	US-09-730-2898-3162	Sequence 3162, Ap
884	14.8	92.5	31	11	US-09-730-2898-3090	Sequence 3090, Ap	957	14.8	92.5	31	11	US-09-730-2898-3163	Sequence 3163, Ap
885	14.8	92.5	31	11	US-09-730-2898-3091	Sequence 3091, Ap	958	14.8	92.5	31	11	US-09-730-2898-3164	Sequence 3164, Ap
886	14.8	92.5	31	11	US-09-730-2898-3092	Sequence 3092, Ap	959	14.8	92.5	31	11	US-09-730-2898-3165	Sequence 3165, Ap
887	14.8	92.5	31	11	US-09-730-2898-3093	Sequence 3093, Ap	960	14.8	92.5	31	11	US-09-730-2898-3166	Sequence 3166, Ap
888	14.8	92.5	31	11	US-09-730-2898-3094	Sequence 3094, Ap	961	14.8	92.5	31	11	US-09-730-2898-3167	Sequence 3167, Ap
889	14.8	92.5	31	11	US-09-730-2898-3095	Sequence 3095, Ap	962	14.8	92.5	31	11	US-09-730-2898-3168	Sequence 3168, Ap
890	14.8	92.5	31	11	US-09-730-2898-3096	Sequence 3096, Ap	963	14.8	92.5	31	11	US-09-730-2898-3169	Sequence 3169, Ap
891	14.8	92.5	31	11	US-09-730-2898-3097	Sequence 3097, Ap	964	14.8	92.5	31	11	US-09-730-2898-3170	Sequence 3170, Ap

```

965 14.8 92.5 31 11 US-09-730-289B-3171 Sequence 3171, Ap
966 14.8 92.5 31 11 US-09-730-289B-3172 Sequence 3172, Ap
967 14.8 92.5 31 11 US-09-730-289B-3173 Sequence 3173, Ap
968 14.8 92.5 31 11 US-09-730-289B-3174 Sequence 3174, Ap
969 14.8 92.5 31 11 US-09-730-289B-3175 Sequence 3175, Ap
970 14.8 92.5 31 11 US-09-730-289B-3176 Sequence 3176, Ap
971 14.8 92.5 31 11 US-09-730-289B-3177 Sequence 3177, Ap
972 14.8 92.5 31 11 US-09-730-289B-3178 Sequence 3178, Ap
973 14.8 92.5 31 11 US-09-730-289B-3179 Sequence 3179, Ap
974 14.8 92.5 31 11 US-09-730-289B-3180 Sequence 3180, Ap
975 14.8 92.5 31 11 US-09-730-289B-3181 Sequence 3181, Ap
976 14.8 92.5 31 11 US-09-730-289B-3182 Sequence 3182, Ap
977 14.8 92.5 31 11 US-09-730-289B-3183 Sequence 3183, Ap
978 14.8 92.5 31 11 US-09-730-289B-3184 Sequence 3184, Ap
979 14.8 92.5 31 11 US-09-730-289B-3185 Sequence 3185, Ap
980 14.8 92.5 31 11 US-09-730-289B-3186 Sequence 3186, Ap
981 14.8 92.5 31 11 US-09-730-289B-3187 Sequence 3187, Ap
982 14.8 92.5 31 11 US-09-730-289B-3188 Sequence 3188, Ap
983 14.8 92.5 31 11 US-09-730-289B-3189 Sequence 3189, Ap
984 14.8 92.5 31 11 US-09-730-289B-3190 Sequence 3190, Ap
985 14.8 92.5 31 11 US-09-730-289B-3191 Sequence 3191, Ap
986 14.8 92.5 31 11 US-09-730-289B-3192 Sequence 3192, Ap
987 14.8 92.5 31 11 US-09-730-289B-3193 Sequence 3193, Ap
988 14.8 92.5 31 11 US-09-730-289B-3194 Sequence 3194, Ap
989 14.8 92.5 31 11 US-09-730-289B-3195 Sequence 3195, Ap
990 14.8 92.5 31 11 US-09-730-289B-3196 Sequence 3196, Ap
991 14.8 92.5 31 11 US-09-730-289B-3197 Sequence 3197, Ap
992 14.8 92.5 31 11 US-09-730-289B-3198 Sequence 3198, Ap
993 14.8 92.5 31 11 US-09-730-289B-3199 Sequence 3199, Ap
994 14.8 92.5 31 11 US-09-730-289B-3200 Sequence 3200, Ap
995 14.8 92.5 31 11 US-09-730-289B-3201 Sequence 3201, Ap
996 14.8 92.5 31 11 US-09-730-289B-3202 Sequence 3202, Ap
997 14.8 92.5 31 11 US-09-730-289B-3203 Sequence 3203, Ap
998 14.8 92.5 31 11 US-09-730-289B-3204 Sequence 3204, Ap
999 14.8 92.5 31 11 US-09-730-289B-3205 Sequence 3205, Ap
1000 14.8 92.5 31 11 US-09-730-289B-3206 Sequence 3206, Ap

```

ALIGNMENTS

```

RESULT 1
US-09-877-526A-21
; Sequence 21, Application US/09877526A
; Patent No. US20020102568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Ueman, Naasim
; APPLICANT: McSwiggen, Jim
; APPLICANT: Zinnen, Shawn
; APPLICANT: Seiwert, Scott
; APPLICANT: Haebertli, Pete
; APPLICANT: Chowrira, Bharat
; APPLICANT: Blact, Larry
; APPLICANT: Valish, Narendra
; TITLE OF INVENTION: A Process for the Detection of Nucleic Acid Using Nucleic Acid Ca
; FILE REFERENCE: MHB00-816-C (700/002)
; CURRENT APPLICATION NUMBER: US/09/877,526A
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,128
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Motif
US-09-877-526A-21
Query Match 92.5%; Score 14.8; DB 10; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;

```

```

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RGCTAGCHACACGA 16
Db 1 RGCTAGCTACACGA 16

```

```

RESULT 2
US-09-866-316B-15
; Sequence 15, Application US/09866316B
; Patent No. US20020142980A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Thompson, Jim
; APPLICANT: McSwiggen, Jim
; APPLICANT: Haebertli, Pete
; APPLICANT: Beigelman, Leo
; APPLICANT: Karpelsky, Alex
; APPLICANT: Bellon, Lauren
; APPLICANT: Reynolds, Mark
; APPLICANT: Zwick, Michael
; APPLICANT: Jarvis, Thale
; APPLICANT: Woolf, Todd
; APPLICANT: Matulic-Adamic, Jasenka
; TITLE OF INVENTION: Nucleic Acid Molecules with No. US20020142980A1 Chemical Compos
; FILE REFERENCE: MHB00,873-H 500/004
; CURRENT APPLICATION NUMBER: US/09/866,316B
; PRIOR FILING DATE: 2002-03-05
; CURRENT APPLICATION NUMBER: US 09/103,656
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: US 60/082,404
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNazyme Motif
US-09-866-316B-15
Query Match 92.5%; Score 14.8; DB 10; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RGCTAGCHACACGA 16
Db 1 RGCTAGCTACACGA 16
RESULT 3
US-09-864-785-3928
; Sequence 3928, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: 400/022 (MHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3928
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

```

OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-3928

Query Match 92.5%; Score 14.8; DB 10; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16
DB 1 RGGCTAGCTACACGA 16

RESULT 4

US-09-992-160-21
Sequence 21, Application US/09992160
Publication No. US2003008295A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc
APPLICANT: Usman, Naasim
APPLICANT: McSwigen, Jim
APPLICANT: Zimen, Shawn
APPLICANT: Seiwert, Scott
APPLICANT: Haebertl, Pete
APPLICANT: Chowitra, Bharat
APPLICANT: Blatt, Larry
TITLE OF INVENTION: Nucleic Acid Sensor Molecules
FILE REFERENCE: MHB00-816-D (700/004)
CURRENT APPLICATION NUMBER: US/09/992,160
CURRENT FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn version 3.0
SEQ ID NO 21
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Motif
US-09-992-160-21

Query Match 92.5%; Score 14.8; DB 11; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16
DB 1 RGGCTAGCTACACGA 16

RESULT 5

US-09-730-289B-3896
Sequence 3896, Application US/09730289B
Publication No. US20030050259A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwigen, Jim
TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
FILE REFERENCE: MHB00-864-A (400/006)
CURRENT APPLICATION NUMBER: US/09/730,289B
CURRENT FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/169,100
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 3897
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3896
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence
US-09-730-289B-3896

Query Match 92.5%; Score 14.8; DB 11; Length 16;

Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16
DB 1 RGGCTAGCTACACGA 16

RESULT 6

US-09-780-533A-6679
Sequence 6679, Application US/09780533A
Publication No. US20030060611A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwigen, Jim
APPLICANT: Chowitra, Bharat
APPLICANT: Haebertl, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MHB00-878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6679
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-533A-6679

Query Match 92.5%; Score 14.8; DB 11; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16
DB 1 RGGCTAGCTACACGA 16

RESULT 7

US-09-877-478-6585
Sequence 6585, Application US/09877478
Publication No. US20030068301A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Diaper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: McSwigen, Jim
APPLICANT: Morrissey, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: MHB00-845-H (400/029)
CURRENT APPLICATION NUMBER: US/09/877,478
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: US 07/882,712
PRIOR FILING DATE: 1992-05-14
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: US 09/696,347
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 08/193,627
PRIOR FILING DATE: 1994-02-07
PRIOR APPLICATION NUMBER: US 08/433,993
PRIOR FILING DATE: 1995-05-04
PRIOR APPLICATION NUMBER: US 08/434,504
PRIOR FILING DATE: 1995-05-04
PRIOR APPLICATION NUMBER: US 09/436,430
PRIOR FILING DATE: 1999-11-08

```

; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6585
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-877-478-6585

Query Match          92.5%; Score 14.8; DB 11; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGGCTAGCHACACGA 16
        |||||:|||||
Db      1 RGGCTAGCTACACGA 16

RESULT 8
US-09-848-754A-9645
; Sequence 9645, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBHB00-958-1 (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 9645
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme Motif
US-09-848-754A-9645

Query Match          92.5%; Score 14.8; DB 11; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGGCTAGCHACACGA 16
        |||||:|||||
Db      1 RGGCTAGCTACACGA 16

RESULT 9
US-09-776-474-2991
; Sequence 2991, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Boober, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Faltzney, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK
; FILE REFERENCE: MBHB00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2991
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-2991

Query Match          92.5%; Score 14.8; DB 11; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGGCTAGCHACACGA 16
        |||||:|||||
Db      1 RGGCTAGCTACACGA 16

RESULT 10
US-09-930-423-4549
; Sequence 4549, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blact, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4549
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-930-423-4549

Query Match          92.5%; Score 14.8; DB 11; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGGCTAGCHACACGA 16
        |||||:|||||
Db      1 RGGCTAGCTACACGA 16

RESULT 11
US-09-780-164-2602
; Sequence 2602, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blact, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2602
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-164-2602

Query Match          92.5%; Score 14.8; DB 11; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGGCTAGCHACACGA 16
```

Db 1 RGGCTAGCTACACGA 16

RESULT 12
US-09-827-395A-2617
; Sequence 2617, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blact
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowitra
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor C
; FILE REFERENCE: MEB00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2617
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Definition of Artificial Sequence: Enzymatic Nucleic Acid
US-09-827-395A-2617

Query Match 92.5%; Score 14.8; DB 11; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RGGCTAGCHACACGA 16
Db 1 RGGCTAGCTACACGA 16

RESULT 13
US-10-366-191-14
; Sequence 14, Application US/10366191
; Publication No. US20030228590A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Susan, Radka
; APPLICANT: Beigelman, Leonid
; APPLICANT: Haeblerl, Peter
; TITLE OF INVENTION: Antibodies Having Specificity for Nucleic Acids
; FILE REFERENCE: 02-030-A (900/047)
; CURRENT APPLICATION NUMBER: US/10/366,191
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-366-191-14

Query Match 92.5%; Score 14.8; DB 12; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RGGCTAGCHACACGA 16
Db 1 RGGCTAGCTACACGA 16

RESULT 14

US-10-435-044A-19
; Sequence 19, Application US/10435044A
; Publication No. US20030228615A1
; GENERAL INFORMATION:
; APPLICANT: Rossi, John J
; APPLICANT: Scherr, Michaela
; APPLICANT: Riggs, Arthur D
; TITLE OF INVENTION: Method For Identifying Accessible Binding Sites on RNA
; FILE REFERENCE: 1954-2851
; CURRENT APPLICATION NUMBER: US/10/435,044A
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US 09/536,393
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/127,529
; PRIOR FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: catalytic core
US-10-435-044A-19

Query Match 92.5%; Score 14.8; DB 12; Length 16;
Best Local Similarity 87.5%; Pred. No. 54;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RGGCTAGCHACACGA 16
Db 1 AGGCTAGCTACACGA 16

RESULT 15
US-10-435-044A-20
; Sequence 20, Application US/10435044A
; Publication No. US20030228615A1
; GENERAL INFORMATION:
; APPLICANT: Rossi, John J
; APPLICANT: Scherr, Michaela
; APPLICANT: Riggs, Arthur D
; TITLE OF INVENTION: Method For Identifying Accessible Binding Sites on RNA
; FILE REFERENCE: 1954-2851
; CURRENT APPLICATION NUMBER: US/10/435,044A
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US 09/536,393
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/127,529
; PRIOR FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: catalytic core
US-10-435-044A-20

Query Match 92.5%; Score 14.8; DB 12; Length 16;
Best Local Similarity 87.5%; Pred. No. 54;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RGGCTAGCHACACGA 16
Db 1 GGGCTAGCTACACGA 16

RESULT 16
US-09-745-237A-4549
; Sequence 4549, Application US/09745237A
; Publication No. US20030143708A1

```
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
FILE REFERENCE: 400/007 (MBH00-918-A)
CURRENT APPLICATION NUMBER: US/09/745,237A
CURRENT FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 4550
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4549
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence
US-09-745-237A-4549

Query Match          92.5%; Score 14.8; DB 13; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAACGA 16
DB 1 RGGCTAGCTACAACGA 16

RESULT 17
US-09-792-818-2304
Sequence 2304, Application US/09792818
Publication No. US20030134806A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Jarvis, Thale
APPLICANT: Von Carlowitz, Ira
APPLICANT: McSwiggen, Jim
APPLICANT: Hamblin, Paul
APPLICANT: Ellis, Jonathan
TITLE OF INVENTION: Method and Reagent for the Inhibition of Grp-2-related with Inse
FILE REFERENCE: MBH00-901-A (400/013)
CURRENT APPLICATION NUMBER: US/09/792,818
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 2304
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2304
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-792-818-2304

Query Match          92.5%; Score 14.8; DB 13; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAACGA 16
DB 1 RGGCTAGCTACAACGA 16

RESULT 18
US-10-279-401-11
Sequence 11, Application US/10279401
Publication No. US20030140362A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
APPLICANT: Macejak, Dennis
APPLICANT: Lee, Patricia
TITLE OF INVENTION: In Vivo Models For Screening Inhibitors of Hepatitis B Virus
FILE REFERENCE: 400/066 (MBH01-1336-B)
CURRENT APPLICATION NUMBER: US/10/279,401
```

```
CURRENT FILING DATE: 2003-01-27
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/335,059
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: PCT/US02/09187
PRIOR FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNAzyme Motif
US-10-279-401-11

Query Match          92.5%; Score 14.8; DB 13; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAACGA 16
DB 1 RGGCTAGCTACAACGA 16

RESULT 19
US-10-201-389A-13
Sequence 13, Application US/10201389A
Publication No. US20030148928A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leonid
APPLICANT: Azharyev, Alex
APPLICANT: Azharyeva, Elena
APPLICANT: Antopol'sky, Maxim
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID PEPTIDE CONJUGATES
FILE REFERENCE: 600/023
CURRENT APPLICATION NUMBER: US/10/201,389A
CURRENT FILING DATE: 2002-07-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNAzyme motif
US-10-201-389A-13

Query Match          92.5%; Score 14.8; DB 13; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAACGA 16
DB 1 RGGCTAGCTACAACGA 16

RESULT 20
US-10-238-700-4666
Sequence 4666, Application US/10238700
Publication No. US20030153521A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Macejak, Dennis
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
FILE REFERENCE: 400/057 (MBH01-1158-A)
CURRENT APPLICATION NUMBER: US/10/238,700
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: PCT/US 02/16840
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US 60/318,471
```

PRIOR FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 4666
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4666
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-238-700-4666

Query Match 92.5%; Score 14.8; DB 13; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16
DB 1 RGGCTAGCTACACGA 16

RESULT 21
US-10-277-494-445
Sequence 445, Application US/10277494
Publication No. US20030186909A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: MCSwigen, Jim
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
FILE REFERENCE: MBH00-958-K (400/064)
CURRENT APPLICATION NUMBER: US/10/277,494
CURRENT FILING DATE: 2002-10-21
NUMBER OF SEQ ID NOS: 446
SOFTWARE: PatentIn version 3.0
SEQ ID NO 445
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Loop Nucleic Acid Sequence
US-10-277-494-445

Query Match 92.5%; Score 14.8; DB 13; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16
DB 1 RGGCTAGCTACACGA 16

RESULT 22
US-10-230-006-2677
Sequence 2677, Application US/10230006
Publication No. US20030191077A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Fosnaugh, Kathy
APPLICANT: MCSwigen, Jim
TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDI
FILE REFERENCE: 400/056 (MBH01-1110)
CURRENT APPLICATION NUMBER: US/10/230,006
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US 60/315,315
PRIOR FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 2678
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2677
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid

US-10-230-006-2677

Query Match 92.5%; Score 14.8; DB 13; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16
DB 1 RGGCTAGCTACACGA 16

RESULT 23
US-10-306-747A-11
Sequence 11, Application US/10306747A
Publication No. US20030216335A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Sandberg, Jennifer
APPLICANT: Pavco, Pam
APPLICANT: Gordon, Glad M.D.
TITLE OF INVENTION: Method and Reagent for the Modulation of Female Reproductive Dise
FILE REFERENCE: 01-1735-A (400/070)
CURRENT APPLICATION NUMBER: US/10/306,747A
CURRENT FILING DATE: 2002-11-27
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-306-747A-11

Query Match 92.5%; Score 14.8; DB 13; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16
DB 1 RGGCTAGCTACACGA 16

RESULT 24
US-10-151-116-12
Sequence 12, Application US/10151116
Publication No. US20030104985A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Matulic-Adamic, Jasenka
APPLICANT: Beigelman, Leo
TITLE OF INVENTION: Conjugates and Compositions for Cellular Delivery
FILE REFERENCE: MBH 01,639-B (600/020)
CURRENT APPLICATION NUMBER: US/10/151,116
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/362,016
PRIOR FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: 60/292,217
PRIOR FILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNazyme motif
US-10-151-116-12

Query Match 92.5%; Score 14.8; DB 15; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16
1 RGGCTAGCTACACGA 16

RESULT 25

US-10-163-552-1997
Sequence 1997, Application US/10163552
Publication No. US20030105051A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: MCSwigen, Jim
TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to level
TITLE OF INVENTION: HER2
FILE REFERENCE: MBH01-1653-A (400/014)
CURRENT APPLICATION NUMBER: US/10/163,552
CURRENT FILING DATE: 2002-06-06
NUMBER OF SEQ ID NOS: 1997
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1997
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Substrate Sequence
US-10-163-552-1997

Query Match 92.5%; Score 14.8; DB 15; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16
1 RGGCTAGCTACACGA 16

RESULT 26

US-10-156-306-8013
Sequence 8013, Application US/10156306
Publication No. US20030119017A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: MCSwigen, James
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
TITLE OF INVENTION: Levels of IKK-Gamma and PKR
FILE REFERENCE: MBH01-664-A (400/050)
CURRENT APPLICATION NUMBER: US/10/156,306
CURRENT FILING DATE: 2002-05-28
NUMBER OF SEQ ID NOS: 8013
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8013
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Substrate sequence
US-10-156-306-8013

Query Match 92.5%; Score 14.8; DB 15; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16
1 RGGCTAGCTACACGA 16

RESULT 27

US-10-157-580A-170
Sequence 170, Application US/10157580A
Publication No. US20030124513A1
GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: MCSwigen, Jim
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions
TITLE OF INVENTION: Related To Levels Of HIV
FILE REFERENCE: MBH01-665-A (400/051)
CURRENT APPLICATION NUMBER: US/10/157,580A
CURRENT FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn version 3.0
SEQ ID NO 170
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Motif
US-10-157-580A-170

Query Match 92.5%; Score 14.8; DB 15; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16
1 RGGCTAGCTACACGA 16

RESULT 28

US-10-201-394A-13
Sequence 13, Application US/10201394A
Publication No. US20030130186A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Vargese, Chandra
APPLICANT: Adams, Jasenka
APPLICANT: Karpelesky, Alexander
APPLICANT: Beigelman, Leonid
APPLICANT: Blat, Lawrence
TITLE OF INVENTION: CONJUGATES AND COMPOSITIONS FOR CELLULAR DELIVERY
FILE REFERENCE: MBH01-882-B (600/022)
CURRENT APPLICATION NUMBER: US/10/201,394A
CURRENT FILING DATE: 2002-07-22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-201-394A-13

Query Match 92.5%; Score 14.8; DB 16; Length 16;
Best Local Similarity 93.8%; Pred. No. 54;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16
1 RGGCTAGCTACACGA 16

RESULT 29

US-10-277-494-334
Sequence 334, Application US/10277494
Publication No. US20030186909A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: MCSwigen, Jim
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related To Level
TITLE OF INVENTION: Epidermal Growth Factor Receptors
FILE REFERENCE: MBH00-958-K (400/064)
CURRENT APPLICATION NUMBER: US/10/277,494
CURRENT FILING DATE: 2002-10-21
NUMBER OF SEQ ID NOS: 446


```
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 334
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-334

Query Match          92.5%; Score 14.8; DB 13; Length 23;
Best Local Similarity 87.5%; Pred. No. 55;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGCTAGCHACACGA 16
        :|||||:|||||
Db      4 GGCTAGCTACACGA 19

RESULT 30
US-10-277-494-335
; Sequence 335, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
; FILE REFERENCE: MBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 335
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-335

Query Match          92.5%; Score 14.8; DB 13; Length 23;
Best Local Similarity 87.5%; Pred. No. 55;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGCTAGCHACACGA 16
        :|||||:|||||
Db      4 GGCTAGCTACACGA 19

RESULT 31
US-10-277-494-336
; Sequence 336, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
; FILE REFERENCE: MBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 336
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-336

Query Match          92.5%; Score 14.8; DB 13; Length 23;
Best Local Similarity 87.5%; Pred. No. 55;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGCTAGCHACACGA 16
        :|||||:|||||
Db      4 GGCTAGCTACACGA 19

RESULT 32
US-10-277-494-337
; Sequence 337, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
; FILE REFERENCE: MBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 337
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-337

Query Match          92.5%; Score 14.8; DB 13; Length 23;
Best Local Similarity 87.5%; Pred. No. 55;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGCTAGCHACACGA 16
        :|||||:|||||
Db      4 GGCTAGCTACACGA 19

RESULT 33
US-10-277-494-338
; Sequence 338, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
; FILE REFERENCE: MBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 338
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-338

Query Match          92.5%; Score 14.8; DB 13; Length 23;
Best Local Similarity 87.5%; Pred. No. 55;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGCTAGCHACACGA 16
        :|||||:|||||
Db      4 GGCTAGCTACACGA 19

RESULT 34
US-10-277-494-339
; Sequence 339, Application US/10277494
; Publication No. US20030186909A1
```

```

LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-341

Query Match      92.5%; Score 14.8; DB 13; Length 23;
Best Local Similarity 87.5%; Pred. No. 55;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGGCTAGCHACAACGA 16
      :|||||:|||||
DB      4 AGGCTAGCTACAACGA 19

RESULT 37
US-10-277-494-342
Sequence 342, Application US/10277494
Publication No. US20030186909A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
FILE REFERENCE: MBH00-958-K (400/064)
CURRENT APPLICATION NUMBER: US/10/277,494
CURRENT FILING DATE: 2002-10-21
NUMBER OF SEQ ID NOS: 446
SOFTWARE: PatentIn version 3.0
SEQ ID NO 342
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-342

Query Match      92.5%; Score 14.8; DB 13; Length 23;
Best Local Similarity 87.5%; Pred. No. 55;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGGCTAGCHACAACGA 16
      :|||||:|||||
DB      4 GCGCTAGCTACAACGA 19

RESULT 38
US-10-277-494-343
Sequence 343, Application US/10277494
Publication No. US20030186909A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
FILE REFERENCE: MBH00-958-K (400/064)
CURRENT APPLICATION NUMBER: US/10/277,494
CURRENT FILING DATE: 2002-10-21
NUMBER OF SEQ ID NOS: 446
SOFTWARE: PatentIn version 3.0
SEQ ID NO 343
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-343

Query Match      92.5%; Score 14.8; DB 13; Length 23;
Best Local Similarity 87.5%; Pred. No. 55;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

Wed Jan 21 10:43:29 2004

OY 1 RGGCTAGCHACACGA 16
 :|||||:|||||
 Db 4 GGGCTAGCTACACGA 19

RESULT 39

US-10-277-494-344
 ; Sequence 344, Application US/10277494
 ; Publication No. US20030186909A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: McSwiggen, Jim
 ; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
 ; TITLE OF INVENTION: Epidermal Growth Factor Receptors
 ; FILE REFERENCE: MBHB00-958-K (400/064)
 ; CURRENT APPLICATION NUMBER: US/10/277,494
 ; CURRENT FILING DATE: 2002-10-21
 ; NUMBER OF SEQ ID NOS: 446
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 344
 ; LENGTH: 23
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
 US-10-277-494-344

Query Match 92.5%; Score 14.8; DB 13; Length 23;

Best Local Similarity 87.5%; Pred. No. 55;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16
 :|||||:|||||
 Db 4 AGGCTAGCTACACGA 19

RESULT 40

US-10-277-494-345
 ; Sequence 345, Application US/10277494
 ; Publication No. US20030186909A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: McSwiggen, Jim
 ; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
 ; TITLE OF INVENTION: Epidermal Growth Factor Receptors
 ; FILE REFERENCE: MBHB00-958-K (400/064)
 ; CURRENT APPLICATION NUMBER: US/10/277,494
 ; CURRENT FILING DATE: 2002-10-21
 ; NUMBER OF SEQ ID NOS: 446
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 345
 ; LENGTH: 23
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
 US-10-277-494-345

Query Match 92.5%; Score 14.8; DB 13; Length 23;

Best Local Similarity 87.5%; Pred. No. 55;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16
 :|||||:|||||
 Db 4 GGGCTAGCTACACGA 19

Search completed: January 21, 2004, 08:22:21
 Job time : 155 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 06:26:43 : Search time 1380 Seconds

(without alignments)
281.791 Million cell updates/sec

Title: US-09-423-035B-122

Perfect score: 16

Sequence: 1 rgsctagchacaaga 16

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 1215238056 residues

Total number of hits satisfying chosen parameters: 452990

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Database :
1: em_estba:*
2: em_esthm:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hrc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hrc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_esthm:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_pro:*
26: em_gss_png:*
27: em_gss_vrt:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12.2	76.2	80	14	CA798147 CAC BL 54
2	11.8	73.8	96	28	AZ431360 1M0216F14
3	11.8	73.8	100	28	AZ658330 1M0535M02
4	11.6	72.5	44	10	BG422154 602448881

5	11.6	72.5	60	29	CNS06E2T
6	11.6	72.5	67	14	CB366166 ZP001-P00
7	11.6	72.5	86	29	TA877090
8	11.6	72.5	88	9	AA953865 on76a12.8
9	11.6	72.5	90	28	AZ602406
10	11.6	72.5	93	28	BH215494 1006027C1
11	11.6	72.5	99	11.6	BG695449 NISC 1v17
12	11.6	72.5	100	13	BQ625306 rd27503.Y
13	11.2	70.0	26	28	BH901408 SALK 0790
14	11.2	70.0	34	28	AQ025306 EP(3)3213
15	11.2	70.0	49	28	BH861777 SALK 0879
16	11.2	70.0	55	9	AA142563 mgs9b11.x
17	11.2	70.0	59	13	BH866082 S062E01.P
18	11.2	70.0	77	14	CA819431 sau78d01.
19	11.2	70.0	85	9	AA183068 mtc8e09.x
20	11.2	70.0	92	28	AZ362937 1M0108B18
21	11.2	70.0	92	29	B2291268 SALK 1200
22	11.2	70.0	95	13	BH867160 S075A07.P
23	11.2	70.0	96	13	BH862306 S014A04.P
24	11.2	70.0	100	9	AW797834 CMO-UM004
25	11.2	70.0	100	12	BM328423 P1C1_29-B
26	11.2	70.0	100	13	BH861867 S007G10.P
27	11.2	70.0	74	29	CC179318 SALK 0678
28	11.2	68.8	79	14	U44372 EMU44372.A8
29	11.2	68.8	82	9	AA594999 n031e06.s
30	11.2	68.8	100	10	BR330980 8032A05.Y
31	11.2	68.8	50	9	AU106358 AU106358
32	10.8	67.5	72	29	B2287687 SALK 0210
33	10.8	67.5	80	28	AZ619815 1M0452D18
34	10.8	67.5	85	29	AL947273 Arabidops
35	10.8	67.5	92	14	W17739 mb77g02.r1
36	10.8	67.5	94	29	BZ291056 SALK 1123
37	10.8	67.5	95	9	AA919502 v220g11.x
38	10.6	66.2	32	28	AZ639727 1M0501D21
39	10.6	66.2	37	14	CB305210 3'EST-NE1
40	10.6	66.2	52	14	H08942 Y193e05.r1
41	10.6	66.2	52	28	BH809438 KG03411-5
42	10.6	66.2	54	29	CC054970 SALK 0804
43	10.6	66.2	55	9	AJ235741 AJ235741
44	10.6	66.2	55	28	AZ759826 1M0552N20
45	10.6	66.2	61	9	AI857338 wmo2h07.x
46	10.6	66.2	67	9	AI931601 u17ic02.y
47	10.6	66.2	67	29	AL945283 Arabidops
48	10.6	66.2	74	14	N98196 AW057152 ca01d12.y
49	10.6	66.2	75	9	AW057152 ca01d12.y
50	10.6	66.2	76	29	BX535085 Arabidops
51	10.6	66.2	78	14	H73809 H73809 Y813h08.s1
52	10.6	66.2	78	28	BH235148 MSAD F06
53	10.6	66.2	79	9	AI323764 mm11h09.x
54	10.6	66.2	79	9	AI736613 sb31c03.y
55	10.6	66.2	79	29	BZ580914 3590_1_41
56	10.6	66.2	81	28	AQ073977 EP(3)3398
57	10.6	66.2	81	28	AF219090 AF219090
58	10.6	66.2	83	9	AA986517 ue14c08.x
59	10.6	66.2	88	28	BH230938 1006160A1
60	10.6	66.2	91	14	CB403169 OSTR002D6
61	10.6	66.2	95	9	AI461140 sa75f01.y
62	10.6	66.2	95	9	AI971673 AL971673
63	10.6	66.2	95	13	BQ823860 1030113D0
64	10.6	66.2	95	28	AQ072923 EP(2)2127
65	10.6	66.2	95	28	AZ603988 1M0423C08
66	10.6	66.2	95	29	TA240A04P AL481566 T. brucei
67	10.6	66.2	96	9	AL644741 AL644741
68	10.6	66.2	96	28	AZ916132 P8C1_3.a8
69	10.6	66.2	98	9	AA487184 ab21d06.s
70	10.6	66.2	98	9	AA487184 ab21d06.s
71	10.6	66.2	99	28	BH813764 SALK 0652
72	10.6	66.2	100	13	BQ758146 Bma01_SQ
73	10.6	66.2	53	14	H18867 ym45h12.r1
74	10.4	65.0	70	29	CC457634 SALK 1111
75	10.4	65.0	81	29	CC457634 SALK 1111
76	10.4	65.0	81	29	CC457634 SALK 1111
77	10.4	65.0	81	29	CC457634 SALK 1111

C 224	10	62.5	85	14	W33866	C 297	9.8	61.3	76	13	BQ764143
C 225	10	62.5	85	28	BH234155	C 298	9.8	61.3	91	29	AA145177
C 226	10	62.5	85	28	BH810968	C 299	9.8	61.3	91	28	AZ595050
C 227	10	62.5	87	9	AI210682	C 300	9.8	61.3	92	10	BP591436
C 228	10	62.5	87	9	AV911031	C 301	9.8	61.3	93	13	BQ766868
C 229	10	62.5	87	13	BQ758477	C 302	9.8	61.3	93	14	CD537206
C 230	10	62.5	87	14	CB384688	C 303	9.8	61.3	95	13	BQ764114
C 231	10	62.5	87	28	AO072951	C 304	9.8	61.3	98	13	BQ815594
C 232	10	62.5	87	28	BH861276	C 305	9.6	60.0	25	28	AZ866918
C 233	10	62.5	87	29	AL942715	C 306	9.6	60.0	25	28	TA138040
C 234	10	62.5	88	9	AA174733	C 307	9.6	60.0	27	28	AZ827952
C 235	10	62.5	88	13	BQ097935	C 308	9.6	60.0	30	28	BH790499
C 236	10	62.5	88	29	AL941037	C 309	9.6	60.0	31	9	AU007544
C 237	10	62.5	89	10	BF013401	C 310	9.6	60.0	31	9	AU007545
C 238	10	62.5	89	28	AZ651121	C 311	9.6	60.0	32	29	BZ763820
C 239	10	62.5	89	28	AZ839180	C 312	9.6	60.0	34	29	AI308456
C 240	10	62.5	90	10	BE566667	C 313	9.6	60.0	34	9	AI762091
C 241	10	62.5	90	28	AO939864	C 314	9.6	60.0	35	29	BX293200
C 242	10	62.5	90	28	AZ933385	C 315	9.6	60.0	37	9	AI119964
C 243	10	62.5	91	12	BM061243	C 316	9.6	60.0	38	28	AZ506380
C 244	10	62.5	91	13	BX294228	C 317	9.6	60.0	39	28	AZ799576
C 245	10	62.5	92	29	BZ663548	C 318	9.6	60.0	40	29	CC055020
C 246	10	62.5	93	9	AI680424	C 319	9.6	60.0	40	29	AL754614
C 247	10	62.5	93	28	AZ433243	C 320	9.6	60.0	41	28	BH909196
C 248	10	62.5	93	28	AZ838229	C 321	9.6	60.0	43	9	AI917489
C 249	10	62.5	93	29	BZ354386	C 322	9.6	60.0	43	28	AZ502070
C 250	10	62.5	94	9	AA420062	C 323	9.6	60.0	43	28	AZ616799
C 251	10	62.5	94	9	AA435359	C 324	9.6	60.0	43	29	AL755953
C 252	10	62.5	94	9	AA512503	C 325	9.6	60.0	46	28	AZ831199
C 253	10	62.5	94	29	AG219003	C 326	9.6	60.0	48	28	AZ438804
C 254	10	62.5	94	29	DMES47254	C 327	9.6	60.0	48	28	BH807268
C 255	10	62.5	95	12	BI972059	C 328	9.6	60.0	49	28	TA84A080
C 256	10	62.5	95	12	BI972059	C 329	9.6	60.0	49	28	AZ484612
C 257	10	62.5	95	14	CA337825	C 330	9.6	60.0	49	29	BZ586070
C 258	10	62.5	95	14	T81028	C 331	9.6	60.0	50	9	AU102833
C 259	10	62.5	95	28	AZ785550	C 332	9.6	60.0	50	9	AU102837
C 260	10	62.5	95	28	BH218664	C 333	9.6	60.0	50	9	AU104296
C 261	10	62.5	95	28	BH218664	C 334	9.6	60.0	50	9	AU105637
C 262	10	62.5	95	28	BH218664	C 335	9.6	60.0	50	9	AU105640
C 263	10	62.5	95	28	BH812878	C 336	9.6	60.0	50	9	AU107549
C 264	10	62.5	96	13	BE588022	C 337	9.6	60.0	50	9	AM246460
C 265	10	62.5	96	13	BQ815321	C 338	9.6	60.0	50	28	AZ931814
C 266	10	62.5	96	28	AZ500728	C 339	9.6	60.0	52	28	AZ636620
C 267	10	62.5	96	28	AZ823238	C 340	9.6	60.0	52	29	BZ287252
C 268	10	62.5	96	28	B42033	C 341	9.6	60.0	53	9	AA166143
C 269	10	62.5	97	9	AA691488	C 342	9.6	60.0	53	9	AA166143
C 270	10	62.5	97	9	AA797348	C 343	9.6	60.0	53	9	AA102062
C 271	10	62.5	97	9	AA969570	C 344	9.6	60.0	53	29	BZ663828
C 272	10	62.5	97	9	AI581819	C 345	9.6	60.0	53	29	TA274C09
C 273	10	62.5	97	9	AM064307	C 346	9.6	60.0	54	28	AZ308458
C 274	10	62.5	97	28	AZ913331	C 347	9.6	60.0	54	29	CC033971
C 275	10	62.5	97	28	BH910232	C 348	9.6	60.0	54	29	AL756050
C 276	10	62.5	98	14	D86759	C 349	9.6	60.0	55	9	AA727100
C 277	10	62.5	99	9	AM271170	C 350	9.6	60.0	55	29	AL942758
C 278	10	62.5	99	12	BI421049	C 351	9.6	60.0	57	10	BF417690
C 279	10	62.5	99	14	CA847174	C 352	9.6	60.0	58	9	AA908619
C 280	10	62.5	99	14	CB405696	C 353	9.6	60.0	58	9	AI324804
C 281	10	62.5	99	28	AZ773743	C 354	9.6	60.0	58	9	AA511964
C 282	10	62.5	99	28	BH418153	C 355	9.6	60.0	58	29	BX288876
C 283	10	62.5	100	9	AI934888	C 356	9.6	60.0	59	14	BF713317
C 284	10	62.5	100	9	AA466564	C 357	9.6	60.0	59	14	CA909971
C 285	10	62.5	100	10	BE874679	C 358	9.6	60.0	61	10	BG513340
C 286	10	62.5	100	10	BG208347	C 359	9.6	60.0	61	10	BE533606
C 287	10	62.5	100	10	BG693567	C 360	9.6	60.0	61	12	BG967103
C 288	10	62.5	100	10	AM860735	C 361	9.6	60.0	61	28	AZ614560
C 289	10	62.5	100	10	BE231350	C 362	9.6	60.0	63	14	CB934157
C 290	10	62.5	100	13	BH203467	C 363	9.6	60.0	63	28	AZ435853
C 291	10	62.5	100	14	CA797445	C 364	9.6	60.0	63	28	BH809023
C 292	10	62.5	100	14	CA797445	C 365	9.6	60.0	63	29	BX188578
C 293	10	62.5	100	14	CA797445	C 366	9.6	60.0	64	9	AI950653
C 294	10	62.5	100	14	CA797445	C 367	9.6	60.0	64	9	AA255961
C 295	10	62.5	100	14	CA797445	C 368	9.6	60.0	64	10	BF400388
C 296	10	62.5	100	14	CA797445	C 369	9.6	60.0	64	10	BE638251

370	9.6	60.0	64	10	BF219646	B219646	SNVUL3CAN	443	9.6	60.0	85	29	BZ765654	BZ765654	SALK 1330	
371	9.6	60.0	64	28	AZ410022	IM018202	AA410022	IM018202	444	9.6	60.0	86	5	AA711608	AA711608	u11e08.r
372	9.6	60.0	64	29	AL770431	ArabiDops	AL770431	ArabiDops	445	9.6	60.0	87	28	AZ776480	AZ776480	2M0010E10
373	9.6	60.0	65	9	AM691706	AM691706	NP048C03S	446	9.6	60.0	87	14	AM722677	AM722677	CAH04nm.r	
374	9.6	60.0	65	13	BQ253384	AM695862	AM695862	AM695862	447	9.6	60.0	87	14	CD395316	CD395316	Gm.cK1531
375	9.6	60.0	65	28	AZ855735	BH904070	3526_1_27	448	9.6	60.0	88	9	AA637658	AA637658	u10f0e.r	
376	9.6	60.0	66	28	BH94070	3526_1_27	449	9.6	60.0	60.0	88	12	BM397069	BM397069	5009-0-28	
377	9.6	60.0	67	9	AM184727	AM184727	f718c09.y	450	9.6	60.0	88	14	CB912348	CB912348	VDI43E08	
378	9.6	60.0	67	28	AZ759905	IM0553C07	BH908636	451	9.6	60.0	88	28	AZ308810	AZ308810	IM0012M07	
379	9.6	60.0	67	28	BH908636	AM694424	NE076C03S	452	9.6	60.0	88	28	BH228507	BH228507	1006147C1	
380	9.6	60.0	68	9	AM694424	AM694424	NE076C03S	453	9.6	60.0	89	28	CA797738	CA797738	Cac.BL.48	
381	9.6	60.0	68	10	BG371736	BG371736	UT-R-CY0-	454	9.6	60.0	89	28	AZ385637	AZ385637	IM0144B16	
382	9.6	60.0	68	14	D45764	D45764	HUMGS02974	455	9.6	60.0	89	28	AZ495357	AZ495357	IM0331F13	
383	9.6	60.0	68	29	BZ595255	BZ595255	SALK_0863	456	9.6	60.0	90	12	BM069470	BM069470	1888A05.x	
384	9.6	60.0	69	10	BG264389	BG264389	daa81D08.	457	9.6	60.0	90	13	BM082152	BM082152	UB24CPE01	
385	9.6	60.0	69	14	H87983	H87983	yw18d06..r1	458	9.6	60.0	90	14	D20584	D20584	HUMGS01559	
386	9.6	60.0	69	28	AZ424099	AZ424099	IM0203F01	459	9.6	60.0	90	28	BH217012	BH217012	1006049E0	
387	9.6	60.0	69	29	AL752981	AL752981	ArabiDops	460	9.6	60.0	90	29	BZ661110	BZ661110	SGT4435-5	
388	9.6	60.0	70	14	W85524	W85524	mf58e04..r1	461	9.6	60.0	90	29	AL796620	AL796620	wh58f01.x	
389	9.6	60.0	70	28	AZ606482	AZ606482	IM0428K13	462	9.6	60.0	91	9	AU259839	AU259839	AM259839	
390	9.6	60.0	70	28	AZ819833	AZ819833	2M0091111	463	9.6	60.0	91	9	AM714722	AM714722	12d04e..r	
391	9.6	60.0	70	29	AL753206	AL753206	ArabiDops	464	9.6	60.0	91	14	H04321	H04321	yj20e10..s1	
392	9.6	60.0	71	9	AA758458	AA758458	z17a04.s	465	9.6	60.0	92	9	AM722670	AM722670	C4Q03nm.r	
393	9.6	60.0	71	9	AA917841	AA917841	on38e04.s	466	9.6	60.0	92	13	BU873432	BU873432	0056806.P	
394	9.6	60.0	71	9	AL1869405	AL1869405	tw40c01.x	467	9.6	60.0	92	13	BU873645	BU873645	Q057G10.P	
395	9.6	60.0	71	12	BU064004	BU064004	ArabiDops	468	9.6	60.0	92	13	BZ438999	BZ438999	IM0229H15	
396	9.6	60.0	71	29	AL937665	AL937665	B145B09..w	469	9.6	60.0	92	28	AZ477507	AZ477507	IM0297H05	
397	9.6	60.0	72	9	AM636306	AM636306	q127742	470	9.6	60.0	92	28	AL942617	AL942617	ArabiDops	
398	9.6	60.0	73	9	AL217742	AL217742	q127742	471	9.6	60.0	92	29	CNS04JG2	CNS04JG2	ArabiDops	
399	9.6	60.0	73	9	AM251001	AM251001	2821159.3	472	9.6	60.0	93	29	AJ301133	AJ301133	ArabiDops	
400	9.6	60.0	73	9	AM499126	AM499126	SNOYAFCP	473	9.6	60.0	93	10	BG057626	BG057626	nah93806.	
401	9.6	60.0	73	12	BI081709	BI081709	602879584	474	9.6	60.0	93	10	BG409079	BG409079	g889903.y	
402	9.6	60.0	73	13	BH870558	BH870558	Q015B11.P	475	9.6	60.0	93	29	AL753208	AL753208	ArabiDops	
403	9.6	60.0	73	14	CB832613	CB832613	SMBWECAY	476	9.6	60.0	93	29	AL753209	AL753209	ArabiDops	
404	9.6	60.0	74	9	AA832576	AA832576	vw43c10..x	477	9.6	60.0	93	29	DME546936	DME546936	nk35a08.s	
405	9.6	60.0	74	10	BG231381	BG231381	na141n05.	478	9.6	60.0	94	29	AA553989	AA553989	v152f01.r	
406	9.6	60.0	74	13	BU894013	BU894013	POSSHO7.P	479	9.6	60.0	94	13	BU869084	BU869084	M125H05.P	
407	9.6	60.0	74	28	AZ919094	AZ919094	1006013H0	480	9.6	60.0	94	13	AZ307695	AZ307695	IM0059G02	
408	9.6	60.0	74	29	BZ661992	BZ661992	SALK_0254	481	9.6	60.0	94	28	AZ307695	AZ307695	IM0059G02	
409	9.6	60.0	74	29	CNS021AA	AL198667	Tetracodon	482	9.6	60.0	94	28	AZ307695	AZ307695	IM0059G02	
410	9.6	60.0	75	10	BF465862	BF465862	UI-M-CQDP	483	9.6	60.0	94	28	BH169272	BH169272	SALK_0009	
411	9.6	60.0	75	10	BR668978	BR668978	601221633	484	9.6	60.0	94	28	BH169272	BH169272	SALK_0009	
412	9.6	60.0	75	12	BI418320	BI418320	LjNBS75e	485	9.6	60.0	94	29	BX291595	BX291595	ArabiDops	
413	9.6	60.0	75	12	BU049481	BU049481	N1SC_nb11	486	9.6	60.0	94	29	BX291595	BX291595	ArabiDops	
414	9.6	60.0	75	14	CB218881	CB218881	N1SC_nb11	487	9.6	60.0	95	10	BG154716	BG154716	sab38D03.	
415	9.6	60.0	76	14	CA914432	CA914432	PCSC15918	488	9.6	60.0	95	12	BI449187	BI449187	dab01A04.	
416	9.6	60.0	76	29	AL753252	AL753252	ArabiDops	489	9.6	60.0	95	14	X85568	X85568	HS241ABST.h	
417	9.6	60.0	76	29	HS2475805	HS2475805	Homo_sapi	490	9.6	60.0	95	29	BX234919	BX234919	Danio_rex	
418	9.6	60.0	77	29	AL940027	AL940027	ArabiDops	491	9.6	60.0	96	14	CD402353	CD402353	Gm.cK2497	
419	9.6	60.0	78	10	BE023116	BE023116	sm90h11.y	492	9.6	60.0	97	14	AA429118	AA429118	zw15c01.r	
420	9.6	60.0	78	13	BQ820346	BQ820346	1030083H0	493	9.6	60.0	97	28	AZ565834	AZ565834	214PVA04	
421	9.6	60.0	79	9	AA657019	AA657019	vr24h01..x	494	9.6	60.0	98	9	AM596808	AM596808	g116h11.y	
422	9.6	60.0	79	9	AA542195	AA542195	vj59a08..x	495	9.6	60.0	98	9	AM709081	AM709081	d2E06n.r	
423	9.6	60.0	79	12	BJ055360	BJ055360	ArabiDops	496	9.6	60.0	98	28	AZ918923	AZ918923	1006013C1	
424	9.6	60.0	79	14	CB367939	CB367939	TGSESTY93	497	9.6	60.0	98	29	AL768784	AL768784	ArabiDops	
425	9.6	60.0	80	9	ALB820251	ALB820251	ALB820251	498	9.6	60.0	99	14	AU244075	AU244075	ArabiDops	
426	9.6	60.0	80	13	BU834191	BU834191	T058A11.P	499	9.6	60.0	99	14	R79054	R79054	y187h02..r1	
427	9.6	60.0	80	14	CB274864	CB274864	ma174G11.	500	9.6	60.0	99	28	BH214808	BH214808	1006004G0	
428	9.6	60.0	80	29	AB082648	AB082648	Drosoph11	501	9.6	60.0	100	9	AI938082	AI938082	sc41G09..x	
429	9.6	60.0	81	9	AI965518	AI965518	ec73b04.y	502	9.6	60.0	100	9	AM102132	AM102132	sdb3f01.y	
430	9.6	60.0	81	13	BQ823042	BQ823042	1030105F0	503	9.6	60.0	100	9	AA428224	AA428224	zw33e07.s	
431	9.6	60.0	81	29	AL752903	AL752903	ArabiDops	504	9.6	60.0	100	12	BG952334	BG952334	PM4-CT056	
432	9.6	60.0	82	9	AA598481	AA598481	z085d12..s	505	9.6	60.0	100	12	BI166011	BI166011	1069P17P	
433	9.6	60.0	82	9	AA598481	AA598481	z085d12..s	506	9.6	60.0	100	14	CB040559	CB040559	4003522.B	
434	9.6	60.0	82	9	AA598481	AA598481	z085d12..s	507	9.6	60.0	100	14	W20655	W20655	EST00021.TE	
435	9.6	60.0	83	12	BJ0000334	BJ0000334	ArabiDops	508	9.6	60.0	100	14	Z20265	Z20265	HSAAABTLU.P	
436	9.6	60.0	83	28	AZ468565	AZ468565	1M0281C11	509	9.6	60.0	100	29	BZ384673	BZ384673	SALK_1358	
437	9.6	60.0	84	9	AI159660	AI159660	ue98c12..x	510	9.6	60.0	100	29	CC026050	CC026050	3591_1_4	
438	9.6	60.0	84	9	AM722919	AM722919	c8g12nm..x	511	9.6	60.0	100	29	AL758309	AL758309	ArabiDops	
439	9.6	60.0	84	28	BH906484	BH906484	SALK_0335	512	9.6	60.0	100	29	CNS04SKX	CNS04SKX	Tetracodon	
440	9.6	60.0	85	9	AV842614	AV842614	ArabiDops	513	9.4	58.8	31	28	AZ588330	AZ588330	IM0396L10	
441	9.6	60.0	85	10	BF785485	BF785485	602111859	514	9.4	58.8	31	9	AA181661	AA181661	zps5c05..x	
442	9.6	60.0	85	12	BI250774	BI250774	602993873	515	9.4	58.8	34	9	AI131979	AI131979	uc35h10.r	

516	9.4	58.8	42	10	BF527907	BF527907 602041058	589	9.4	58.8	96	10	BG261692	BG261692 602373363
C 517	9.4	58.8	42	28	BH904167	BH904167 SALK 1040	C 590	9.4	58.8	96	14	CA592488	CA592488 behl.p00
C 518	9.4	58.8	45	29	CC018920	CC018920 3591_112	C 591	9.4	58.8	97	14	AI122377	AI122377 uc61d05.x
C 519	9.4	58.8	48	29	BK178275	BK178275 Danilo rer	C 592	9.4	58.8	97	28	AQ025077	AQ025077 EP(3)0409
C 520	9.4	58.8	49	28	BH904166	BH904166 SALK 1040	C 593	9.4	58.8	97	29	AL942149	AL942149 Arabidops
C 521	9.4	58.8	49	28	BH904172	BH904172 SALK 1040	C 594	9.4	58.8	98	14	CD260607	CD260607 pema009xk
C 522	9.4	58.8	49	29	B2384940	B2384940 SALK 1362	C 595	9.4	58.8	98	29	CNS0306B	AL262028 Tetradon
C 523	9.4	58.8	53	28	AZ625652	AZ625652 IM045A24	C 596	9.4	58.8	99	9	AA676894	AA676894 z165e11.s
C 524	9.4	58.8	57	9	AI973877	AI973877 bd13a08.y	C 597	9.4	58.8	99	9	AM078836	AM078836 xbl17ho7.x
C 525	9.4	58.8	58	9	AA242953	AA242953 zrf65c12.r	C 598	9.4	58.8	100	6	AL812919	AL812919 Triticum
C 526	9.4	58.8	60	13	B0899083	B0899083 mai145602.	C 599	9.4	58.8	100	6	AA207795	AA207795 mw81c01.x
C 527	9.4	58.8	60	13	B0965007	B0965007 sac05c07.	C 600	9.4	58.8	100	10	BF953180	BF953180 CM3-NN118
C 528	9.4	58.8	60	14	W85304	W85304 mfe2509.r1	C 601	9.4	58.8	100	13	B0820967	B0820967 DB17CPB02
C 529	9.4	58.8	63	9	AA785298	AA785298 g6d01a1.f	C 602	9.4	58.8	100	14	Z20729	Z20729 HSAACITM V
C 530	9.4	58.8	63	29	BX196015	BX196015 Danilo rer	C 603	9.4	58.8	100	28	BH218154	BH218154 1006077D0
C 531	9.4	58.8	64	11	CNS09MTR	BK065659 Single re	C 604	9.2	57.5	22	29	TA330H07Q	AL492002 T. brucei
C 532	9.4	58.8	64	14	CB830802	CB830802 r109e05.y	C 605	9.2	57.5	23	28	AZ785047	AZ785047 2M0028M02
C 533	9.4	58.8	65	9	AV671702	AV671702 AV671702	C 606	9.2	57.5	28	9	AI625681	AI625681 ty59c06.x
C 534	9.4	58.8	65	28	AQ025771	AQ025771 1(2)K0581	C 607	9.2	57.5	31	9	AI677827	AI677827 wc80h06.x
C 535	9.4	58.8	65	29	AL951726	AL951726 Arabidops	C 608	9.2	57.5	31	28	AZ386571	AZ386571 IM0145C09
C 536	9.4	58.8	66	13	B0581139	B0581139 mah98507.	C 609	9.2	57.5	33	29	BZ358119	BZ358119 SALK 1319
C 537	9.4	58.8	66	28	AZ537250	AZ537250 AST-2P031	C 610	9.2	57.5	36	28	AZ836165	AZ836165 2M0130E23
C 538	9.4	58.8	67	28	AZ848671	AZ848671 2M0149F16	C 611	9.2	57.5	37	9	AA985715	AA985715 ue13d01.y
C 539	9.4	58.8	68	9	AU256518	AU256518 AU256518	C 612	9.2	57.5	37	9	AA387998	AA387998 mx3c01.x
C 540	9.4	58.8	68	11	CNS08M76	BX018190 Single re	C 613	9.2	57.5	37	9	AA238798	AA199679 zq74g06.r
C 541	9.4	58.8	68	14	CB353381	CB353381 ZP001-P00	C 614	9.2	57.5	40	9	AA199679	W53067 md14f07.r1
C 542	9.4	58.8	68	28	BH644273	BH644273 1008043C0	C 615	9.2	57.5	40	14	W53067	AL953755 Arabidops
C 543	9.4	58.8	70	9	AA879217	AA879217 nw85d10.s	C 616	9.2	57.5	40	29	AL953755	AL460414 T. brucei
C 544	9.4	58.8	70	14	AA953289	AA953289 o087h06.s	C 617	9.2	57.5	41	29	TA77D03Q	BH630486 1007088F1
C 545	9.4	58.8	70	14	CD487659	CD487659 Gm_cK424	C 618	9.2	57.5	42	28	BH630486	AZ834022 2M0116D04
C 546	9.4	58.8	73	28	BH789293	BH789293 SALK 0016	C 619	9.2	57.5	43	9	AI789785	AZ834022 2M0116D04
C 547	9.4	58.8	75	12	B1909149	B1909149 603052150	C 620	9.2	57.5	43	28	AZ789583	BH635864 1008007F0
C 548	9.4	58.8	76	9	AI746553	AI746553 u108e06.x	C 621	9.2	57.5	44	28	AZ324242	CC037245 3591_1-86
C 549	9.4	58.8	76	10	BE058589	BE058589 en18b03.y	C 622	9.2	57.5	44	29	AL764168	AL495350 T. brucei
C 550	9.4	58.8	77	28	BH789294	BH789294 SALK 0016	C 623	9.2	57.5	45	29	BX191644	AL495350 T. brucei
C 551	9.4	58.8	77	29	BZ761975	BZ761975 SALK 0839	C 624	9.2	57.5	46	14	H28362	BH907194 SALK 0386
C 552	9.4	58.8	79	9	AM646530	AM646530 cm65h09.w	C 625	9.2	57.5	46	28	AZ834022	B0899105 ma145S08.
C 553	9.4	58.8	80	9	AA836179	AA836179 cd21g05.8	C 626	9.2	57.5	46	28	BH635864	AU106744 AU106744
C 554	9.4	58.8	80	11	CNS08D04	BX0062728 Single re	C 627	9.2	57.5	46	29	CC037245	AU106745 AU106745
C 555	9.4	58.8	80	13	B0861991	B0861991 S009H05 P	C 628	9.2	57.5	47	29	TA359H02Q	AU106748 AU106748
C 556	9.4	58.8	81	9	AA207801	AA207801 mw81e01.r	C 629	9.2	57.5	48	28	BH907194	AI106750 AU106750
C 557	9.4	58.8	81	9	AV732653	AV732653 AV732653	C 630	9.2	57.5	49	13	B0899105	AI106750 AU106750
C 558	9.4	58.8	82	28	AZ586406	AZ586406 IM0392J16	C 631	9.2	57.5	50	9	AU106744	CB053396 NISC q114
C 559	9.4	58.8	82	9	AW718858	AW718858 i7e03nm.f	C 632	9.2	57.5	50	9	AU106745	AZ774755 2M0004E01
C 560	9.4	58.8	83	10	BF463412	BF463412 UI-M-CG0P	C 633	9.2	57.5	50	9	AU106748	AI203858 qf76g06.x
C 561	9.4	58.8	85	9	AL896449	AL896449 AL896449	C 634	9.2	57.5	50	9	AU106750	AI281257 qv22e08.x
C 562	9.4	58.8	85	9	AM064494	AM064494 SP1094 KR	C 635	9.2	57.5	53	28	BH790547	CB274957 ku73e02.y
C 563	9.4	58.8	85	12	BJ036891	BJ036891 B0036891	C 636	9.2	57.5	53	29	TA305R05Q	BL488934 T. brucei
C 564	9.4	58.8	86	9	AA236075	AA236075 z805a05.r	C 637	9.2	57.5	54	12	B1261027	BI261027 602972214
C 565	9.4	58.8	86	29	DME546383	DME546383 Drosophi1	C 638	9.2	57.5	54	9	AI610009	AI610009 tf78h03.x
C 566	9.4	58.8	86	29	DME546642	DME546642 Drosophi1	C 639	9.2	57.5	55	12	BI447971	BI447971 d6h90d02.
C 567	9.4	58.8	87	14	CB353686	CB353686 ZP001-P00	C 640	9.2	57.5	55	13	B0634625	B0634625 011G09 1n
C 568	9.4	58.8	88	9	AM064494	AM064494 SP1094 KR	C 641	9.2	57.5	55	28	B45110	B45110 HS-1060-B1-
C 569	9.4	58.8	88	14	R22567	R22567 yH24a08.s1	C 642	9.2	57.5	56	14	CB274974	CB274974 ku74h09.y
C 570	9.4	58.8	88	29	AG217414	AG217414 Drosophi1	C 643	9.2	57.5	56	28	BH652317	BH652317 SALK 0744
C 571	9.4	58.8	89	9	AI781871	AI781871 AL781871	C 644	9.2	57.5	58	9	AI195289	AI195289 ue71a03.r
C 572	9.4	58.8	89	9	AA283436	AA283436 RTH191 HT	C 645	9.2	57.5	58	12	BI944444	BI944444 s6d21d05.
C 573	9.4	58.8	89	29	BU0552018	BU0552018 mai24G04.	C 646	9.2	57.5	58	12	BI944444	BI944444 s6d21d05.
C 574	9.4	58.8	89	29	CC033596	CC033596 3591_1 64	C 647	9.2	57.5	58	29	BZ380332	BZ380332 T. brucei
C 575	9.4	58.8	90	11	CNS09692	CNS09692 Single re	C 648	9.2	57.5	58	29	TA113A05Q	TA113A05Q T. brucei
C 576	9.4	58.8	91	14	CB3944112	CB3944112 OSTRL1H4	C 649	9.2	57.5	59	28	AZ487775	AZ487775 IM0317112
C 577	9.4	58.8	91	14	CD029357	CD029357 mgcwo16xm	C 650	9.2	57.5	59	28	AQ254664	AQ254664 EP(3)0887
C 578	9.4	58.8	91	28	BH851397	BH851397 SALK 0729	C 651	9.2	57.5	60	10	BF471331	BF471331 UI-M-BH3-
C 579	9.4	58.8	92	28	AZ778554	AZ778554 2M0013M10	C 652	9.2	57.5	60	14	CB277341	CB277341 ku64c10.y
C 580	9.4	58.8	93	12	BI689678	BI689678 wo39g12.x	C 653	9.2	57.5	60	28	AZ782748	AZ782748 2M0023F07
C 581	9.4	58.8	93	12	BI689678	BI689678 603316173	C 654	9.2	57.5	60	29	BX323254	BX323254 Danilo rer
C 582	9.4	58.8	93	29	AB082060	AB082060 Drosophi1	C 655	9.2	57.5	60	29	BX323254	BX323254 Danilo rer
C 583	9.4	58.8	94	28	AL821922	AL821922 AL821922	C 656	9.2	57.5	60	29	BX323254	BX323254 Danilo rer
C 584	9.4	58.8	94	28	AZ822068	AZ822068 2M0095D02	C 657	9.2	57.5	60	29	BX323254	BX323254 Danilo rer
C 585	9.4	58.8	94	28	AZ827884	AZ827884 2M0104N03	C 658	9.2	57.5	60	29	BX323254	BX323254 Danilo rer
C 586	9.4	58.8	95	14	CB930289	CB930289 r193b02.y	C 659	9.2	57.5	60	29	BX323254	BX323254 Danilo rer
C 587	9.4	58.8	95	14	CB930289	CB930289 r193b02.y	C 660	9.2	57.5	60	29	BX323254	BX323254 Danilo rer
C 588	9.4	58.8	95	29	AL943193	AL943193 Arabidops	C 661	9.2	57.5	60	29	BX323254	BX323254 Danilo rer

662	9.2	57.5	61	9	AA682677	735	9.2	57.5	79	9	AI619804
C 663	9.2	57.5	61	9	AI469429	736	9.2	57.5	79	10	BF507191
C 664	9.2	57.5	61	13	BQ759608	C 737	9.2	57.5	79	12	BG942642
C 665	9.2	57.5	61	28	AZ916244	C 738	9.2	57.5	79	12	BJ059037
C 666	9.2	57.5	61	29	BZ762614	C 739	9.2	57.5	79	29	BZ563346
C 667	9.2	57.5	62	9	AF211691	740	9.2	57.5	80	9	AU256734
C 668	9.2	57.5	62	28	AZ920963	C 741	9.2	57.5	80	13	BQ822592
C 669	9.2	57.5	62	28	BZ764789	C 742	9.2	57.5	80	13	BU743537
C 670	9.2	57.5	63	13	BQ786079	C 743	9.2	57.5	80	13	BU743537
C 671	9.2	57.5	63	28	BH146129	744	9.2	57.5	80	29	BZ748860
C 672	9.2	57.5	64	12	BH192407	745	9.2	57.5	80	29	TAG19040
C 673	9.2	57.5	64	14	CB277338	746	9.2	57.5	81	9	AI494432
C 674	9.2	57.5	64	28	AZ930397	747	9.2	57.5	82	14	F35562
C 675	9.2	57.5	65	9	AI926212	C 748	9.2	57.5	82	28	AZ800630
C 676	9.2	57.5	65	14	CB274956	C 749	9.2	57.5	82	28	BH847053
C 677	9.2	57.5	65	28	AZ921399	C 750	9.2	57.5	83	9	AI130837
C 678	9.2	57.5	65	28	BH856885	C 751	9.2	57.5	83	13	BQ246646
C 679	9.2	57.5	65	29	BX535185	C 752	9.2	57.5	83	29	BZ383815
C 680	9.2	57.5	66	10	BG563372	C 753	9.2	57.5	84	9	AI318731
C 681	9.2	57.5	66	28	AZ809229	C 754	9.2	57.5	84	10	BG700680
C 682	9.2	57.5	66	29	AG216222	C 755	9.2	57.5	84	13	BQ274157
C 683	9.2	57.5	67	9	AA576816	C 756	9.2	57.5	85	28	BH863008
C 684	9.2	57.5	67	28	AZ588886	C 757	9.2	57.5	85	9	AA693766
C 685	9.2	57.5	67	29	BZ384630	C 758	9.2	57.5	85	13	BU870526
C 686	9.2	57.5	68	9	AI593371	759	9.2	57.5	85	14	T25066
C 687	9.2	57.5	68	10	BE463636	C 760	9.2	57.5	85	14	T63730
C 688	9.2	57.5	68	14	CB365575	C 761	9.2	57.5	85	28	BH856791
C 689	9.2	57.5	68	28	AQ025753	762	9.2	57.5	86	28	AZ809289
C 690	9.2	57.5	68	28	AZ808394	C 763	9.2	57.5	86	29	AL758982
C 691	9.2	57.5	68	29	CC156334	764	9.2	57.5	87	9	AM100540
C 692	9.2	57.5	69	28	AZ783790	C 765	9.2	57.5	87	10	BF382023
C 693	9.2	57.5	69	28	BH905447	C 766	9.2	57.5	87	12	BI781815
C 694	9.2	57.5	69	29	BZ357591	C 767	9.2	57.5	87	13	BU651003
C 695	9.2	57.5	70	9	AA271393	C 768	9.2	57.5	88	9	AA172789
C 696	9.2	57.5	70	9	AI869405	769	9.2	57.5	88	10	BF213975
C 697	9.2	57.5	71	9	AJ239810	C 770	9.2	57.5	88	28	BH172590
C 698	9.2	57.5	71	9	AA592935	C 771	9.2	57.5	88	9	AI537937
C 699	9.2	57.5	71	28	AZ377782	772	9.2	57.5	89	9	AV964569
C 700	9.2	57.5	72	10	DB7503	C 773	9.2	57.5	89	14	CB664411
C 701	9.2	57.5	72	14	CB217416	774	9.2	57.5	89	28	AF149519
C 702	9.2	57.5	72	28	AZ666486	775	9.2	57.5	89	28	AZ921956
C 703	9.2	57.5	72	28	BH632561	C 776	9.2	57.5	90	14	CB384048
C 704	9.2	57.5	72	28	AA709286	777	9.2	57.5	90	28	BH216178
C 705	9.2	57.5	73	9	AA531660	C 778	9.2	57.5	91	9	AA814152
C 706	9.2	57.5	73	28	AZ666427	C 779	9.2	57.5	91	9	AA821125
C 707	9.2	57.5	73	29	TA138A01P	780	9.2	57.5	91	10	AI119900
C 708	9.2	57.5	74	9	AA066266	781	9.2	57.5	91	10	BE399488
C 709	9.2	57.5	74	9	AI686239	782	9.2	57.5	91	10	BE546379
C 710	9.2	57.5	74	9	AI972803	783	9.2	57.5	91	14	CB884950
C 711	9.2	57.5	74	14	F26038	784	9.2	57.5	91	14	CD029310
C 712	9.2	57.5	74	28	AZ676904	C 785	9.2	57.5	91	28	AZ483571
C 713	9.2	57.5	74	28	AZ801962	C 786	9.2	57.5	92	9	AM615574
C 714	9.2	57.5	75	9	AI355788	C 787	9.2	57.5	92	13	BQ548581
C 715	9.2	57.5	75	28	AZ960154	788	9.2	57.5	92	28	AZ967063
C 716	9.2	57.5	75	28	BH908296	C 789	9.2	57.5	93	29	BZ597501
C 717	9.2	57.5	75	29	AI757185	790	9.2	57.5	94	10	BE270887
C 718	9.2	57.5	76	9	AV963354	791	9.2	57.5	94	12	BM178932
C 719	9.2	57.5	76	10	BE310567	C 792	9.2	57.5	94	28	BH901682
C 720	9.2	57.5	76	14	NB3035	C 793	9.2	57.5	94	29	BZ597364
C 721	9.2	57.5	76	28	AZ498839	794	9.2	57.5	95	9	AM614303
C 722	9.2	57.5	76	28	AZ775650	795	9.2	57.5	95	14	CA760949
C 723	9.2	57.5	76	29	CC156096	796	9.2	57.5	95	28	AZ575790
C 724	9.2	57.5	76	29	CC156096	C 797	9.2	57.5	95	29	BZ706369
C 725	9.2	57.5	77	14	T78711	798	9.2	57.5	95	29	BX293366
C 726	9.2	57.5	77	14	AG226570	C 799	9.2	57.5	96	28	AZ923126
C 727	9.2	57.5	78	10	BF215196	800	9.2	57.5	96	28	BH220277
C 728	9.2	57.5	78	28	AZ833373	801	9.2	57.5	96	29	AL752611
C 729	9.2	57.5	78	28	AZ920507	802	9.2	57.5	97	9	AA936843
C 730	9.2	57.5	78	28	BH413515	803	9.2	57.5	97	9	AA971988
C 731	9.2	57.5	78	29	CC156074	804	9.2	57.5	97	10	BG278602
C 732	9.2	57.5	79	9	AI18547	805	9.2	57.5	97	28	BH906651
C 733	9.2	57.5	79	9	AI422565	806	9.2	57.5	97	29	BZ384181
C 734	9.2	57.5	79	9	AI422565	807	9.2	57.5	98	9	AU077062

AI619804	ly53d10.x
BF507191	2912P-22d
BG942642	ax27g11.x
BJ059037	BJ059037
BZ563346	SALK_0924
AU256734	AU256734
BQ822592	1030101H0
BU743537	me133d10.
N55635	ESTG183 Rat
BZ748860	EY01909-5
AL460997	T. brucei
AI494432	GY99f03.x
F35562	HSPD1395B.H
AZ800630	ZM0038E14
BH847053	SALK_0129
AI130837	ta43a11.x
BQ246646	TAB15007E
BZ383815	SALK_1345
AI318731	a1e01m.f
BG700680	602682317
BQ274157	Kc47h04.Y
BH863008	SALK_0929
AA693766	z147h12.s
BU870526	0013P07.P
T25066	EST641.Huma
T63730	Yc16h02.r1
BH856791	3526_15
AZ809289	ZM0073A14
AL758982	Arabidops
AM100540	sds6e05.Y
BF382023	601816344
BI781815	kh01903.Y
BU651003	1112090FO
AA172789	m857c01.r
BF213975	601847455
BH172590	SALK_0059
AI537937	lp27a05.x
AV964569	AY964569
CB664411	Br01D_04h
AF149519	AF149519
AZ921956	HRC02G04
CB384048	TGSEST.yh5
BH216178	1006040H1
AA814152	cb25e02.s
AA821125	v41a01.r
AI119900	uc22a11.r
BE399488	WHE0036.H
BE546379	601071061
CB884950	M617065.H
CD029310	mgcW012XD
AZ483571	1N0309D20
AM615574	ba12a09.x
BQ548581	rd33f09.Y
AZ967063	ZM0237P14
BZ597501	SALK_1093
BE270887	600943706
BM178932	eej61c04.
BH901682	SALK_0844
BZ597364	SALK_1020
CA760949	BR060009A
AZ575790	AST-r31B0
BZ706369	SM276B2-G
BX293366	Arabidops
AZ923126	4908.ge87
BH220277	1006093B0
AL752611	Arabidops
AA936843	ch89f08.s
AA971988	op76c07.B
BG278602	as512np.f
BH906651	SALK_0351
BZ384181	SALK_1351
AU077062	AU077062

808	9.2	57.5	98	13	BU763747	BU763747	sas874d07.
809	9.2	57.5	98	28	AZ777342	AZ777342	2M001IM07
810	9.2	57.5	98	28	BH807347	BH807347	1008104F0
811	9.2	57.5	98	29	DR26H11T	DR26H11T	Al984461
812	9.2	57.5	99	9	AA785099	AA785099	g5a02a1.f
813	9.2	57.5	99	9	Al687258	Al687258	cp94c11.x
814	9.2	57.5	99	9	Al828637	Al828637	Al828637
815	9.2	57.5	99	9	Al828637	Al828637	Al828637
816	9.2	57.5	99	9	AY948472	AY948472	AV948472
817	9.2	57.5	99	10	BG152001	BG152001	naq72e07.
818	9.2	57.5	99	10	BG236505	BG236505	na144c09.
819	9.2	57.5	99	14	H92491	H92491	y86c10..81
820	9.2	57.5	99	29	B2424500	B2424500	100013609
821	9.2	57.5	99	29	CC248975	CC248975	XH952 Bay
822	9.2	57.5	100	9	Al888803	Al888803	wn36G05.x
823	9.2	57.5	100	9	Al196242	Al196242	zpz9f04.x
824	9.2	57.5	100	10	BE479484	BE479484	164197 BA
825	9.2	57.5	100	13	BQ819795	BQ819795	1030080E0
826	9.2	57.5	100	13	BQ820336	BQ820336	1030083G1
827	9.2	57.5	100	14	CB366608	CB366608	ZF001-P00
828	9.2	57.5	100	28	AQ845808	AQ845808	LMaJFV1_1
829	9.2	57.5	100	28	AZ325011	AZ325011	1M0047A15
830	9.2	57.5	100	28	BH847984	BH847984	SALX_0673
831	9.2	57.5	100	29	BZ355837	BZ355837	SALX_1276
832	9.2	57.5	100	29	TA384D04P	TA384D04P	Al498667 T. brucei
833	9.2	57.5	20	28	AZ774560	AZ774560	2M0004H08
834	9.2	57.5	21	28	TA387G01Q	TA387G01Q	Al498325 T. brucei
835	9.2	57.5	28	29	AZ589405	AZ589405	1M0398B20
836	9.2	57.5	30	10	BE274322	BE274322	601121015
837	9.2	57.5	30	10	BE276866	BE276866	601178428
838	9.2	57.5	30	10	BE277260	BE277260	601178250
839	9.2	57.5	30	10	BE279576	BE279576	601157461
840	9.2	57.5	30	10	BE280898	BE280898	601155490
841	9.2	57.5	30	10	BE384678	BE384678	601276956
842	9.2	57.5	30	10	BE384733	BE384733	601273335
843	9.2	57.5	30	10	BE386356	BE386356	601273503
844	9.2	57.5	30	10	BE389833	BE389833	601284336
845	9.2	57.5	30	10	BE359533	BE359533	601345383
846	9.2	57.5	30	10	BE3561270	BE3561270	601344283
847	9.2	57.5	30	10	BE3727688	BE3727688	601564370
848	9.2	57.5	30	10	BE371660	BE371660	601567046
849	9.2	57.5	30	10	BE374581	BE374581	601594894
850	9.2	57.5	30	10	BE3900191	BE3900191	601673121
851	9.2	57.5	31	10	BE261494	BE261494	601148665
852	9.2	57.5	31	10	BE384502	BE384502	601277869
853	9.2	57.5	31	10	BE409249	BE409249	601301117
854	9.2	57.5	31	10	BE729154	BE729154	601561047
855	9.2	57.5	31	10	BE731925	BE731925	601568932
856	9.2	57.5	31	28	AZ386571	AZ386571	1M0145C09
857	9.2	57.5	31	28	TA235H03Q	TA235H03Q	Al481228 T. brucei
858	9.2	57.5	32	10	BE277724	BE277724	601119930
859	9.2	57.5	32	10	BE547551	BE547551	601475188
860	9.2	57.5	32	10	BE561225	BE561225	601344209
861	9.2	57.5	32	10	BE901763	BE901763	601675392
862	9.2	57.5	33	10	BE385013	BE385013	601276895
863	9.2	57.5	33	10	BF026570	BF026570	601672580
864	9.2	57.5	34	9	Al662934	Al662934	uj69c01.y
865	9.2	57.5	34	9	BE268227	BE268227	601125649
866	9.2	57.5	34	10	BE277022	BE277022	601178905
867	9.2	57.5	34	10	BE277727	BE277727	601119937
868	9.2	57.5	34	10	BE561483	BE561483	601346552
869	9.2	57.5	34	10	CC458064	CC458064	SALX_1154
870	9.2	57.5	34	29	AV961052	AV961052	AV961052
871	9.2	57.5	35	9	AZ666284	AZ666284	1M0548P10
872	9.2	57.5	35	28	BE408356	BE408356	601302740
873	9.2	57.5	36	10	Al446151	Al446151	tj07e11.x
874	9.2	57.5	37	9	BE548155	BE548155	6010773138
875	9.2	57.5	37	10	BF122604	BF122604	601760322
876	9.2	57.5	37	12	BI524368	BI524368	603052253
877	9.2	57.5	37	18	AZ595462	AZ595462	1M0408P03
878	9.2	57.5	37	28	Al945039	Al945039	ArabiDops
879	9.2	57.5	37	29	TA15F12P	TA15F12P	Al462847 T. brucei
880	9.2	57.5	37	29			
881	9.2	57.5	37	29	TA380C04P	TA380C04P	
882	9.2	57.5	38	29	TA50D020	TA50D020	
883	9.2	57.5	39	10	BE392354	BE392354	
884	9.2	57.5	39	28	BH848585	BH848585	
885	9.2	57.5	41	28	AZ467358	AZ467358	1M0278M07
886	9.2	57.5	41	28	AZ804585	AZ804585	2M0065B10
887	9.2	57.5	41	28	BH851307	BH851307	SALX_0728
888	9.2	57.5	41	28	BH851308	BH851308	SALX_0728
889	9.2	57.5	42	9	AU006856	AU006856	
890	9.2	57.5	42	10	BE278008	BE278008	
891	9.2	57.5	42	28	AZ629604	AZ629604	1M0482N12
892	9.2	57.5	42	28	AZ823130	AZ823130	2M0097A04
893	9.2	57.5	43	9	Al868103	Al868103	c036a07..x
894	9.2	57.5	43	9	AV962413	AV962413	
895	9.2	57.5	43	10	BE272940	BE272940	601171229
896	9.2	57.5	43	12	BI829531	BI829531	603080362
897	9.2	57.5	43	12	W62611	W62611	md58c07..x1
898	9.2	57.5	43	29	AL756475	AL756475	ArabiDops
899	9.2	57.5	44	9	AA930614	AA930614	vy67a03..x
900	9.2	57.5	44	9	AV845599	AV845599	
901	9.2	57.5	44	10	BE909560	BE909560	601502734
902	9.2	57.5	45	12	BI761191	BI761191	603043417
903	9.2	57.5	45	28	AZ832673	AZ832673	2M0113G22
904	9.2	57.5	45	28	BH855837	BH855837	1008025C0
905	9.2	57.5	45	28	BH855537	BH855537	SALX_0849
906	9.2	57.5	45	29	TA17A04P	TA17A04P	Al45403 T. brucei
907	9.2	57.5	45	29	TA372A04P	TA372A04P	Al496098 T. brucei
908	9.2	57.5	46	9	AV849366	AV849366	
909	9.2	57.5	46	28	AZ513841	AZ513841	1M0360B12
910	9.2	57.5	46	28	AZ603730	AZ603730	1M0423A18
911	9.2	57.5	47	28	BH789255	BH789255	SALX_0013
912	9.2	57.5	47	28	BH849286	BH849286	SALX_0694
913	9.2	57.5	47	29	BZ382871	BZ382871	SALX_1190
914	9.2	57.5	47	29	CC057374	CC057374	SALX_1409
915	9.2	57.5	47	29	TA120G01P	TA120G01P	Al464568 T. brucei
916	9.2	57.5	48	10	BE377446	BE377446	601228923
917	9.2	57.5	48	12	BI757791	BI757791	603029775
918	9.2	57.5	48	28	AZ339937	AZ339937	1M0071F09
919	9.2	57.5	48	28	AZ767769	AZ767769	1M0567H13
920	9.2	57.5	48	28	BH790348	BH790348	SALX_0568
921	9.2	57.5	48	29	DME547336	DME547336	droB0Dh11
922	9.2	57.5	49	9	Al499383	Al499383	co11b02..x
923	9.2	57.5	49	9	Al800933	Al800933	wq14q11..x
924	9.2	57.5	49	12	BI407152	BI407152	602919431
925	9.2	57.5	49	28	AZ309933	AZ309933	1M0017G23
926	9.2	57.5	49	29	CC459657	CC459657	SALX_1379
927	9.2	57.5	49	29	DME546869	DME546869	droB0Dh11
928	9.2	57.5	50	9	AU102552	AU102552	
929	9.2	57.5	50	9	AU102609	AU102609	
930	9.2	57.5	50	9	AU102610	AU102610	
931	9.2	57.5	50	9	AU102612	AU102612	
932	9.2	57.5	50	9	AU102613	AU102613	
933	9.2	57.5	50	9	AU102614	AU102614	
934	9.2	57.5	50	9	AU103873	AU103873	
935	9.2	57.5	50	9	AU103884	AU103884	
936	9.2	57.5	50	9	AU103886	AU103886	
937	9.2	57.5	50	9	AU103933	AU103933	
938	9.2	57.5	50	9	AU103934	AU103934	
939	9.2	57.5	50	9	AU103935	AU103935	
940	9.2	57.5	50	9	AU103936	AU103936	
941	9.2	57.5	50	9	AU107477	AU107477	
942	9.2	57.5	50	9	AU107480	AU107480	
943	9.2	57.5	50	9	AM783902	AM783902	5..Al12 G11
944	9.2	57.5	50	13	BQ387587	BQ387587	NtSC_mn24
945	9.2	57.5	50	29	BZ769258	BZ769258	SALX_1418
946	9.2	57.5	50	29	BZ769259	BZ769259	SALX_1418
947	9.2	57.5	51	29	AL953339	AL953339	ArabiDops
948	9.2	57.5	52	9	AA797759	AA797759	vx66g03..x
949	9.2	57.5	52	28	AZ455027	AZ455027	1M0257B13
950	9.2	57.5	53	28	AZ826318	AZ826318	2M0101022
951	9.2	57.5	54	12	BI111668	BI111668	602896049
952	9.2	57.5	54	28	AZ447232	AZ447232	1M0244L13
953	9.2	57.5	54	28	AZ592301	AZ592301	1M0403B10

C 954 56.2 54 28 BH25617 BH25617 1006127C0
 C 955 56.2 55 9 A1689325 A1689325 CX33H03.X
 C 956 56.2 55 9 AA469546 AA469546 VF67D07.X
 C 957 56.2 55 12 BM342998 BM342998 FW50D05.Y
 C 958 56.2 55 28 AF149501 AF149501 AF149501 AF149501
 C 959 56.2 55 28 A2845377 A2845377 2M0145H09
 C 960 56.2 55 28 A2919058 A2919058 1006013G1
 C 961 56.2 55 29 A2942758 A2942758 Arabidops
 C 962 56.2 56 9 A1904001 A1904001 MR-BT039-
 C 963 56.2 56 10 BF312405 BF312405 601898946
 C 964 56.2 56 10 BF315275 BF315275 601902673
 C 965 56.2 56 12 B1906543 B1906543 603064110
 C 966 56.2 56 29 BX122063 BX122063 Danio rer
 C 967 56.2 57 9 AA531356 AA531356 nj61b01.s
 C 968 56.2 57 12 BM566536 BM566536 K163112.Y
 C 969 56.2 57 14 CB914166 CB914166 VDD009E07
 C 970 56.2 57 29 AA769106 AA769106 Arabidops
 C 971 56.2 58 9 A1035939 A1035939 Arabidops
 C 972 56.2 58 9 A1626254 A1626254 Arabidops
 C 973 56.2 58 9 A1626254 A1626254 Arabidops
 C 974 56.2 58 9 A1626254 A1626254 Arabidops
 C 975 56.2 58 12 BM342544 BM342544 Arabidops
 C 976 56.2 58 14 CD028622 CD028622 mgcm002XP
 C 977 56.2 58 28 AF219062 AF219062 Arabidops
 C 978 56.2 58 28 A2317235 A2317235 1M0035K12
 C 979 56.2 58 28 A2616246 A2616246 1M0446M06
 C 980 56.2 58 29 BZ592795 BZ592795 SALX 0291
 C 981 56.2 59 12 B1036242 B1036242 Arabidops
 C 982 56.2 60 10 BE316566 BE316566 NP057A06L
 C 983 56.2 60 10 BE318074 BE318074 NP062F01L
 C 984 56.2 60 10 BE325120 BE325120 NP114F06S
 C 985 56.2 60 14 R95416 R95416 SMNHADA0090
 C 986 56.2 60 28 BH790816 BH790816 SALX 0579
 C 987 56.2 60 28 BH811589 BH811589 SALX 0591
 C 988 56.2 61 9 AA627880 AA627880 mg66D02.s
 C 989 56.2 61 9 AA189463 AA189463 mg79F06.r
 C 990 56.2 61 9 AA594724 AA594724 n002811.s
 C 991 56.2 61 14 CB007034 CB007034 VVC040G11
 C 992 56.2 62 9 A1149923 A1149923 qf33d06.x
 C 993 56.2 62 28 AZ775430 AZ775430 2M0007B20
 C 994 56.2 62 29 AG219377 AG219377 Lotus jap
 C 995 56.2 63 9 A1748404 A1748404 db52d06.Y
 C 996 56.2 63 9 AU009048 AU009048 AU009048
 C 997 56.2 63 9 AU009049 AU009049 AU009049
 C 998 56.2 63 9 AU009103 AU009103 AU009103
 C 999 56.2 63 9 AU009104 AU009104 AU009104
 C 1000 56.2 63 9 AM762943 AM762943 ut68G08.Y

ALIGNMENTS

RESULT 1 80 bp mRNA linear EST 05-DEC-2002
 CA798147 Cac BL 5432 Cac BL (Bean and Leaf from Amelonardo type cacao)
 LOCUS Theobroma cacao CDNA clone Cac BL_5432 5', mRNA sequence.
 DEFINITION Theobroma cacao CDNA clone Cac BL_5432 5', mRNA sequence.
 CA798147
 VERSION CA798147.1 GI:26055233
 KEYWORDS EST.
 SOURCE Theobroma cacao (cacao)
 ORGANISM Theobroma cacao
 EST. Theobroma cacao
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 1; eustosids II; Malvales; Myricaceae; Byttnerioideae; Theobroma.
 1 (bases 1 to 80)
 Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D., Retzel
 E.R. and Jones, C.A.
 Gene discovery and microarray analysis of cacao (Theobroma cacao
 L.) varieties
 Plant 216 (2), 255-264 (2002)
 JOURNAL 22337596
 MEDLINE 12447539
 PUBMED

COMMENT

Contact: Jones, Paul
 Masterfoods
 3d Dundee Road, Slough, Berkshire, UK, SL1 4UG
 Tel: +44 1664 416644
 Email: Paul.Jones@eu.affem.com
 Seg primer: 73.
 Location/Qualifiers
 1..80
 /organism="Theobroma cacao"
 /mol_type="mRNA"
 /strain="Amelonardo type"
 /db_xref="taxon:3641"
 /clone="Cac BL 5432"
 /issue_type="Mature leaf and mature bean"
 /cell_type="Whole organ"
 /dev_stage="maturity"
 /lab_host="XL-1 Blue MRF"
 /clone_11b="Cac BL (Bean and Leaf from Amelonardo type
 Cacao)"
 /note="Vector: pBK-CMV; Bean and Leaf tissue from an
 Amelonardo type Cacao tree."

FEATURES

source

BASE COUNT

15 a 17 c 27 g 18 t 3 others

ORIGIN

Query Match 76.2%; Score 12.2; DB 14; Length 80;
 Best Local Similarity 80.0%; Pred. No. 1.2e+04;
 Matches 12; Conservative 2; Mismatches 1; Gaps 0;

Qy 1 RGCGTACGACACG 15
 Db 36 GCGGTACTACTACG 50

RESULT 2

A2431360 96 bp DNA linear GSS 03-OCT-2000
 LOCUS 1M0216F14F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
 DEFINITION clone UGCG1M0216F14 F, genomic survey sequence.
 A2431360
 VERSION A2431360.1 GI:10555373
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 96)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0216 Row: F Column: 14
 Seq primer: CGTTGTAACACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 96.
 Location/Qualifiers
 1..96
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG1M0216F14"

JOURNAL

COMMENT Unpublished
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0216 Row: F Column: 14
 Seq primer: CGTTGTAACACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 96.
 Location/Qualifiers
 1..96
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG1M0216F14"

FEATURES

source

/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g1/4732114[gb]/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 31 a 32 c 12 g 21 t
ORIGIN

Query Match 73.8%; Score 11.8; DB 28; Length 96;
Best Local Similarity 84.6%; Pred. No. 2.1e+04;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 RGCTAGACCA 13
:|||||:
4 GGCTAGCCACA 16

Db

RESULT 3
AZ658330 100 bp DNA linear GSS 14-DEC-2000
LOCUS clone UUCGCM0535M02 F, genomic survey sequence.
DEFINITION
ACCESSION AZ658330.1 GI:11795476
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 (bases 1 to 100)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0535 row: M column: 02
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 100.
Location/Qualifiers
1. 100
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"

FEATURES
source

/clone="UUCGCM0535M02"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g1/4732114[gb]/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 23 a 13 c 36 g 28 t
ORIGIN

Query Match 73.8%; Score 11.8; DB 28; Length 100;
Best Local Similarity 84.6%; Pred. No. 2.2e+04;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 RGCTAGACCA 13
:|||||:
5 GGCTAGCCACA 17

Db

RESULT 4
BG422154 44 bp mRNA linear EST 14-MAR-2001
LOCUS 602448881F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4567189 5', mRNA sequence.
DEFINITION
ACCESSION BG422154
VERSION BG422154.1 GI:13328660
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 44)
NIH-MGC http://mgc.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.jnl.gov
Plate: LNCM317 row: b column: 22
High quality sequence stop: 44.
Location/Qualifiers
1. 44
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4567189"
/tissue_type="renal cell adenocarcinoma"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 14"
/note="Organ: kidney; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally

FEATURES
source

ORIGIN

Query Match 72.5%; Score 11.6; DB 14; Length 67;
 Best Local Similarity 75.0%; Pred. No. 2.4e+04;
 Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RGGCTAGGCHACACGA 16
 |||||:|||||
 33 GGCTAGCCACACACA 48

RESULT 7
 T8A7H09Q
 LOCUS

DEFINITION T. brucei sheared genomic DNA clone 87h09, reverse sequence,
 genomic survey sequence.

ACCESSION AL459831
 VERSION AL459831.1 GI:11861863
 KEYWORDS
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 1 (bases 1 to 86)
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 Direct Submission
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk
 Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, ed. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: neilsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers

FEATURES
 source 1..86
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="87h09"
 BASE COUNT 23 a 23 c 18 g 22 t
 ORIGIN

Query Match 72.5%; Score 11.6; DB 29; Length 86;
 Best Local Similarity 85.7%; Pred. No. 2.6e+04;
 Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 GCTAGCHACACGA 16
 |||||:|||||
 31 GCTAGACACACGA 44

RESULT 8
 AA953865
 LOCUS

DEFINITION on76a12.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone
 IMAGE:1562590 3' similar to TR:Q92615 Q92615 MYELOBLAST KIA0217 ;,
 mRNA sequence.

ACCESSION AA953865
 VERSION AA953865.1 GI:3116783
 KEYWORDS
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 86)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: -40m3 fwd. RT from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES
 source 1..86
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1562590"
 /lab_host="DH10B"
 /clone_1lb="Soares NFL_T_GBC_S1"
 /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
 a modified polylinker; Site 1: Not I; Site 2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung NDHL19W, testis NRT, and B-cell
 NCI-CGAP GCB1) were mixed, and 88 circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 1.M.A.G.E. clones 297480-302087, 682632-687239,
 726408-728711, and 729096-731399. Subtraction by Bento
 Soares and M. Fatima Bonaldo."
 BASE COUNT 17 a 20 c 34 g 17 t
 ORIGIN

Query Match 72.5%; Score 11.6; DB 9; Length 88;
 Best Local Similarity 85.7%; Pred. No. 2.7e+04;
 Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGCTAGCHACACG 15
 |||||:|||||
 61 GGCTGGCCACACG 74

RESULT 9
 AZ602406
 LOCUS

DEFINITION IM0421H09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0421H09 F, genomic survey sequence.

ACCESSION AZ602406
 VERSION AZ602406.1 GI:11724596
 KEYWORDS
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 90)
 Dunn, P., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE Unpublished
 JOURNAL
 COMMENT Contact: Robert B. Weis
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606

Fax: 801 585 7177
Email: ddun@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0421 row: H column: 09
Seq primer: CGTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 90.

FEATURES

SOURCE

1..90

Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U06C1M0421H09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid U06C1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF159072.1) a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

14 a 18 c 28 g 30 t

ORIGIN

Query Match 72.5%; Score 11.6; DB 28; Length 90;
Best Local Similarity 75.0%; Pred. No. 2.7e+04;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RGGCTAGCHACACGA 16
: |||||:|||||
Db 65 AGGCTGGCCACACACTA 50

RESULT 10
BH215494/c 93 bp DNA linear GSS 08-NOV-2001
LOCUS BH215494
DEFINITION 1006027C12.2EL y2 1006 - RescueMu Grid G Zea mays genomic, genomic survey sequence.
ACCESSION BH215494
VERSION BH215494.1 GI:16806152
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 93)
Walbot, V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.
Plate: 1006027 row: 42
Class: transposon-tagged.
Location/Qualifiers

FEATURES

SOURCE

1..93

Location/Qualifiers

/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A186/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1006 - RescueMu Grid G"
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.instate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT

15 a 17 c 39 g 22 t

ORIGIN

Query Match 72.5%; Score 11.6; DB 28; Length 93;
Best Local Similarity 85.7%; Pred. No. 2.7e+04;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGTAGCHACACG 15
||| |||||
Db 17 GCGAAGCACACACG 4

RESULT 11
BG695449/c 99 bp mRNA linear EST 04-MAY-2001
LOCUS BG695449
DEFINITION NISC iV17E07.w2 Soares NMBP2 pituitary Mus musculus cDNA clone IMAGE:4318212 5', mRNA sequence.
ACCESSION BG695449
VERSION BG695449.1 GI:13955375
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 99)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
cDNA Library Preparation: M. Bento Soares Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
MGI:1598980
Plate: L14M9923 row: K column: 13
Seq primer: T7 primer.
Location/Qualifiers

FEATURES

SOURCE

1..99

Location/Qualifiers

/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:4318212"
/tissue_type="pituitary gland"


```

/dev stage="embryo, 14 dpc"
/lab host="DH10B (phage-resistant)"
/clone_lib="Soares NMMP2 pituitary"
/note="Organ: Brain; Vector: pT73D-Pac; Site 1: NotI;
Site 2: EcoRI; 1st strand cDNA was primed with a NotI -
oligo(dT) primer
5'-AATCGAAGATTGGGGCGGGCGGCTTTTCTTTTCTTTT-3';
double-stranded cDNA was ligated to EcoRI adaptors
5'-AATCGGACGACAG-3' AND 5'-CTGTGTCG-3' (Pharmacia),
digested with NotI and cloned into the NotI and EcoRI
sites of the pT73D-Pac vector. Library went through one
round of normalization, and was constructed in the
laboratory of M. Bento Soares (University of Iowa)."
```

BASE COUNT 10 a 21 c 33 g 35 t

ORIGIN

Query Match 72.5%; Score 11.6; DB 10; Length 99;
Best Local Similarity 75.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16
|||||:|||||
76 GGGTTAGCACACACAA 61

Db

RESULT 12
B0625306 100 bp mRNA linear EST 01-JUL-2002
LOCUS rd27g03.y1 Meloidogyne incognita egg SL1 TOPO v1 Meloidogyne
DEFINITION incognita cDNA 5', mRNA sequence.
B0625306
VERSION B0625306.1 GI:21652484
KEYWORDS EST.
SOURCE Meloidogyne incognita (southern root-knot nematode)
ORGANISM Meloidogyne incognita
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heterodera; Meloidogyninae; Meloidogyne.
1 (bases 1 to 100)
McCartter,J., Clifton,S., Chiapelli,B., Page,D., Martin,J., Wyle,T.,
Dante,M., Maria,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.,
Gibbons,M., Rifter,E., Bennett,J., Franklin,C., Tsagarisvili,R.,
Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe
,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,
Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterton,R. and
Wilson,R.
The Washington Univ. Nematode EST Project, 1999
Unpublished
Contact: McCartter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: eswatson.wustl.edu
The library was constructed by Claire Murphy and Dr. James McCartter
at Washington University, St. Louis. Meloidogyne incognita eggs
were provided by Andrew Kloek of Divergence Inc., St. Louis, MO.
Putative full length read
The vector to vector length is 101
Seq primer: -40R from Gibco.
Location/Qualifiers
1..100
/oranism="Meloidogyne incognita"
/mol type="mRNA"
/db xref="taxon:6306"
/dev stage="eggs"
/lab host="DH10B (Invitrogen)"
/clone_lib="Meloidogyne incognita egg SL1 TOPO v1"
/note="Vector: pCR11-TOPO (Invitrogen); Site 1: EcoRI;
Site 2: EcoRI; The library was constructed by Claire
Murphy and Dr. James McCartter at Washington University,
St. Louis. Oligo(dT)-SL1 PCR based library. cDNA PCR
products of size >400 nucleotides containing SL1 on the 5'.

```

end and oligo(dT) on the 3' end were non-directionally
cloned into pCR11-TOPO(Invitrogen) following the TOPO TA
cloning protocol. Meloidogyne incognita eggs were provided
by Andrew Kloek of Divergence Inc., St. Louis, MO."
```

BASE COUNT 39 a 29 c 15 g 17 t

ORIGIN

Query Match 72.5%; Score 11.6; DB 13; Length 100;
Best Local Similarity 75.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16
|||||:|||||
30 AGCCGACGACACACAA 45

Db

RESULT 13
BH901408/c 26 bp DNA linear GSS 04-SEP-2002
LOCUS SALK_079024.36.15.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_079024.36.15.x, genomic
survey sequence.
BH901408
ACCESSION BH901408.1 GI:22712289
VERSION BH901408
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (chale crese)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosid II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 26)
Alonso,J.M., Leisbe,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckersalk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1..26
/oranism="Arabidopsis thaliana"
/mol type="genomic DNA"
/strain="Columbia 0"
/db xref="taxon:3702"
/clone="SALK_079024.36.15.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 6 a 6 c 3 g 11 t

ORIGIN

Query Match 70.0%; Score 11.2; DB 28; Length 26;
Best Local Similarity 91.7%; Pred. No. 2.8e+04;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 GGGTACGACACAA 13
|||||:|||||
21 GGGTACGACACAA 10

Db

RESULT 14
 A0025306/c 34 bp DNA linear GSS 23-AUG-2000
 LOCUS EP(3)313 Drosophila melanogaster EP line Drosophila melanogaster
 DEFINITION genomic Sequence recovered from 5' end of P element, genomic survey
 sequence.
 ACCESSION A0025306
 VERSION A0025306.1 GI:3265658
 KEYWORDS GSS.
 SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydriidea; Drosophilidae; Drosophila.
 REFERENCE Liao,G.-C., Rehm,E.J. and Rubin,G.M.
 1 (bases 1 to 34)
 Insertion site preferences of the P transposable element in
 Drosophila melanogaster
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3347-3351 (2000)
 JOURNAL 20202638
 MEDLINE 10716700
 PUBMED
 COMMENT Contact: Gerald Rubin
 Berkeley Drosophila Genome Project
 University of California, Berkeley
 USA Building, Berkeley, CA 94720-3200, USA
 Fax: 5106439947
 Email: gerry@fruitfly.berkeley.edu
 Sequence recovery method was inverse PCR.
 Sequence orientation is forward strand relative to 5' end of P
 element
 The P element insertion position is base 27 in the 34 bases. This
 insertion position refers to the first base of the 8 base target
 recognition sequence.
 Class: transposon-tagged.
 FEATURES
 source Location/Qualifiers
 1..34
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /db_xref="taxon:7227"
 /clone_lib="Drosophila melanogaster EP line"
 /note="Inverse PCR was performed on Drosophila
 melanogaster strains each of which contains a single EP
 transposable element insertion. (The generation of these
 insertion strains is described in Rorth P, Szabo K, Bailey
 A, Laverly T, Rehm J, Rubin GM, Weigmann K, Milan M, Benes
 V, Ansoerge W, Cohen SM. 1998. Systematic gain-of-function
 genetics in Drosophila. Development 6:1049-1057.) The
 resultant fragment for each strain was directly sequenced
 to determine the genomic sequence at the site of
 insertion. Details of the protocols used can be found at
 http://fruitfly.berkeley.edu/P_distrupt/inverse_pcr.html."

BASE COUNT
 ORIGIN 4 a 13 c 10 g 7 t

Query Match 70.0%; Score 11.2; DB 28; Length 34;
 Best Local Similarity 78.6%; Pred. No. 3.1e+04;
 Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGGCTAGCGACAC 14
 :|||||:|||||
 Db 28 AGGCTGCGACAC 15

RESULT 15
 BH861777/c 49 bp DNA linear GSS 05-AUG-2002
 LOCUS BH861777
 DEFINITION SALK_087974 Arabidopsis thaliana TDNA insertion lines Arabidopsis
 thaliana genomic clone SALK_087974, genomic survey sequence.
 ACCESSION BH861777
 VERSION BH861777.1 GI:22097103
 KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
 1 (bases 1 to 49)
 A sequence-indexed library of insertion mutations in the
 Arabidopsis Genome
 TITLE Arabidopsis Genome
 JOURNAL Unpublished
 COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: eckers@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within an annotated exon of At5g01330.
 Class: TDNA tagged.

FEATURES
 source Location/Qualifiers
 1..49
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_087974"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT
 ORIGIN 7 a 9 c 15 g 18 t

Query Match 70.0%; Score 11.2; DB 28; Length 49;
 Best Local Similarity 91.7%; Pred. No. 3.6e+04;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 TAGCGACACGA 16
 :|||||:|||||
 Db 12 TAGCGACACGA 1

RESULT 16
 BH861778/c 49 bp DNA linear GSS 05-AUG-2002
 LOCUS BH861778
 DEFINITION SALK_087975 Arabidopsis thaliana TDNA insertion lines Arabidopsis
 thaliana genomic clone SALK_087975, genomic survey sequence.
 ACCESSION BH861778
 VERSION BH861778.1 GI:22097104
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
 1 (bases 1 to 49)
 A sequence-indexed library of insertion mutations in the
 Arabidopsis Genome
 TITLE Arabidopsis Genome
 JOURNAL Unpublished
 COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752


```

LOCUS          CA819431                77 bp    mRNA    linear    EST 09-DEC-2002
DEFINITION     sau78801.y1 Gm-cl071 glycine max cDNA clone SOYBEAN CLONE ID:
VERSION        CA819431
KEYWORDS       CA819431.1  GI:26268368
SOURCE         EST.
ORGANISM       Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseolae;
Glycine.
REFERENCE      1 (bases 1 to 77)
AUTHORS        Shoemaker R., Keim, P., Vodkin, L., Erpelting, J., Correll, V., Khanna
               'A', Bolla, B., Mairra, M., Hillier, L., Kuabada, T., Martin, J., Beck, C.,
               Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
               'Y', Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
               'R', Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
               'R', Waterston, R. and Wilson, R.
COMMENT        Public Soybean EST Project
               Unpublished
               Contact: Shoemaker R./Public Soybean EST Project
               Washington University School of Medicine
               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
               Tel: 314 286 1800
               Fax: 314 286 1810
               Email: est@wustl.edu
               This clone is available through: Reagen, Invitrogen Corp. 2130
               South Memorial Parkway Huntzville, AL 35801 For further information
               call: (800)-533-4363 or contact: csw@reagen.com web site:
               www.reagen.com
               Putative full length read
               vector to vector length is 78
               Seq primer: -40RP from Gibco.
FEATURES
  source
    1..77
    /organism="Glycine max"
    /mol_type="mRNA"
    /db_xref="taxon:3847"
    /clone="SOYBEAN CLONE ID: Gm-cl071-7058"
    /tissue_type="immature pods (-2cm long) of greenhouse
    grown plants"
    /lab_host="DH10B"
    /clone_1fb="Gm-cl071"
    /note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; The
    cDNA library was constructed from mRNA isolated from
    immature pods (approximately 2cm long) of greenhouse grown
    plants. The library was prepared using the Life
    Technologies SuperScript cDNA library construction kit.
    Complementary DNA was synthesised from mRNA using a
    poly(dT) sequence with a NotI restriction site. SalI
    linkers adapters were ligated to the blunt-ended cDNA
    fragments followed by NotI digestion. The cDNA fragments
    were directionally cloned into the NotI-SalI restriction
    site of the pSPORT1 vector. The ligated cDNA fragments
    were transformed into E.coli Electromax DH10B host cells.
    This library was constructed in the laboratory of Dr. Lila
    Vodkin by Anu Khanna at the University of Illinois at
    Urbana-Champaign. email: l-vodkin@uiuc.edu"
BASE COUNT    18 a      14 c      17 g      28 t
ORIGIN
Query Match   70.0%; Score 11.2; DB 14; Length 77;
Best Local Similarity 91.7%; Pred. No. 4.3e+04;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
4 CTAGGACACAGC 15
|||||:|||||
Db              65 CTAGGCACACAGC 76

```

Accession	Version	Keywords	Source	Organism	Reference	Authors	Title	Journal	Comment	Features	Source
AI183068											
LOCUS	85 bp	mRNA									
DEFINITION	AI183068 85 bp mRNA linear EST 07-JAN-1997										
ACCESSION	m86609.r1 Soares mouse lymph node NbM1N Mus musculus cDNA clone										
VERSION	IMAGE:636808.5 similar to TR:GI203965 GI203965 BONE-DERIVED GROWTH										
KEYWORDS	FACTOR, mRNA sequence.										
SOURCE	AI183068										
ORGANISM	AI183068.1 GI:1766724										
	EST.										
	Mus musculus (house mouse)										
	Mus musculus										
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.										
	1 (bases 1 to 85)										
	Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Schellenger, K., Stepien, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.										
	The WashU-HMI Mouse EST Project										
	Unpublished										
	Contact: Marra M/Mouse EST Project										
	WashU-HMI Mouse EST Project										
	Washington University School of Medicine										
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108										
	Tel: 314 286 1800										
	Fax: 314 286 1810										
	Email: mouseest@watsn.wustl.edu										
	This clone is available royalty-free through LNL; contact the										
	IMAGE Consortium (info@image.lnl.gov) for further information.										
	MGI:388800										
	Trace considered overall poor quality										
	Possible reversed clone: similarity on wrong strand										
	Seq primer: -28M13 rev2 from Amersham										
	High quality sequence stop: 1.										
	Location/Qualifiers										
	1..85										
	/organism="Mus musculus"										
	/mol_type="mRNA"										
	/strain="C57BL/6J"										
	/db_xref="taxon:10090"										
	/clone="IMAGE:636808"										
	/sex="male"										
	/tissue_type="lymph node"										
	/dev_stage="4 weeks"										
	/lab_host="DH10B"										
	/clone_id="Soares mouse lymph node NbM1N"										
	/note="Organ: lymph node; Vector: pT73D-Pac (Pharmacia)										
	with a modified polylinker; Site 1: Not I; Site 2: Eco RI;										
	1st strand cDNA was primed with a Not I - oligo(dT) primer										
	15'										
	TGTTACCAATCTGAAGTGGAGCGCGGCGGACTTTTTTTTTTTTTTTTTTTTTT										
	3'; double-stranded cDNA was ligated to Eco RI adaptors										
	(Pharmacia), digested with Not I and cloned into the Not I										
	and Eco RI sites of the modified pT73 vector. RNA										
	provided by Dr. Bertrand Jordan. Library constructed and										
	normalized by Bento Soares and M.Fatima Bonaldo."										
	15'										
	TGTTACCAATCTGAAGTGGAGCGCGGCGGACTTTTTTTTTTTTTTTTTTTTTT										
	3'; double-stranded cDNA was ligated to Eco RI adaptors										
	(Pharmacia), digested with Not I and cloned into the Not I										
	and Eco RI sites of the modified pT73 vector. RNA										
	provided by Dr. Bertrand Jordan. Library constructed and										
	normalized by Bento Soares and M.Fatima Bonaldo."										
	15'										
	TGTTACCAATCTGAAGTGGAGCGCGGCGGACTTTTTTTTTTTTTTTTTTTTTT										
	3'; double-stranded cDNA was ligated to Eco RI adaptors										
	(Pharmacia), digested with Not I and cloned into the Not I										
	and Eco RI sites of the modified pT73 vector. RNA										
	provided by Dr. Bertrand Jordan. Library constructed and										
	normalized by Bento Soares and M.Fatima Bonaldo."										
	15'										
	TGTTACCAATCTGAAGTGGAGCGCGGCGGACTTTTTTTTTTTTTTTTTTTTTT										
	3'; double-stranded cDNA was ligated to Eco RI adaptors										
	(Pharmacia), digested with Not I and cloned into the Not I										
	and Eco RI sites of the modified pT73 vector. RNA										
	provided by Dr. Bertrand Jordan. Library constructed and										
	normalized by Bento Soares and M.Fatima Bonaldo."										
	15'										
	TGTTACCAATCTGAAGTGGAGCGCGGCGGACTTTTTTTTTTTTTTTTTTTTTT										
	3'; double-stranded cDNA was ligated to Eco RI adaptors										
	(Pharmacia), digested with Not I and cloned into the Not I										
	and Eco RI sites of the modified pT73 vector. RNA										
	provided by Dr. Bertrand Jordan. Library constructed and										
	normalized by Bento Soares and M.Fatima Bonaldo."										
	15'										
	TGTTACCAATCTGAAGTGGAGCGCGGCGGACTTTTTTTTTTTTTTTTTTTTTT										
	3'; double-stranded cDNA was ligated to Eco RI adaptors										
	(Pharmacia), digested with Not I and cloned into the Not I										
	and Eco RI sites of the modified pT73 vector. RNA										
	provided by Dr. Bertrand Jordan. Library constructed and										
	normalized by Bento Soares and M.Fatima Bonaldo."										
	15'										
	TGTTACCAATCTGAAGTGGAGCGCGGCGGACTTTTTTTTTTTTTTTTTTTTTT										
	3'; double-stranded cDNA was ligated to Eco RI adaptors										
	(Pharmacia), digested with Not I and cloned into the Not I										
	and Eco RI sites of the modified pT73 vector. RNA										
	provided by Dr. Bertrand Jordan. Library constructed and										
	normalized by Bento Soares and M.Fatima Bonaldo."										
	15'										
	TGTTACCAATCTGAAGTGGAGCGCGGCGGACTTTTTTTTTTTTTTTTTTTTTT										
	3'; double-stranded cDNA was ligated to Eco RI adaptors										
	(Pharmacia), digested with Not I and cloned into the Not I										
	and Eco RI sites of the modified pT73 vector. RNA										
	provided by Dr. Bertrand Jordan. Library constructed and										
	normalized by Bento Soares and M.Fatima Bonaldo."										
	15'										
	TGTTACCAATCTGAAGTGGAGCGCGGCGGACTTTTTTTTTTTTTTTTTTTTTT										
	3'; double-stranded cDNA was ligated to Eco RI adaptors										
	(Pharmacia), digested with Not I and cloned into the Not I										
	and Eco RI sites of the modified pT73 vector. RNA										
	provided by Dr. Bertrand Jordan. Library constructed and										
	normalized by Bento Soares and M.Fatima Bonaldo."										
	15'										
	TGTTACCAATCTGAAGTGGAGCGCGGCGGACTTTTTTTTTTTTTTTTTTTTTT										
	3'; double-stranded cDNA was ligated to Eco RI adaptors										

ACCESSION AZ362937
 VERSION AZ362937.1 GI:10476637
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 92)
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A., and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 TITLE Unpublished
 JOURNAL Unpublished
 COMMENT Contact: Robert B. Weiss
 University of Utah
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0108 row: B column: 18
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 92.
 Location/Qualifiers
 1..92
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0108B18"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114[gbl/AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 21 a 25 c 30 g 16 t
 ORIGIN

Query Match 70.0%; Score 11.2; DB 28; Length 92;
 Best Local Similarity 78.6%; Pred. No. 4.6e+04;
 Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGCTAGACAC 14
 |||||:|||||
 Db 68 GGGCTACCAAC 81

RESULT 22 B2291268 92 bp DNA linear GSS 24-OCT-2002
 LOCUS B2291268
 DEFINITION SALK_120055.25.10.x Arabidopsis thaliana TMA insertion lines

Arabidopsis thaliana genomic clone SALK_120055.25.10.x, genomic survey sequence.
 ACCESSION B2291268
 VERSION B2291268.1 GI:24336251
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 1 (bases 1 to 92)
 REFERENCE Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Ecker, J.R.
 A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
 TITLE Unpublished
 JOURNAL Unpublished
 COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of TMA. This sequence lies within an annotated exon of At4g17970.
 Class: TMA tagged.
 Location/Qualifiers
 1..92
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_120055.25.10.x"
 /clone_lib="Arabidopsis thaliana TMA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TMA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/cdna_protocols.html"

BASE COUNT 25 a 32 c 17 g 18 t
 ORIGIN

Query Match 70.0%; Score 11.2; DB 29; Length 92;
 Best Local Similarity 91.7%; Pred. No. 4.6e+04;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 CTAGCHCAACG 15
 |||||:|||||
 Db 48 CTAGCAACACG 59

RESULT 23 B2291268 95 bp mRNA linear EST 16-OCT-2002
 LOCUS B2291268
 DEFINITION 5075A07 Populus imbric seed cDNA library Populus tremula x Populus tremuloides cDNA 5 prime, mRNA sequence.
 ACCESSION B2291268
 VERSION B2291268.1 GI:24057814
 KEYWORDS EST.
 SOURCE Populus tremula x Populus tremuloides
 ORGANISM Populus tremula x Populus tremuloides
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 1 (bases 1 to 95)
 REFERENCE Umeberg, P., Bhalerao, R.R., Jansson, S., and Sterky, F.
 The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries
 JOURNAL Unpublished
 COMMENT Contact: BHALERAO RUPALI R.
 Umea Plant Science Center

Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupall.bhalerao@plantphys.umu.se.
Location/Qualifiers

FEATURES

source

1.95
/organism="Populus tremula x Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:47664"
/tissue_type="imbibed seed"
/clone_lib="Populus imbibed seed cDNA library"
25 a 28 c 16 g 26 t

BASE COUNT

ORIGIN

Query Match 70.0%; Score 11.2; DB 13; Length 95;
Best Local Similarity 78.6%; Pred. No. 4.6e+04;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAC 14
:|||||||:
74 AGGCTAGCTAGAAC 61

RESULT 24

BU862306 96 bp mRNA linear EST 16-OCT-2002
LOCUS BU862306/c
DEFINITION Sol14A04 Populus imbibed seed cDNA library Populus tremula x Populus tremuloides cDNA 5 prime, mRNA sequence.

ACCESSION BU862306
VERSION BU862306.1 GI:24048366
KEYWORDS EST.
SOURCE Populus tremula x Populus tremuloides
ORGANISM Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eucosids I; Malpighiales; Salicaceae; Populus.
1 (bases 1 to 96)
Unneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
The poplar tree transcriptome: Analysis of expressed sequence tags
from multiple libraries
Unpublished
Contact: BHALERAO RUPALI R.
Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupall.bhalerao@plantphys.umu.se.
Location/Qualifiers

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES

source

1.96
/organism="Populus tremula x Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:47664"
/tissue_type="imbibed seed"
/clone_lib="Populus imbibed seed cDNA library"
27 a 27 c 16 g 26 t

BASE COUNT

ORIGIN

Query Match 70.0%; Score 11.2; DB 13; Length 96;
Best Local Similarity 78.6%; Pred. No. 4.6e+04;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACAC 14
:|||||||:
46 AGGCTAGCTAGAAC 33

Db 46 AGGCTAGCTAGAAC 33

RESULT 25

AW797834 100 bp mRNA linear EST 16-MAY-2000
LOCUS AW797834/c
DEFINITION CM0-UM0042-020300-261-e05 UM0042 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW797834

VERSION AW797834.1 GI:7849704
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 100)

REFERENCE

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsushima, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL MEDLINE
PUBMED
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=CM0-UM0042-020
300-261-e05&cl3=2000-03-02&cl4=1)
Seq primer: puc 18 forward
Seq quality sequence start: 8
High quality sequence stop: 100.
Location/Qualifiers

FEATURES

source

1.100
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/def_string="Adult"
/clone_lib="UM0042"
/note="Organ: uterus; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
16 a 34 c 26 g 24 t

BASE COUNT

ORIGIN

Query Match 70.0%; Score 11.2; DB 9; Length 100;
Best Local Similarity 91.7%; Pred. No. 4.7e+04;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 TAGCCACACCA 16
:|||||||:
15 TAGCCACACCA 4

Db 15 TAGCCACACCA 4

RESULT 26
BM328423 100 bp mRNA linear EST 04-JAN-2002
LOCUS BM328423/c
DEFINITION PIC1_29_B03_g1_A002 Pathogen-infected compatible 1 (PIC1) Sorghum
bicolor cDNA, mRNA sequence.

ACCESSION BM328423
VERSION BM328423.1 GI:18067560
KEYWORDS EST.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACMAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 100)

REFERENCE
BM328423 100 bp mRNA linear EST 04-JAN-2002
LOCUS BM328423/c
DEFINITION PIC1_29_B03_g1_A002 Pathogen-infected compatible 1 (PIC1) Sorghum
bicolor cDNA, mRNA sequence.

ACCESSION BM328423
VERSION BM328423.1 GI:18067560
KEYWORDS EST.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACMAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 100)

REFERENCE
BM328423 100 bp mRNA linear EST 04-JAN-2002
LOCUS BM328423/c
DEFINITION PIC1_29_B03_g1_A002 Pathogen-infected compatible 1 (PIC1) Sorghum
bicolor cDNA, mRNA sequence.

ACCESSION BM328423
VERSION BM328423.1 GI:18067560
KEYWORDS EST.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACMAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 100)

AUTHORS Cordonnier-Pratt, M.-M., Gingle, A., Pang, G.C., Dean, R., Wang, R., Sudan, M. and Pratt, L.H.
TITLE An EST database from Sorghum: plants infected with a compatible pathogen
JOURNAL Unpublished
COMMENT Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Km. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu
 Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20. Three-prime sequences, which are obtained with PolyTrak or 17 sequencing primer, are presented as the reverse complement.
 Seq primer: 17
 High quality sequence start: 30
 High quality sequence stop: 100
 PolyA=yes

FEATURES
 source
 1..100
 /organism="Sorghum bicolor"
 /mol_type="mRNA"
 /cultivar="BTx623"
 /db_xref="taxon:4558"
 /tissue_type="leaves"
 /dev_stage="4-week-old seedlings infected with Colletotrichum graminicola"
 /clone_lib="Pathogen-infected compatible 1 (PIC1)"
 /note="Vector: phuscript II SK(-) from lambda Zap II, Site 1: XhoI, Site 2: EcoRI. Four-week-old sorghum seedlings were sprayed with spore suspension prepared from 3-week-old RM421, a sorghum isolate of the anthracnose pathogen Colletotrichum graminicola. Inoculated plants were kept in a 25 C dark growth chamber with 100% relative humidity for 24 hr, followed by 12/12 hr of light/dark cycle at 25 C with 90% relative humidity for another 24 hr. All leaves were harvested and quick frozen with liquid nitrogen and stored in a -80 C freezer. The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision.
 WARNING: While most or all ESTs are expected to derive from the host plant, no effort was made to eliminate ESTs deriving from the pathogen."

BASE COUNT
 30 a 15 c 24 g 31 t

ORIGIN

Query Match 70.0%; Score 11.2; DB 12; Length 100;
 Best Local Similarity 91.7%; Pred. No. 4.7e+04;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 4 CTAGCACAACG 15
 |||||
 26 CTAGCACAACG 15

Db 26 CTAGCACAACG 15

RESULT 27
 BUB61867 100 bp mRNA linear EST 16-OCT-2002
 BUB61867/c
 LOCUS
 DEFINITION S007G10 Populus imbed seed cDNA library Populus tremula x Populus tremuloides cDNA 5 prime, mRNA sequence.
 ACCESSION BUB61867
 VERSION BUB61867.1 GI:24047927
 KEYWORDS
 SOURCE
 ORGANISM Populus tremula x Populus tremuloides
 Populus tremula x Populus tremuloides
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eurosids 1; Malpighiales; Salicaceae; Populus.
 1 (bases 1 to 100)
 Uneberg, P., Bhalero, R.R., Jansson, S. and Steky, F.
 The poplar tree transcriptome: Analysis of expressed sequence tags

JOURNAL from multiple libraries
COMMENT Unpublished
 Contact: BHALERU RUPALI R.
 Umea Plant Science Center
 Department of Plant Physiology
 University of Umea, 901 87 Umea, Sweden
 Tel: +46 90 786 5279
 Fax: +46 90 786 6676
 Email: rupali.bhalero@plantphys.umu.se

FEATURES
 source
 1..100
 /organism="Populus tremula x Populus tremuloides"
 /mol_type="mRNA"
 /db_xref="taxon:47664"
 /tissue_type="imbibed seed"
 /clone_lib="Populus imbed seed cDNA library"
 22 a 29 c 20 g 29 t

BASE COUNT
 22 a 29 c 20 g 29 t

ORIGIN

Query Match 70.0%; Score 11.2; DB 13; Length 100;
 Best Local Similarity 78.6%; Pred. No. 4.7e+04;
 Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 1 RGCTAGCACAAC 14
 :|||
 37 AGCTAGCACAAC 24

Db 37 AGCTAGCACAAC 24

RESULT 28
 CC179318 74 bp DNA linear GSS 02-MAY-2003
 BALK_067813.35.30.x Arabidopsis thaliana TDNA insertion lines
 LOCUS Arabidopsis thaliana genomic clone SALK_067813.35.30.x, genomic survey sequence.
 DEFINITION
 ACCESSION CC179318
 VERSION CC179318
 KEYWORDS
 SOURCE GSS.
 ORGANISM Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eurosids 1; Brassicales; Brassicaceae; Arabidopsie.
 1 (bases 1 to 74)
 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
 A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
 Unpublished
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: eckere@salk.edu
 This is single pass sequence recovered from the left border of TDNA.
 Class: TDNA tagged.

FEATURES
 source
 1..74
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 27 a 9 c 13 g 25 t
 ORIGIN

Query Match 68.8%; Score 11; DB 29; Length 74;
 Best Local Similarity 80.0%; Pred. No. 5.4e+04;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGCTAGCACAACA 16
 |||||
 64 GGCTGCAACAATGA 50

RESULT 29
 U44372/c
 LOCUS U44372 79 bp mRNA linear EST 03-APR-1996
 DEFINITION EN04372 Aspergillus nidulans cleistothecium Emericella nidulans
 CDNA clone SE0877, mRNA sequence.
 ACCESSION U44372
 VERSION U44372.1 GI:1245035
 KEYWORDS EST.
 SOURCE Emericella nidulans (anamorph: Aspergillus nidulans)
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Eukaryotes; Trichocomaceae; Emericella.
 REFERENCE 1 (bases 1 to 79)
 AUTHORS Lee, D., Lee, S., Hwang, H., Kim, J. and Chae, K.
 TITLE Quantitative analysis of gene expression in sexual structures of Aspergillus nidulans by sequencing of 3'-directed CDNA clones
 JOURNAL FEMS Microbiol. Lett. 138 (1), 71-76 (1996)
 MEDLINE 96236220
 PUBMED 8674973
 COMMENT Contact: Keon-Sang Chae
 Chonbuk National University
 Chonju, 561-756, S. Korea
 Tel: +82-652-70-3340
 Fax: +82-652-70-3345
 Email: chaeks@chonbukns.chonbuk.ac.kr.
 Location/Qualifiers
 FEATURES
 source
 1..79
 /organism="Emericella nidulans"
 /mol_type="mRNA"
 /strain="FGSC4"
 /db_xref="taxon:162425"
 /clone="SE0877"
 /issue_type="cleistothecium"
 /cell_type="hull cell"
 /dev_stage="sexual"
 /clone_id="Aspergillus nidulans cleistothecium"
 /note="3'-directed CDNA clones; single-pass sequencing"

BASE COUNT 24 a 9 c 20 g 26 t
 ORIGIN

Query Match 68.8%; Score 11; DB 14; Length 79;
 Best Local Similarity 80.0%; Pred. No. 5.6e+04;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGCTAGCACAACA 16
 |||||
 49 GACTGACCAACAAGA 35

RESULT 30
 AA594999 82 bp mRNA linear EST 26-SEP-1997
 LOCUS AA594999
 DEFINITION n031806.81 NCI CGAP Pr22 Homo sapiens CDNA clone IMAGE:1102306 3'
 similar to TR:G1234841 G1234841 LIM PROTEIN MLP.; mRNA sequence.
 ACCESSION AA594999
 VERSION AA594999.1 GI:2410349
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 82)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished
 COMMENT Contact: Robert Straubeberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
 www-bio.livn.gov/bdrp/image/image.html

Trace considered overall poor quality
 Insert Length: 968 Std Error: 0.00
 Seg primer: -40ml3 fwd. RT from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1..82
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1102306"
 /sex="male"
 /tissue_type="normal prostate"
 /lab_host="DH10B"
 /clone_id="NCI CGAP Pr22"
 /note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)
 with a modified polylinker; 1st strand cDNA was prepared
 from normal prostate bulk tissue, and was then primed with
 a Not I - oligo(dT) primer. Double-stranded cDNA was
 ligated to Eco RI adaptors (Pharmacia), digested with Not
 I and cloned into the Not I and Eco RI sites of the
 modified pT73 vector. Library is normalized, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 23 a 25 c 21 g 13 t
 ORIGIN

Query Match 68.8%; Score 11; DB 9; Length 82;
 Best Local Similarity 80.0%; Pred. No. 5.7e+04;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGCTAGCACAACA 16
 |||||
 63 GACTTGCCACAACA 77

RESULT 31
 BE330980 100 bp mRNA linear EST 04-DEC-2001
 LOCUS BE330980
 DEFINITION s092a05.v1 Gm-c1041 Glycine max CDNA clone GENOME SYSTEMS CLONE ID:
 Gm-c1041-777 5' similar to TR:Q42897 Q42897 UBIQUITIN-CONJUGATING
 ENZYME E2.; mRNA sequence.
 ACCESSION BE330980
 VERSION BE330980.1 GI:9204756
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 100)
 1 (bases 1 to 100)
 REFERENCES
 1 (bases 1 to 100)
 AUTHORS Shoemaker, R., Keim, P., Vodkin, L., Expelling, J., Coryell, V., Khanna
 A., Bolla, B., Merrin, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
 Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers
 R., Peterson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
 R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
 R., Waterston, R. and Willson, R.
 TITLE Public Soybean EST Project

JOURNAL
COMMENT

Unpublished
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
Trace considered overall poor quality This clone is available
through: Resgen, Invitrogen Corp, 2130 South Memorial Parkway
Huntersville, AL 35801 For further information call: (800)-533-4363
or contact via email: cc@resgen.com
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

source

1. .100
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl041-777"
/issue_type="Sensitizing leaves, mature plant, greenhouse
grown"
/lab_host="DH10B"
/clone_id="Gm-cl041"
/note="Vector: pRT3Pac (Pharmacia); Site 1: EcoRI,
Site 2: HindIII. This library was constructed from mRNA
isolated from senescing leaf tissue of mature greenhouse
grown plants of the cultivar Williams. Complementary DNA
was synthesized from mRNA using a 3' anchored poly(dT)
primer. EcoRI adapters were ligated to the blunt-ended
cDNA fragments followed by digestion with EcoRI and
HindIII. The cDNA fragments were directionally cloned
into the EcoRI-HindIII restriction site of the pRT3-Pac
vector. The ligated cDNA fragments were transformed into
DH10B host cells. This library was constructed by Dr.
Randy Shoemaker."

BASE COUNT
ORIGIN

29 a 25 c 27 g 19 t

Query Match 68.8%; Score 11; DB 10; Length 100;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGCTAGGACACGA 16
Db 78 GGCAAGCAACATGA 92

RESULT 32
AUI06358/c 50 bp mRNA linear EST 30-AUG-2001
LOCUS AUI06358 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP02980, mRNA sequence.
ACCESSION AUI06358
VERSION AUI06358.1 GI:13555879
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tanoda, T., Minushima, Sugano, J., Sese, J., Hara
, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929

COMMENT

JOURNAL
MEDLINE
PUBMED
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
, S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers

FEATURES

source

1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP02980"
/clone_id="Sugano Homo sapiens cDNA library"
Location/Qualifiers

BASE COUNT
ORIGIN

3 a. 20 c 12 g 15 t

Query Match 67.5%; Score 10.8; DB 9; Length 50;
Best Local Similarity 85.7%; Pred. No. 6.1e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGCTAGGACACGA 16
Db 31 GGCAAGCAACGA 18

RESULT 33
BZ287687 72 bp DNA linear GSS 24-OCT-2002
LOCUS SALK_021065.27.75.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_021065.27.75.x, genomic
survey sequence.
ACCESSION BZ287687
VERSION BZ287687.1 GI:24325988
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
1 (bases 1 to 72)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadgil, N.
, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.,
, Zimmerman, J. and Ecker, J.R.
A sequence-indexed library of insertion mutations in the
Arabidopsis Genome
Unpublished
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers

FEATURES

source

1. .72
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_id="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocol.html"

BASE COUNT
ORIGIN

22 a 12 c 14 g 24 t

Query Match 67.5%; Score 10.8; DB 29; Length 72;
Best Local Similarity 85.7%; Pred. No. 7e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCTAGCACACGA 16
 Db 52 GCTAGCACACATGA 65

RESULT 34
 AZ619815/c 80 bp DNA linear GSS 13-DEC-2000
 LOCUS 1M0452018F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 DEFINITION clone UGCGIM0452018 F, genomic survey sequence.
 ACCESSION AZ619815
 VERSION AZ619815.1 GI:11742005
 KEYWORDS GSS.
 ORGANISM Mus musculus (house mouse)
 SOURCE Mus musculus
 REFERENCE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 80)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
 and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE Unpublished
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 1000 Std Error: 0.00
 Plate: 0452 row: D column: 18
 Seq primer: CGTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 80.
 Location/Qualifiers
 1..80
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGIM0452018"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 20 a 15 c 21 g 24 t
 ORIGIN
 Query Match 67.5%; Score 10.8; DB 28; Length 80;
 Best Local Similarity 83.3%; Pred. No. 7.3e+04;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGGCTAGCHACA 12
 Db 28 AGGCTAGCTACA 17

RESULT 35
 AL947273 85 bp DNA linear GSS 24-OCT-2002
 LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-303A09-015560,
 DEFINITION genomic survey sequence.
 ACCESSION AL947273
 VERSION AL947273.1 GI:24403895
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; euroside II; Brassicales; Brassicaceae; Arabidopsis.
 1
 Strizhov, N., Li, Y., Rosso, M., Viehoveer, P., Dekker, K., Saedler, H.
 and Weisshaar, B.
 A pipeline for automated high-throughput generation of FSTs
 (flanking sequence tags) from Arabidopsis thaliana T-DNA
 transformed lines
 Unpublished
 2
 Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B.
 A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
 for flanking sequence tag based reverse genetics
 Unpublished
 3 (bases 1 to 85)
 Li, Y., Strizhov, N., Rosso, M. and Weisshaar, B.
 Direct Submission
 Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence is recovered from the left border of the T-DNA. It
 indicates an insertion close to or within gene At3g25560. The
 sequences are generated at the MPI for Plant Breeding Research in
 the context of the GABI-Kat project. GABI-Kat is part of the German
 Plant Genomics program designated 'GABI'. Information on line
 availability can be found at:
 http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES
 source
 1..85
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-303A09-015560"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /note="PCR was performed on DNA from Arabidopsis thaliana
 plants (T1) which were transformed with the T-DNA from
 vector PAC161. The lines contain one or more T-DNA
 insertions. The DNA fragment(s) resulting from the PCR
 were directly sequenced to determine the genomic sequence
 flanking the insertion. Sequences displaying significant
 similarity to the A. thaliana nuclear genome sequence were
 processed for submission. T-DNA derived sequences were
 removed"

BASE COUNT 27 a 19 c 18 g 21 t
 ORIGIN
 Query Match 67.5%; Score 10.8; DB 29; Length 85;
 Best Local Similarity 83.3%; Pred. No. 7.5e+04;
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGGCTAGCHACA 12
 Db 26 AGGCTAGCACACA 37

RESULT 36
W17739
LOCUS
DEFINITION m7792.r1 Soares mouse p3M919.5 Mus musculus cDNA clone
IMAGE:335474 5', mRNA sequence.
ACCESSION W17739
VERSION W17739.1 GI:1292123
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 92)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Teisberg, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished
COMMENT Contact: Marra M/Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LMLT; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MW:216874
Seq primer: mob, REGA+RT
High quality sequence stop: 85.
Location/Qualifiers
1. .92
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:335474"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares mouse p3M919.5"
/note="Vector: pRTT3 (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCATTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRTT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."
BASE COUNT 30 a 25 c 25 g 12 t
ORIGIN

Query Match 67.5%; Score 10.8; DB 14; Length 92;
Best Local Similarity 83.3%; Pred. No. 7.7e+04;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RGCTAGACCA 12
Db 74 GGCTAGACCA 85

RESULT 37
BZ291056/c
LOCUS
DEFINITION BZ291056 94 bp DNA linear GSS 24-OCT-2002
SALK_112368.45.85.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_112368.45.85.x, genomic survey sequence.
ACCESSION BZ291056
VERSION BZ291056.1 GI:24335637
KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
REFERENCE 1 (bases 1 to 94)
Alonso, J.M., Lejse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shum, P., Zimmerman, J., and Ecker, J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At5g04660.
Class: TDNA tagged.
Location/Qualifiers
1. .94
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_112368.45.85.x"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/dna_protocols.html"
BASE COUNT 18 a 24 c 19 g 33 t
ORIGIN

Query Match 67.5%; Score 10.8; DB 29; Length 94;
Best Local Similarity 85.7%; Pred. No. 7.8e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 GCTAGACCA 16
Db 35 GCTAGACCA 22

RESULT 38
AA919502
LOCUS
DEFINITION AA919502 95 bp mRNA linear EST 20-APR-1998
v220g11.r1 Stragene mouse heart (#937316) Mus musculus cDNA clone
IMAGE:1316324 5' similar to TR:060961 Q60961 MEMBRANE TRANSPORTER
PROTEIN; mRNA sequence.
ACCESSION AA919502
VERSION AA919502.1 GI:3066281
KEYWORDS EST.
SOURCE Mus musculus
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 95)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Teisberg, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished
COMMENT Contact: Marra M/Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mousesest@atson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:686620
 Seq primer: -28m3 rev1 ET from Amersham
 High quality sequence stop: 70.
 Location/Qualifiers

FEATURES

source

1. .95
 /organism="Mus musculus"
 /mol_type="RNA"
 /strain="NIH Swiss"
 /db_xref="taxon:10090"
 /clone="IMAGE:1316324"
 /sex="pooled"
 /tissue_type="heart"
 /dev_stage="13 day embryos"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="Stratagene mouse heart (#937316)"
 /note="Organ: heart; Vector: pBluescript SK-; Site: 1:
 EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
 Oligo dt. 93 pooled NIH/Swiss 13 day embryo hearts.
 Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'
 adaptor sequence: 5' GATTCGGCAGAG 3' ~3' adaptor
 sequence: 5' CTCGAGTTTCTTTTCTTTT 3'"

BASE COUNT

20 a 24 c 33 g 18 t

ORIGIN

Query Match 67.5%; Score 10.8; DB 9; Length 95;
 Best Local Similarity 75.0%; Pred. No. 7.8e+04;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 RGGCTAGCHACACGA 16
 : |||||
 Db 32 GCGCTGGGAGACGA 47

RESULT 39

AZ639727 32 bp DNA linear GSS 14-DEC-2000
 LOCUS 1M0501D21F Mouse 10kb plasmid UGSCIM library Mus musculus genomic
 DEFINITION clone UGSCIM0501D21 F, genomic survey sequence.

ACCESSION AZ639727.1 GI:11763127

VERSION

AZ639727

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 32)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islem, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

Unpublished

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0501 row: D column: 21
 Seq primer: CGTGTAAACGACGCGCACT
 Class: plasmid ends
 High quality sequence stop: 32.
 Location/Qualifiers

FEATURES

1. .32

BASE COUNT

11 a 9 c 3 g 9 t

ORIGIN

Query Match 66.2%; Score 10.6; DB 28; Length 32;
 Best Local Similarity 84.6%; Pred. No. 6.6e+04;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 4 CTAGCHACACGA 16
 : |||||
 Db 1 CTAGCCACACTA 13

RESULT 40

CB305210 37 bp RNA linear EST 01-JUN-2003
 LOCUS 3'EST-NFly-025 Drosophila melanogaster cDNA library Drosophila
 DEFINITION melanogaster cDNA 3', mRNA sequence.

ACCESSION CB305210.1 GI:31297614

VERSION

CB305210

KEYWORDS

EST.

SOURCE

Drosophila melanogaster (fruit fly)

ORGANISM

Drosophila melanogaster

REFERENCE

1 (bases 1 to 37)

AUTHORS

Lee, S., Zhou, G., Bao, J., Shapiro, J., Xu, J., Sun, M., Lin, W., Zhang,
 R., Chen, J., Clark, T., Sun, M., Wang, J., Johnson, D., Tseng, C., Yang,
 H., Wang, J., Du, W., Wu, C. I., Zhang, X. and Wang, S. M.

TITLE

Novel SAGE tags represent a significant number of novel genes in
 Drosophila genome

JOURNAL

Unpublished

COMMENT

Contact: Wang SM

Hem/Onc

University of Chicago Medical Center
 5841 S. Maryland Ave., MC2115, Chicago, IL 60637, USA
 Tel: 773-702-6788
 Fax: 773-702-3002
 Email: swangl@midway.uchicago.edu

This EST was detected from Drosophila melanogaster cDNA library
 with GLG technique (Generation of longer cDNA fragments from SAGE
 tags for Gene Identification, Proc. Natl. Acad. Sci. USA 97, 349,
 2000). A high-throughput GLG procedure for converting a large
 number of SAGE tag sequences into 3' ESTs. Genes, Chromosomes &
 Cancers 33:252-261, 2002), which covers from the 3' end of cDNA
 till the first CATTG.

Seq primer: M13 Forward.
FEATURES
Location/Qualifiers
Source
1..37
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone_lib="Drosophila melanogaster cDNA Library"
BASE COUNT
7 a 9 c 8 g 13 t
ORIGIN
Query Match 66.2%; Score 10.6; DB 14; Length 37;
Best Local Similarity 84.6%; Pred. No. 7e+04;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 4 CTAGCHACACGA 16
|||:|||||
Db 12 CTAGCCACGACGA 24

Search completed: January 21, 2004, 08:16:38
Job time : 1412 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 05:18:03 ; Search time 151.5 Seconds
(without alignments)
285.089 Million cell updates/sec

Title: US-09-423-035B-122

Perfect score: 16

Sequence: 1 rgcgtacgacaacga 16

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 2722628

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database :

N_Geneseq 19Jun03:*

1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
1	14.8	92.5	16	20	AAV82954		Enzymatic DNA core
2	14.8	92.5	16	20	AAV82953		Enzymatic DNA core
3	14.8	92.5	16	21	AA63474		DNAzyme catalytic
4	14.8	92.5	16	21	AA63475		DNAzyme catalytic
5	14.8	92.5	16	22	AA802749		DNAzyme motif SEQ
6	14.8	92.5	16	22	AAH97756		DNAzyme motif SEQ
7	14.8	92.5	16	23	ABK09278		DNAzyme motif. SY
8	14.8	92.5	16	24	ABK61076		Human CLKAI gene e

9	14.8	92.5	16	24	ABK22719		DNAzyme motif. SY
10	14.8	92.5	16	25	ACA10109		Necrosis factor ka
11	14.8	92.5	17	25	ABZ58432		DNAzyme motif. SY
12	14.8	92.5	16	25	ABZ66525		Human HER2 synthe
13	14.8	92.5	27	25	ABZ66527		Nucleic acid-based
14	14.8	92.5	29	20	AAZ34361		Nucleic acid-based
15	14.8	92.5	29	20	AAZ34363		Hammerhead ribozym
16	14.8	92.5	29	21	AAZ34363		Hammerhead ribozym
17	14.8	92.5	29	25	ABZ66526		Human HER2 synthe
18	14.8	92.5	29	25	ABZ66528		Human HER2 synthe
19	14.8	92.5	29	25	ABZ66529		Human HER2 synthe
20	14.8	92.5	29	25	ABZ66549		Human HIV enzymati
21	14.8	92.5	29	25	ABZ66550		Human HIV enzymati
22	14.8	92.5	29	25	ABZ66551		Human HIV enzymati
23	14.8	92.5	29	25	ABZ66552		Human HIV enzymati
24	14.8	92.5	29	25	ABZ66553		Human HIV enzymati
25	14.8	92.5	29	25	ABX13988		Deoxy-ribozyme, c1
26	14.8	92.5	29	25	ABX13989		Deoxy-ribozyme, c1
27	14.8	92.5	29	25	ABX13990		Deoxy-ribozyme, c1
28	14.8	92.5	29	25	ABX13991		Deoxy-ribozyme, c1
29	14.8	92.5	29	25	ABX13992		Deoxy-ribozyme, c1
30	14.8	92.5	29	25	ABX13993		Deoxy-ribozyme, c1
31	14.8	92.5	29	25	ABX13994		Deoxy-ribozyme, c1
32	14.8	92.5	29	25	ABX13995		Deoxy-ribozyme, c1
33	14.8	92.5	29	25	ABX13996		Deoxy-ribozyme, c1
34	14.8	92.5	29	25	ABX13997		Deoxy-ribozyme, c1
35	14.8	92.5	29	25	ABX13998		Deoxy-ribozyme, c1
36	14.8	92.5	29	25	ABX13999		Deoxy-ribozyme, c1
37	14.8	92.5	29	25	ABX14001		Deoxy-ribozyme, c1
38	14.8	92.5	29	25	ABX14002		Deoxy-ribozyme, c1
39	14.8	92.5	30	21	AA414525		Oligonucleotide 5'
40	14.8	92.5	30	21	AAZ87648		Human short protei
41	14.8	92.5	30	22	AAZ87648		Synthetic oligodeo
42	14.8	92.5	30	25	ACA10089		Necrosis factor ka
43	14.8	92.5	30	25	ACA10090		Necrosis factor ka
44	14.8	92.5	30	25	ACA10091		Necrosis factor ka
45	14.8	92.5	30	25	ACA10092		Necrosis factor ka
46	14.8	92.5	30	25	ACA10093		Necrosis factor ka
47	14.8	92.5	30	25	ABX14000		Deoxy-ribozyme, c1
48	14.8	92.5	31	20	AAZ34380		Nucleic acid-based
49	14.8	92.5	31	20	AAZ34383		Nucleic acid-based
50	14.8	92.5	31	20	AAZ34383		Nucleic acid-based
51	14.8	92.5	31	20	AAZ34386		Nucleic acid-based
52	14.8	92.5	31	20	AAZ34389		Nucleic acid-based
53	14.8	92.5	31	20	AAZ34393		Nucleic acid-based
54	14.8	92.5	31	20	AAZ21117		Nucleic acid-based
55	14.8	92.5	31	21	AAZ52572		HCV RNA-binding c1
56	14.8	92.5	31	21	AAZ91150		HPV mRNA-cleaving
57	14.8	92.5	31	22	ABZ62611		HPV6 targeted DNA
58	14.8	92.5	31	22	ABZ62642		HPV16 targeted DNA
59	14.8	92.5	31	22	ABZ62643		HPV16 targeted DNA
60	14.8	92.5	31	22	ABZ62644		HPV16 targeted DNA
61	14.8	92.5	31	22	ABZ62645		HPV16 targeted DNA
62	14.8	92.5	31	22	ABZ62646		HPV16 targeted DNA
63	14.8	92.5	31	22	ABZ62647		HPV16 targeted DNA
64	14.8	92.5	31	22	ABZ62648		HPV16 targeted DNA
65	14.8	92.5	31	22	ABZ62649		HPV16 targeted DNA
66	14.8	92.5	31	22	ABZ62650		HPV16 targeted DNA
67	14.8	92.5	31	22	ABZ62651		HPV16 targeted DNA
68	14.8	92.5	31	22	ABZ62652		HPV11 targeted DNA
69	14.8	92.5	31	22	ABZ62653		HPV11 targeted DNA
70	14.8	92.5	31	22	ABZ62654		HPV11 targeted DNA
71	14.8	92.5	31	22	ABZ62655		HBV targeted DNA
72	14.8	92.5	31	22	ABZ62657		HBV targeted DNA
73	14.8	92.5	31	22	ABZ62658		HBV targeted DNA
74	14.8	92.5	31	22	ABZ62659		HBV targeted DNA
75	14.8	92.5	31	22	AAH96952		Human Chk1 ribozym
76	14.8	92.5	31	22	AAH96953		Human Chk1 ribozym
77	14.8	92.5	31	22	AAH96954		Human Chk1 ribozym
78	14.8	92.5	31	22	AAH96955		Human Chk1 ribozym
79	14.8	92.5	31	22	AAH96956		Human Chk1 ribozym
80	14.8	92.5	31	22	AAH96957		Human Chk1 ribozym
81	14.8	92.5	31	22	AAH96958		Human Chk1 ribozym

812	14.8	92.5	31	23	ABR06330	Human	NOGO	DNAzyme	885	14.8	92.5	31	23	ABR06403	Human	NOGO	DNAzyme
813	14.8	92.5	31	23	ABR06331	Human	NOGO	DNAzyme	886	14.8	92.5	31	23	ABR06404	Human	NOGO	DNAzyme
814	14.8	92.5	31	23	ABR06332	Human	NOGO	DNAzyme	887	14.8	92.5	31	23	ABR06405	Human	NOGO	DNAzyme
815	14.8	92.5	31	23	ABR06333	Human	NOGO	DNAzyme	888	14.8	92.5	31	23	ABR06406	Human	NOGO	DNAzyme
816	14.8	92.5	31	23	ABR06334	Human	NOGO	DNAzyme	889	14.8	92.5	31	23	ABR06407	Human	NOGO	DNAzyme
817	14.8	92.5	31	23	ABR06335	Human	NOGO	DNAzyme	890	14.8	92.5	31	23	ABR06408	Human	NOGO	DNAzyme
818	14.8	92.5	31	23	ABR06336	Human	NOGO	DNAzyme	891	14.8	92.5	31	23	ABR06409	Human	NOGO	DNAzyme
819	14.8	92.5	31	23	ABR06337	Human	NOGO	DNAzyme	892	14.8	92.5	31	23	ABR06410	Human	NOGO	DNAzyme
820	14.8	92.5	31	23	ABR06338	Human	NOGO	DNAzyme	893	14.8	92.5	31	23	ABR06411	Human	NOGO	DNAzyme
821	14.8	92.5	31	23	ABR06339	Human	NOGO	DNAzyme	894	14.8	92.5	31	23	ABR06412	Human	NOGO	DNAzyme
822	14.8	92.5	31	23	ABR06340	Human	NOGO	DNAzyme	895	14.8	92.5	31	23	ABR06413	Human	NOGO	DNAzyme
823	14.8	92.5	31	23	ABR06341	Human	NOGO	DNAzyme	896	14.8	92.5	31	23	ABR06414	Human	NOGO	DNAzyme
824	14.8	92.5	31	23	ABR06342	Human	NOGO	DNAzyme	897	14.8	92.5	31	23	ABR06415	Human	NOGO	DNAzyme
825	14.8	92.5	31	23	ABR06343	Human	NOGO	DNAzyme	898	14.8	92.5	31	23	ABR06416	Human	NOGO	DNAzyme
826	14.8	92.5	31	23	ABR06344	Human	NOGO	DNAzyme	899	14.8	92.5	31	23	ABR06417	Human	NOGO	DNAzyme
827	14.8	92.5	31	23	ABR06345	Human	NOGO	DNAzyme	900	14.8	92.5	31	23	ABR06418	Human	NOGO	DNAzyme
828	14.8	92.5	31	23	ABR06346	Human	NOGO	DNAzyme	901	14.8	92.5	31	23	ABR06419	Human	NOGO	DNAzyme
829	14.8	92.5	31	23	ABR06347	Human	NOGO	DNAzyme	902	14.8	92.5	31	23	ABR06420	Human	NOGO	DNAzyme
830	14.8	92.5	31	23	ABR06348	Human	NOGO	DNAzyme	903	14.8	92.5	31	23	ABR06421	Human	NOGO	DNAzyme
831	14.8	92.5	31	23	ABR06349	Human	NOGO	DNAzyme	904	14.8	92.5	31	23	ABR06422	Human	NOGO	DNAzyme
832	14.8	92.5	31	23	ABR06350	Human	NOGO	DNAzyme	905	14.8	92.5	31	23	ABR06423	Human	NOGO	DNAzyme
833	14.8	92.5	31	23	ABR06351	Human	NOGO	DNAzyme	906	14.8	92.5	31	23	ABR06424	Human	NOGO	DNAzyme
834	14.8	92.5	31	23	ABR06352	Human	NOGO	DNAzyme	907	14.8	92.5	31	23	ABR06425	Human	NOGO	DNAzyme
835	14.8	92.5	31	23	ABR06353	Human	NOGO	DNAzyme	908	14.8	92.5	31	23	ABR06426	Human	NOGO	DNAzyme
836	14.8	92.5	31	23	ABR06354	Human	NOGO	DNAzyme	909	14.8	92.5	31	23	ABR06427	Human	NOGO	DNAzyme
837	14.8	92.5	31	23	ABR06355	Human	NOGO	DNAzyme	910	14.8	92.5	31	23	ABR06428	Human	NOGO	DNAzyme
838	14.8	92.5	31	23	ABR06356	Human	NOGO	DNAzyme	911	14.8	92.5	31	23	ABR06429	Human	NOGO	DNAzyme
839	14.8	92.5	31	23	ABR06357	Human	NOGO	DNAzyme	912	14.8	92.5	31	23	ABR06430	Human	NOGO	DNAzyme
840	14.8	92.5	31	23	ABR06358	Human	NOGO	DNAzyme	913	14.8	92.5	31	23	ABR06431	Human	NOGO	DNAzyme
841	14.8	92.5	31	23	ABR06359	Human	NOGO	DNAzyme	914	14.8	92.5	31	23	ABR06432	Human	NOGO	DNAzyme
842	14.8	92.5	31	23	ABR06360	Human	NOGO	DNAzyme	915	14.8	92.5	31	23	ABR06433	Human	NOGO	DNAzyme
843	14.8	92.5	31	23	ABR06361	Human	NOGO	DNAzyme	916	14.8	92.5	31	23	ABR06434	Human	NOGO	DNAzyme
844	14.8	92.5	31	23	ABR06362	Human	NOGO	DNAzyme	917	14.8	92.5	31	23	ABR06435	Human	NOGO	DNAzyme
845	14.8	92.5	31	23	ABR06363	Human	NOGO	DNAzyme	918	14.8	92.5	31	23	ABR06436	Human	NOGO	DNAzyme
846	14.8	92.5	31	23	ABR06364	Human	NOGO	DNAzyme	919	14.8	92.5	31	23	ABR06437	Human	NOGO	DNAzyme
847	14.8	92.5	31	23	ABR06365	Human	NOGO	DNAzyme	920	14.8	92.5	31	23	ABR06438	Human	NOGO	DNAzyme
848	14.8	92.5	31	23	ABR06366	Human	NOGO	DNAzyme	921	14.8	92.5	31	23	ABR06439	Human	NOGO	DNAzyme
849	14.8	92.5	31	23	ABR06367	Human	NOGO	DNAzyme	922	14.8	92.5	31	23	ABR06440	Human	NOGO	DNAzyme
850	14.8	92.5	31	23	ABR06368	Human	NOGO	DNAzyme	923	14.8	92.5	31	23	ABR06441	Human	NOGO	DNAzyme
851	14.8	92.5	31	23	ABR06369	Human	NOGO	DNAzyme	924	14.8	92.5	31	23	ABR06442	Human	NOGO	DNAzyme
852	14.8	92.5	31	23	ABR06370	Human	NOGO	DNAzyme	925	14.8	92.5	31	23	ABR06443	Human	NOGO	DNAzyme
853	14.8	92.5	31	23	ABR06371	Human	NOGO	DNAzyme	926	14.8	92.5	31	23	ABR06444	Human	NOGO	DNAzyme
854	14.8	92.5	31	23	ABR06372	Human	NOGO	DNAzyme	927	14.8	92.5	31	23	ABR06445	Human	NOGO	DNAzyme
855	14.8	92.5	31	23	ABR06373	Human	NOGO	DNAzyme	928	14.8	92.5	31	23	ABR06446	Human	NOGO	DNAzyme
856	14.8	92.5	31	23	ABR06374	Human	NOGO	DNAzyme	929	14.8	92.5	31	23	ABR06447	Human	NOGO	DNAzyme
857	14.8	92.5	31	23	ABR06375	Human	NOGO	DNAzyme	930	14.8	92.5	31	23	ABR06448	Human	NOGO	DNAzyme
858	14.8	92.5	31	23	ABR06376	Human	NOGO	DNAzyme	931	14.8	92.5	31	23	ABR06449	Human	NOGO	DNAzyme
859	14.8	92.5	31	23	ABR06377	Human	NOGO	DNAzyme	932	14.8	92.5	31	23	ABR06450	Human	NOGO	DNAzyme
860	14.8	92.5	31	23	ABR06378	Human	NOGO	DNAzyme	933	14.8	92.5	31	23	ABR06451	Human	NOGO	DNAzyme
861	14.8	92.5	31	23	ABR06379	Human	NOGO	DNAzyme	934	14.8	92.5	31	23	ABR06452	Human	NOGO	DNAzyme
862	14.8	92.5	31	23	ABR06380	Human	NOGO	DNAzyme	935	14.8	92.5	31	23	ABR06453	Human	NOGO	DNAzyme
863	14.8	92.5	31	23	ABR06381	Human	NOGO	DNAzyme	936	14.8	92.5	31	23	ABR06454	Human	NOGO	DNAzyme
864	14.8	92.5	31	23	ABR06382	Human	NOGO	DNAzyme	937	14.8	92.5	31	23	ABR06455	Human	NOGO	DNAzyme
865	14.8	92.5	31	23	ABR06383	Human	NOGO	DNAzyme	938	14.8	92.5	31	23	ABR06456	Human	NOGO	DNAzyme
866	14.8	92.5	31	23	ABR06384	Human	NOGO	DNAzyme	939	14.8	92.5	31	23	ABR06457	Human	NOGO	DNAzyme
867	14.8	92.5	31	23	ABR06385	Human	NOGO	DNAzyme	940	14.8	92.5	31	23	ABR06458	Human	NOGO	DNAzyme
868	14.8	92.5	31	23	ABR06386	Human	NOGO	DNAzyme	941	14.8	92.5	31	23	ABR06459	Human	NOGO	DNAzyme
869	14.8	92.5	31	23	ABR06387	Human	NOGO	DNAzyme	942	14.8	92.5	31	23	ABR06460	Human	NOGO	DNAzyme
870	14.8	92.5	31	23	ABR06388	Human	NOGO	DNAzyme	943	14.8	92.5	31	23	ABR06461	Human	NOGO	DNAzyme
871	14.8	92.5	31	23	ABR06389	Human	NOGO	DNAzyme	944	14.8	92.5	31	23	ABR06462	Human	NOGO	DNAzyme
872	14.8	92.5	31	23	ABR06390	Human	NOGO	DNAzyme	945	14.8	92.5	31	23	ABR06463	Human	NOGO	DNAzyme
873	14.8	92.5	31	23	ABR06391	Human	NOGO	DNAzyme	946	14.8	92.5	31	23	ABR06464	Human	NOGO	DNAzyme
874	14.8	92.5	31	23	ABR06392	Human	NOGO	DNAzyme	947	14.8	92.5	31	23	ABR06465	Human	NOGO	DNAzyme
875	14.8	92.5	31	23	ABR06393	Human	NOGO	DNAzyme	948	14.8	92.5	31	23	ABR06466	Human	NOGO	DNAzyme
876	14.8	92.5	31	23	ABR06394	Human	NOGO	DNAzyme	949	14.8	92.5	31	23	ABR06467	Human	NOGO	DNAzyme
877	14.8	92.5	31	23	ABR06395	Human	NOGO	DNAzyme	950	14.8	92.5	31	23	ABR06468	Human	NOGO	DNAzyme
878	14.8	92.5	31	23	ABR06396	Human	NOGO	DNAzyme	951	14.8	92.5	31	23	ABR06469	Human	NOGO	DNAzyme
879	14.8	92.5	31	23	ABR06397	Human	NOGO	DNAzyme	952	14.8	92.5	31	23	ABR06470	Human	NOGO	DNAzyme
880	14.8	92.5	31	23	ABR06398	Human	NOGO	DNAzyme	953	14.8	92.5	31	23	ABR06471	Human	NOGO	DNAzyme
881	14.8	92.5	31	23	ABR06399	Human	NOGO	DNAzyme	954	14.8	92.5	31	23	ABR06472	Human	NOGO	DNAzyme
882	14.8	92.5	31	23	ABR06400	Human	NOGO	DNAzyme	955	14.8	92.5	31	23	ABR06473	Human	NOGO	DNAzyme
883	14.8	92.5	31	23	ABR06401	Human	NOGO	DNAzyme	956	14.8	92.5	31	23	ABR06474	Human	NOGO	DNAzyme
884	14.8	92.5	31	23	ABR06402	Human	NOGO	DNAzyme	957	14.8	92.5	31	23	ABR06475	Human	NOGO	DNAzyme

958	14.8	92.5	31	23	ABK06476	Human NOGO DNAzyme
959	14.8	92.5	31	23	ABK06477	Human NOGO DNAzyme
960	14.8	92.5	31	23	ABK06478	Human NOGO DNAzyme
961	14.8	92.5	31	23	ABK06479	Human NOGO DNAzyme
962	14.8	92.5	31	23	ABK06480	Human NOGO DNAzyme
963	14.8	92.5	31	23	ABK06481	Human NOGO DNAzyme
964	14.8	92.5	31	23	ABK06482	Human NOGO DNAzyme
965	14.8	92.5	31	23	ABK06483	Human NOGO DNAzyme
966	14.8	92.5	31	23	ABK06484	Human NOGO DNAzyme
967	14.8	92.5	31	23	ABK06485	Human NOGO DNAzyme
968	14.8	92.5	31	23	ABK06486	Human NOGO DNAzyme
969	14.8	92.5	31	23	ABK06487	Human NOGO DNAzyme
970	14.8	92.5	31	23	ABK06488	Human NOGO DNAzyme
971	14.8	92.5	31	23	ABK06489	Human NOGO DNAzyme
972	14.8	92.5	31	23	ABK06490	Human NOGO DNAzyme
973	14.8	92.5	31	23	ABK06491	Human NOGO DNAzyme
974	14.8	92.5	31	23	ABK06492	Human NOGO DNAzyme
975	14.8	92.5	31	23	ABK06493	Human NOGO DNAzyme
976	14.8	92.5	31	23	ABK06494	Human NOGO DNAzyme
977	14.8	92.5	31	23	ABK06495	Human NOGO DNAzyme
978	14.8	92.5	31	23	ABK06496	Human NOGO DNAzyme
979	14.8	92.5	31	23	ABK06497	Human NOGO DNAzyme
980	14.8	92.5	31	23	ABK06498	Human NOGO DNAzyme
981	14.8	92.5	31	23	ABK06499	Human NOGO DNAzyme
982	14.8	92.5	31	23	ABK06500	Human NOGO DNAzyme
983	14.8	92.5	31	23	ABK06501	Human NOGO DNAzyme
984	14.8	92.5	31	23	ABK06502	Human NOGO DNAzyme
985	14.8	92.5	31	23	ABK06503	Human NOGO DNAzyme
986	14.8	92.5	31	23	ABK06504	Human NOGO DNAzyme
987	14.8	92.5	31	23	ABK06505	Human NOGO DNAzyme
988	14.8	92.5	31	23	ABK06506	Human NOGO DNAzyme
989	14.8	92.5	31	23	ABK06507	Human NOGO DNAzyme
990	14.8	92.5	31	23	ABK06508	Human NOGO DNAzyme
991	14.8	92.5	31	23	ABK06509	Human NOGO DNAzyme
992	14.8	92.5	31	23	ABK06510	Human NOGO DNAzyme
993	14.8	92.5	31	23	ABK06511	Human NOGO DNAzyme
994	14.8	92.5	31	23	ABK06512	Human NOGO DNAzyme
995	14.8	92.5	31	23	ABK06513	Human NOGO DNAzyme
996	14.8	92.5	31	23	ABK06514	Human NOGO DNAzyme
997	14.8	92.5	31	23	ABK06515	Human NOGO DNAzyme
998	14.8	92.5	31	23	ABK06516	Human NOGO DNAzyme
999	14.8	92.5	31	23	ABK06517	Human NOGO DNAzyme
1000	14.8	92.5	31	25	AA153699	Prostate cancer ma

ALIGNMENTS

RESULT 1
AAV82954
ID AAV82954 standard; DNA; 16 BP.

XX AAV82954;
AC
XX
DT 05-MAR-1999 (first entry)
XX
XX Enzymatic DNA core motif region 10-23.
DE
XX Enzyme; catalysis; cleavage; target; pharmaceutical; medical; substrate;
KW regulator; detergent; dental hygiene; meat tenderiser; ss.
XX
OS Synthetic.
XX
XX WO9849346-A1.
XX
XX 05-NOV-1998.
XX
XX 29-APR-1998; 98WO-US08677.
XX
XX 29-APR-1997; 97US-0045228.
XX
XX (SCRI) SCRIPPS RES INST.
XX

PI Breaker RR, Joyce GF;
XX
XX WPI; 1999-034670/03.
DR
XX
PT New catalytic DNA molecules - having site-specific endonuclease
PT activity in a substrate nucleic acid, used for cleaving target
PT nucleic acid sequences
XX
PS Claim 1; Page 96; 161pp; English.

This sequence is used in a method which involves the production of catalytic DNA molecules which can be used for cleaving target nucleic acid molecules. Such DNA molecules can be used in pharmaceutical and medical products (e.g. for wound debridement, clot dissolution), as well as in household items (e.g. detergents, dental hygiene products, meat tenderisers). Other suitable substrates include those comprising or produced by picornaviruses, hepadnaviridae (e.g. HBV, HCV), papillomaviruses (e.g. HPV), gammaherpesvirinae (e.g. EBV), lymphocryptoviruses, leukemia viruses (e.g. HTLV-1 and -II), flaviviruses, togaviruses, herpesviruses (including alphaherpesvirus and betaherpesviruses), cytomegaloviruses (CMV), influenza viruses, and retroviruses contributing to immunodeficiency diseases and syndromes (e.g. HIV-1 and -2), simian and feline immunodeficiency viruses and bovine leukemia viruses. They can also be used as regulators of gene expression.

Sequence 16 BP; 5 A; 4 C; 4 G; 1 T; 2 other;

Query Match 92.5%; Score 14.8; DB 20; Length 16;
Best local similarity 100.0%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGCGTAGCHACACGA 16
DB 1 RGGCTAGCHACACGA 16

RESULT 2
AAV82953
ID AAV82953 standard; DNA; 16 BP.

XX AAV82953;
AC
XX
DT 05-MAR-1999 (first entry)
XX
XX Enzymatic DNA core motif region.
DE
XX Enzyme; catalysis; cleavage; target; pharmaceutical; medical; substrate;
KW regulator; detergent; dental hygiene; meat tenderiser; ss.
XX
OS Synthetic.
XX
XX WO9849346-A1.
XX
XX 05-NOV-1998.
XX
XX 29-APR-1998; 98WO-US08677.
XX
XX 29-APR-1997; 97US-0045228.
XX
XX (SCRI) SCRIPPS RES INST.
XX
XX Breaker RR, Joyce GF;
XX
XX WPI; 1999-034670/03.
XX
XX New catalytic DNA molecules - having site-specific endonuclease
PT activity in a substrate nucleic acid, used for cleaving target
PT nucleic acid sequences
XX
XX Claim 1; Page 96; 161pp; English.
XX
XX This sequence is used in a method which involves the production of

DE DNzyme motif SEQ ID NO 21.
 XX Nucleic acid sensor molecule; detection; infection; disease diagnosis;
 XX physiological abnormality; electronic; signalling molecule; ribozyme;
 KW nucleoside analogue; DNzyme; ss.
 XX Synthetic.
 OS WO200166721-A2.
 PN 13-SEP-2001.
 XX 06-MAR-2001; 2001WO-US07163.
 PF 06-MAR-2000; 2000US-187128P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA Usman N, McSwiggen JA, Zinnen S, Seiwert S, Haeblerli P;
 PI Chowrita B, Blatt L;
 XX WPI; 2001-616242/71.
 DR New nucleic acid sensor molecule useful in diagnostic applications,
 XX nucleic acid-based electronics and functional genomics, comprises an
 PT enzymatic nucleic acid and one or more sensors
 XX
 PS Disclosure; Fig 4; 115pp; English.
 XX The invention relates to a nucleic acid sensor molecule (I) comprising an
 CC enzymatic nucleic acid component and one or more sensor components, (I)
 CC is useful in diagnostic applications to identify the presence of genes
 CC and/or gene products indicative of a particular genotype and/or
 CC phenotype, e.g. a disease state or infection and for diagnosis of disease
 CC states or physiological abnormalities related to the expression of viral,
 CC bacterial or cellular RNA and DNA. (I) is useful in nucleic acid-based
 CC electronics, for the detection of specific target signalling molecules,
 CC in assays to assess the specificity, toxicity and effectiveness of
 CC various small molecules, nucleoside analogues or non-nucleic acid drugs
 CC or for detection of pathogens, biochemicals, organic or inorganic
 CC compounds. The present sequence is that of a DNzyme motif of the
 CC invention.
 XX
 XX Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;
 SQ
 Query Match 92.5%; Score 14.8; DB 22; Length 16;
 Best Local Similarity 93.8%; Pred. No. 89;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 RGGCTAGCHACACGA 16
 Db 1 RGGCTAGCTACACGA 16
 RESULT 6
 AAH97756
 ID AAH97756 standard; DNA; 16 BP.
 XX AAH97756;
 AC
 XX 09-OCT-2001 (first entry)
 DT
 XX DNzyme ribozyme motif SEQ ID NO: 3186.
 DE Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;
 KW RNA cleavage; cancer; ss.
 XX Unidentified.
 OS WO200157206-A2.
 XX 09-AUG-2001.
 PD
 XX

PF 02-FEB-2001; 2001WO-US03504.
 XX 03-FEB-2000; 2000US-0179983.
 PR (RIBO-) RIBOZYME PHARM INC.
 PA (PAT/) PATTAIEY A R.
 XX Fattaey AR, Jarvis T, McSwiggen J, Booher RN, Holman PS;
 PI WPI; 2001-496922/54.
 DR Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid
 PT molecules, which downregulates expression of a checkpoint kinase-1
 PT gene, useful for treating colorectal, lung, breast or prostate cancers
 PT
 PS Claim 8; Fig 5; 115pp; English.
 XX The present invention provides nucleic acid molecules capable of
 CC downregulating the expression of the human checkpoint kinase-1 (Chk1)
 CC gene. These may be antisense or ribozyme sequences, and are useful in the
 CC treatment of diseases associated with conditions affected by Chk1 levels,
 CC including cancer. The present sequence is an oligonucleotide described in
 CC the exemplification of the invention.
 XX
 XX Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;
 SQ
 Query Match 92.5%; Score 14.8; DB 22; Length 16;
 Best Local Similarity 93.8%; Pred. No. 89;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 RGGCTAGCHACACGA 16
 Db 1 RGGCTAGCTACACGA 16
 RESULT 7
 ABR09278
 ID ABR09278 standard; DNA; 16 BP.
 XX ABR09278;
 AC
 XX 12-MAR-2002 (first entry)
 DT
 XX DNzyme motif.
 DE Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNzyme; inozyme; G-cleaver; amberyze; zinzyne; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX Synthetic.
 OS WO200159103-A2.
 PN 16-AUG-2001.
 XX 09-FEB-2001; 2001WO-US04273.
 XX 11-FEB-2000; 2000US-181797P.
 PR 28-FEB-2000; 2000US-185516P.
 PR 06-MAR-2000; 2000US-187128P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA

PA (MCSW/J) MCSWIGGEN J.
 PA (CHOW/J) CHOWIRIRA B M.
 P1 Blact L, McSwiggen J, Chowirira BM;
 DR WPI, 2001-607195/69.
 XX
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
 PT and central nervous system injury
 PS
 XX Disclosure; Fig 5; 200pp; English.
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOCO).
 CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNAzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NTN
 CC motif) or an amberzyme (cleaving RNA with an NGN triplet), a zinczyme
 CC (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used
 CC to cleave RNA of CD20 in the presence of a divalent cation that is
 CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce
 CC CD20 activity of the cell and treat a patient having a condition
 CC associated with the level of CD20. The treatment may further comprise the
 CC use of one or more therapies. In particular, the CD20 targeting
 CC nucleic acid may be used to treat lymphoma, leukemia, B-cell
 CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
 CC low-grade or follicular NHL, lymphocytic leukaemia, HIV (human
 CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
 CC immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune
 CC thrombocytopenia, and inflammatory arthropathy. The NOCO-targeting
 CC nucleic acid is used to cleave RNA of the NOCO gene in the presence of a
 CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid
 CC may be contacted with a cell to reduce NOCO activity of the cell and
 CC treat a patient having a condition associated with the level of NOCO. The
 CC treatment may further comprise the use of one or more therapies.
 CC In particular, the NOCO-targeting nucleic acid may be used to treat
 CC central nervous system (CNS) injury and cerebrovascular accident (CVA,
 CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOCO expression. The
 CC present sequence is a DNAzyme molecule of the invention.
 CC
 XX
 SQ Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;
 QY Query Match 92.5%; Score 14.8; DB 23; Length 16;
 Best Local Similarity 93.8%; Pred. No. 89;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RGGCTAGCHACACGA 16
 DB 1 RGGCTAGCTACACGA 16
 D6
 RESULT 8
 ABR61076
 ID ABR61076 standard; DNA, 16 BP.
 AC ABR61076;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Human CLCA1 gene enzymatic nucleic acid #5445.
 XX
 KW Human, chloride channel calcium activated 1; CLCA1, ss; antiasthmatic;
 KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
 KW acetylcysteine.

XX
 OS Homo sapiens.
 XX
 EN WO200211674-A2.
 XX
 PD 14-FEB-2002.
 XX
 PF 09-AUG-2001; 2001WO-US24970.
 XX
 PR 09-AUG-2000; 2000US-224383P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (SYNT) SYNTEX USA LLC.
 PA (THOM/J) THOMPSON J.
 P1 Thompson J, McSwiggen J, McKenzie T, Ayers D, Szymkowski DE;
 P1 Grape A;
 DR WPI, 2002-217145/27.
 XX
 PT Enzymatic polynucleotide that down regulates expression of chloride
 PT channel calcium activated gene, useful for treating Chronic obstructive
 PT pulmonary disease (COPD), chronic bronchitis and asthma
 PS
 XX Disclosure; Fig 4; 152pp; English.
 CC The invention relates to enzymatic nucleic acid molecules that down
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are
 CC useful as pharmaceutical agents for treating conditions such as chronic
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
 CC that are related to or will respond to the levels of CLCA1 in a cell or
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
 CC hence, are useful for treatment of a patient having a condition
 CC associated with the level of CLCA1, where the invention further comprises
 CC the use of one or more therapies under conditions suitable for the
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
 CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
 CC nucleic acids of the invention are also used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of CLCA1 RNA in a cell. This sequence represents an
 CC enzymatic nucleic acid molecule of the invention.
 CC
 XX
 SQ Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;
 QY Query Match 92.5%; Score 14.8; DB 24; Length 16;
 Best Local Similarity 93.8%; Pred. No. 89;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RGGCTAGCHACACGA 16
 DB 1 RGGCTAGCTACACGA 16
 D6
 RESULT 9
 ABR22719
 ID ABR22719 standard; RNA, 16 BP.
 AC ABR22719;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE DNAzyme motif.
 XX
 KW Human; hammerhead ribozyme; cytosstatic; antitumour; antidiabetic;
 KW ophthalmological; antiarthritic; antipneumatic; viricide; osteopathic;
 KW vulnery; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
 KW angiofibroma of tuberosus sclerosis; port-wine stain; wound healing;
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
 KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;

KW amberzyme.
 XX Synthetic.
 OS
 XX WO20018124-A2.
 XX
 XX 22-NOV-2001.
 XX
 XX 16-MAY-2001; 2001WO-US15866.
 XX
 XX 16-MAY-2000; 2000US-0572021.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX (GLAXO) GLAXO GROUP LTD.
 XX
 XX Jarvis T, Von Carlowitz I, McSwiggen JA, McLaughlin F, Randi AM;
 PI WPI; 2002-082995/11.
 DR
 XX
 XX Novel polynucleotide which down regulates expression of Bts-related
 PT gene, useful for treating cancer, diabetic retinopathy, macular
 PT degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber
 PT syndrome -
 XX
 XX Disclosure; Figure 5; 149pp; English.
 PS
 XX The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Bts-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumor angiosarcoma, myopic degeneration, macular degeneration, verruca
 CC vulgaris, angiodysplasia of tuberosus sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Redu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg²⁺. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK7354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention.
 XX
 XX Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;
 SQ
 Query Match 92.5%; Score 14.8; DB 24; Length 16;
 Best Local Similarity 93.8%; Pred. No. 89;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGGCTAGCTACACGA 16
 DB 1 RGGCTAGCTACACGA 16
 RESULT 10
 ACA10109
 ID ACA10109 standard; DNA; 16 BP.
 XX
 XX ACA10109;
 AC
 XX 03-JUN-2003 (first entry)
 XX
 XX DT
 XX Necrosis factor kappa B (NFkB) modulating DNAzyme motif.
 DB
 XX

KW Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinczyme;
 KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer;
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
 KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
 KW cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;
 KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; leukaemia;
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
 KW allergic airway inflammation; inflammatory bowel disease; infection;
 KW
 XX
 XX Synthetic.
 XX
 XX US2002177568-A1.
 XX
 XX 28-NOV-2002.
 XX
 XX 23-MAY-2001; 2001US-0864785.
 XX
 XX 15-AUG-1994; 94US-0291932.
 XX 07-DEC-1992; 92US-0987132.
 XX 18-MAY-1994; 94US-0245466.
 XX 23-DEC-1996; 96US-0777916.
 XX
 XX (STIN)/ STINCHOMB D T.
 XX (MCSW)/ MCSWIGGEN J.
 XX (DRAP)/ DRAPER K G.
 XX
 XX Stinchcomb DT, Mcswiggen J, Draper KG;
 PI WPI; 2003-340953/32.
 DR
 XX Novel enzymatic nucleic acid molecules which down regulates expression
 PT of a sequence encoding a subunit of nuclear factor kappa B useful for
 PT treating cancer, inflammatory disorders and autoimmune diseases -
 PT
 XX
 XX Fig 4; SEQ ID NO 3928; 72pp; English.
 PS
 XX The invention describes an enzymatic nucleic acid molecule (I) which down
 CC regulates expression of a sequence encoding a subunit of nuclear factor
 CC kappa B (NFkB), where (I) is an inozyme, zinczyme, G-cleaver or amberzyme
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat
 CC cancer and is useful for down-regulating REL-A activity in a cell, for
 CC treating a patient having a condition associated with the level of REL-A.
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
 CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
 CC antisense nucleic acid molecules are useful for treating breast, lung,
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
 CC multidrug resistant cancer. The method involves use of other drug
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
 CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
 CC acid molecules are also useful for treating inflammatory disease such as
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
 CC rejection, gene therapy applications, ischaemia/reperfusion injury
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or
 CC infection. This sequence represents a motif of an enzymatic nucleic acid
 CC used to modulate the function of a necrosis factor kappa B sub-unit.
 XX
 XX Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;
 SQ
 Query Match 92.5%; Score 14.8; DB 25; Length 16;
 Best Local Similarity 93.8%; Pred. No. 89;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGGCTAGCTACACGA 16
 DB 1 RGGCTAGCTACACGA 16

OY 1 RGGCTAGCHACACGA 16
|||:|||||
Db 1 RGGCTAGCTACACGA 16

RESULT 11

ID AB258432 standard; DNA; 16 BP.

AC AB258432;

DT 08-MAY-2003 (first entry)

DE DNazyme motif.

KM DNazyme; enzymatic nucleic acid; enzyme; transporter; drug
KW delivery; cytosolic; virucide; gene therapy; ss.

OS Synthetic.

XX WO2003008628-A2.

XX 30-JAN-2003.

XX 22-JUL-2002; 2002WO-US23324.

XX 20-JUL-2001; 2001US-306995P.

XX (RIBO-) RIBOZYME PHARM INC.

PI Beigelman L, Azharyev A, Azharyeva E;

DR WPI; 2003-247828/25.

PT New transporter compounds useful for delivering molecules into
PT biological system such as cells, and for treating cancer and viral
PT infections -

PS Disclosure; Fig 4; 88pp; English.

XX The present sequence is an example of a DNazyme, an enzymatic
CC nuclear acid (ENA) that does not require the presence of a 2'-OH
CC group for its activity. DNazymes can be used as the ENA moiety in
CC novel ENA peptide conjugates (1) of the invention that facilitate
CC delivery of molecules into biological systems, such as cells. The
CC peptide part of the conjugate is typically a fusogenic peptide such
CC as a peptide given in ABP72298-ABP72305. The conjugates can be
CC used to treat a cancer patient, where the cancer is breast, lung,
CC colorectal, brain, oesophageal, stomach, bladder, pancreas, cervix,
CC head and neck or ovary cancer, melanoma, lymphoma, glioma or
CC multidrug resistant cancer, or to treat a virus infection, where
CC the virus is HIV, hepatitis B virus, hepatitis C virus,
CC cytomegalovirus, Rous sarcoma virus, herpes simplex virus,
CC poliovirus, influenza virus, rhinovirus, west nile virus, Ebola
CC virus, foot and mouth disease virus or papilloma virus (all
CC claimed). (1) are useful for introducing nucleotides,
CC nucleosides, nucleic acid molecules, lipids, peptides, proteins
CC and/or non-nucleosidic small molecules into a cell and to detect
CC the presence of a target molecule in a biological system such as
CC tissue, cell or cell lysate. They are useful as diagnostic tools
CC to examine genetic drift and mutations within diseased cells or to
CC detect the presence of a disease-related RNA in a cell.

XX Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;

Query Match 92.5%; Score 14.8; DB 25; Length 16;

Best Local Similarity 93.8%; Pred. No. 89;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16
|||:|||||
Db 1 RGGCTAGCTACACGA 16

RESULT 12

ID AB266525 standard; RNA; 27 BP.

AC AB266525;

DT 21-MAR-2003 (first entry)

DE Human HER2 synthetic DNazyme #1.

KM Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;
KW anti-thematic; cancer; AIDS; ss.

OS Homo sapiens.

XX WO200297114-A2.

XX 05-DEC-2002.

XX 29-MAY-2002; 2002WO-US16840.

XX 29-MAY-2001; 2001US-294140P.

XX 06-JUN-2001; 2001US-296249P.

XX 10-SEP-2001; 2001US-318471P.

XX (RIBO-) RIBOZYME PHARM INC.

PI Mcswiggen J;

DR WPI; 2003-140484/13.

PT Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX Claim 3; Page 153; 185pp; English.

XX The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytosolic, anti-HIV, and
CC anti-rheumatic activity. The nucleic acid molecules are useful for
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
CC acids are also useful for treating breast, ovarian, colorectal, lung,
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
CC The sequences shown in AB262217 - AB264543, AB265532 - AB265519,
CC AB266525 - AB266529, AB266586 - AB266558 represent human ribozymes of the
CC invention.

XX Sequence 27 BP; 6 A; 6 C; 10 G; 2 T; 3 U; 0 other;

Query Match 92.5%; Score 14.8; DB 25; Length 27;

Best Local Similarity 87.5%; Pred. No. 92;

Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16
|||:|||||

Db 6 AGGCTAGCTACACGA 21

RESULT 13

ID AB266527 standard; RNA; 27 BP.

AC AB266527;

DT 21-MAR-2003 (first entry)

DE Human HER2 synthetic DNazyme #3.

XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;
 KW anti-rheumatic; cancer; AIDS; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200297114-A2.
 XX
 PD 05-DEC-2002.
 XX
 PF 29-MAY-2002; 2002WO-US16840.
 XX
 PR 29-MAY-2001; 2001US-294140P.
 PR 06-JUN-2001; 2001US-296249P.
 PR 10-SEP-2001; 2001US-318471P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Mcswiggen J;
 XX
 DR WPI; 2003-140484/13.
 XX
 PT Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
 XX
 PS Claim 3; Page 153; 185pp; English.
 XX
 CC The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytosolic, anti-HIV, and
 CC anti-rheumatic activity. The nucleic acid molecules are useful for
 CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
 CC acids are also useful for treating breast, ovarian, colorectal, lung,
 CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
 CC The sequences shown in AB262217 - AB264543, AB265532 - AB265519,
 CC AB266525 - AB266529, AB266586 - AB266658 represent human ribozymes of the
 CC invention.
 XX
 SQ Sequence 27 BP; 11 A; 8 C; 6 G; 2 T; 0 other;

Query Match 92.5%; Score 14.8; DB 25; Length 27;
 Best Local Similarity 87.5%; Pred. No. 92;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGGCHACACGA 16
 : |||||: |||||
 Db 6 AGGCTAGCTACACGA 21

RESULT 14
 AA234361
 ID AA234361 standard; DNA; 29 BP.
 XX
 AC AA234361;
 XX
 DT 14-DEC-1999 (first entry)
 XX
 DE Nucleic acid-based diagnostic exemplification oligonucleotide #23.
 XX
 KW Catalytic nucleic acid-based diagnostic method; determination; AIDS;
 KW mutation; ribozyme; target; cleavage; amplification; PCR primer;
 KW probe; cancer; human immune deficiency virus; cystic fibrosis; HIV; ss.
 XX
 OS Synthetic.
 XX
 PN WO9950452-A1.
 XX
 PD 07-OCT-1999.
 XX

PR 16-MAR-1999; 99WO-IB00848.
 XX
 XX 27-MAR-1998; 98US-0079651.
 PR
 PA (JOHN) JOHNSON & JOHNSON RES PTY LTD.
 XX
 PI Todd AV, Fuery CJ, Cairns MJ;
 XX
 DR WPI; 1999-591332/50.
 XX
 PT Detecting diseases associated with a known mutation by amplification
 PT and cleavage with catalytic nucleic acids, particularly for cancer,
 PT human immune deficiency virus and cystic fibrosis -
 XX
 PS Disclosure; Page 20; 57pp; English.
 XX
 CC The present invention describes a method for determining whether a
 CC subject is afflicted with a disorder characterised by the presence of
 CC a known nucleic acid. The method comprises: (i) amplifying, in an
 CC isolated sample from the subject, the nucleic acid segment that, in an
 CC affected individual contains (A), (ii) treating the amplicons with a
 CC catalytic nucleic acid (I) that specifically recognizes and cleaves a
 CC target sequence present in either the mutated or wild-type segments,
 CC but not in both; and (iii) detecting any cleavage caused by (I). Step
 CC (ii) may be performed concurrently with (i). The method is specifically
 CC used to diagnose cancer (especially), acquired immune deficiency
 CC syndrome and cystic fibrosis. (I) recognises as few as two bp to create
 CC a cleavage site (contrast at least 4 bp required by enzymes used in
 CC restriction fragment length polymorphism (RFLP) analysis); such sites
 CC occur more frequently than restriction enzyme sites, and mismatched
 CC primers can be used to induce cleavage sites for (I). The method is
 CC potentially more flexible than RFLP and does not require any enzymes or
 CC toxic compounds. AA234339 to AA234450 represent oligonucleotide
 CC sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 29 BP; 10 A; 5 C; 10 G; 3 T; 1 other;

Query Match 92.5%; Score 14.8; DB 20; Length 29;
 Best Local Similarity 87.5%; Pred. No. 93;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGGCHACACGA 16
 : |||||: |||||
 Db 8 AGGCTAGCTACACGA 23

RESULT 15
 AA234363
 ID AA234363 standard; DNA; 29 BP.
 XX
 AC AA234363;
 XX
 DT 14-DEC-1999 (first entry)
 XX
 DE Nucleic acid-based diagnostic exemplification oligonucleotide #25.
 XX
 KW Catalytic nucleic acid-based diagnostic method; determination; AIDS;
 KW mutation; ribozyme; target; cleavage; amplification; PCR primer;
 KW probe; cancer; human immune deficiency virus; cystic fibrosis; HIV; ss.
 XX
 OS Synthetic.
 XX
 PN WO9950452-A1.
 XX
 PD 07-OCT-1999.
 XX
 PR 16-MAR-1999; 99WO-IB00848.
 XX
 PR 27-MAR-1998; 98US-0079651.
 XX
 PA (JOHN) JOHNSON & JOHNSON RES PTY LTD.
 XX
 PI Todd AV, Fuery CJ, Cairns MJ;

PS Disclosure; Fig 13; 39pp; German.

CC The invention relates to a novel short interfering RNA (siRNA) nucleic

CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytosstatic, anti-HIV, and
CC anti-rheumatic activity. The nucleic acid molecules are useful for
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
CC acids are also useful for treating breast, ovarian, colorectal, lung,
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
CC The sequences shown in ABZ62217 - ABZ64543, ABZ65532 - ABZ65519,
CC ABZ66525 - ABZ66529, ABZ66586 - ABZ66658 represent human ribozymes of the
CC invention.

XX
SQ Sequence 29 BP; 11 A; 7 C; 7 G; 2 T; 2 U; 0 other;

QY
Query Match 92.5%; Score 14.8; DB 25; Length 29;
Best Local Similarity 87.5%; Pred. No. 93;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1 RGGCTAGCHACACGA 16
7 AGGCTAGCTACACGA 22

RESULT 18
ABZ66528
ID ABZ66528 standard; RNA; 29 BP.
XX
AC ABZ66528;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human HER2 synthetic DNAzyme #4.
XX
KM Human, ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
KM anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J;
XX
DR WPI; 2003-140484/13.
XX
PT Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX
PS Claim 3; Page 153; 185pp; English.

CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytosstatic, anti-HIV, and
CC anti-rheumatic activity. The nucleic acid molecules are useful for
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
CC acids are also useful for treating breast, ovarian, colorectal, lung,
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
CC The sequences shown in ABZ62217 - ABZ64543, ABZ65532 - ABZ65519,
CC ABZ66525 - ABZ66529, ABZ66586 - ABZ66658 represent human ribozymes of the
CC invention.

XX
SQ Sequence 29 BP; 9 A; 5 C; 11 G; 2 T; 2 U; 0 other;

QY
Query Match 92.5%; Score 14.8; DB 25; Length 29;
Best Local Similarity 87.5%; Pred. No. 93;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1 RGGCTAGCHACACGA 16
7 AGGCTAGCTACACGA 22

RESULT 19
ABZ66529
ID ABZ66529 standard; RNA; 29 BP.
XX
AC ABZ66529;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human HER2 synthetic DNAzyme #5.
XX
KM Human, ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
KM anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J;
XX
DR WPI; 2003-140484/13.
XX
PT Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX
PS Claim 3; Page 153; 185pp; English.

CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytosstatic, anti-HIV, and
CC anti-rheumatic activity. The nucleic acid molecules are useful for
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
CC acids are also useful for treating breast, ovarian, colorectal, lung,
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
CC The sequences shown in ABZ62217 - ABZ64543, ABZ65532 - ABZ65519,
CC ABZ66525 - ABZ66529, ABZ66586 - ABZ66658 represent human ribozymes of the
CC invention.

XX
SQ Sequence 29 BP; 7 A; 4 C; 11 G; 2 T; 5 U; 0 other;

QY
Query Match 92.5%; Score 14.8; DB 25; Length 29;
Best Local Similarity 87.5%; Pred. No. 93;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1 RGGCTAGCHACACGA 16
7 AGGCTAGCTACACGA 22

RESULT 20
ABZ66649 standard; RNA; 29 BP.
XX
AC ABZ66649;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human HIV enzymatic nucleic acid #1.
XX
KM Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
KM anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-US16840.
XX
PR 29-MAY-2001; 2001US-294140P.
PR 06-JUN-2001; 2001US-296249P.
PR 10-SEP-2001; 2001US-318471P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcawiggen J;
XX
DR WPI; 2003-140484/13.
XX
PT Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX
PS Claim 122; Page 159; 185pp; English.
XX
CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytosstatic, anti-HIV, and
CC anti-rheumatic activity. The nucleic acid molecules are useful for
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
CC acids are also useful for treating breast, ovarian, colorectal, lung,
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
CC The sequences shown in ABZ62217 - ABZ64543, ABZ65532 - ABZ65519,
CC ABZ66525 - ABZ66529, ABZ66586 - ABZ66658 represent human ribozymes of the
CC invention.
XX
SQ Sequence 29 BP; 7 A; 11 C; 5 G; 2 T; 4 U; 0 other;
XX
Query Match 92.5%; Score 14.8; DB 25; Length 29;
Best Local Similarity 87.5%; Pred. No. 93;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 RGGCTAGCHACACGA 16
:|||||:|||||
DB 7 AGGCTAGCTACACGA 22

RESULT 21
ABZ66650 standard; RNA; 29 BP.
XX
AC ABZ66650;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human HIV enzymatic nucleic acid #2.
XX

KM Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
KM anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-US16840.
XX
PR 29-MAY-2001; 2001US-294140P.
PR 06-JUN-2001; 2001US-296249P.
PR 10-SEP-2001; 2001US-318471P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcawiggen J;
XX
DR WPI; 2003-140484/13.
XX
PT Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX
PS Claim 122; Page 159; 185pp; English.
XX
CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytosstatic, anti-HIV, and
CC anti-rheumatic activity. The nucleic acid molecules are useful for
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
CC acids are also useful for treating breast, ovarian, colorectal, lung,
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
CC The sequences shown in ABZ62217 - ABZ64543, ABZ65532 - ABZ65519,
CC ABZ66525 - ABZ66529, ABZ66586 - ABZ66658 represent human ribozymes of the
CC invention.
XX
SQ Sequence 29 BP; 7 A; 9 C; 5 G; 2 T; 6 U; 0 other;
XX
Query Match 92.5%; Score 14.8; DB 25; Length 29;
Best Local Similarity 87.5%; Pred. No. 93;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 RGGCTAGCHACACGA 16
:|||||:|||||
DB 7 GGCTAGCTACACGA 22

RESULT 22
ABZ66651 standard; RNA; 29 BP.
XX
AC ABZ66651;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human HIV enzymatic nucleic acid #3.
XX
KM Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
KM anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-US16840.

XX 29-MAY-2001; 2001US-294140P.
 PR 06-JUN-2001; 2001US-296249P.
 PR 10-SEP-2001; 2001US-318471P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Mcswiggen J;
 XX
 DR WPI; 2003-140484/13.
 XX
 PT Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
 PS Claim 122; Page 159; 185pp; English.
 CC
 CC The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytosstatic, anti-HIV, and
 CC anti-rheumatic activity. The nucleic acid molecules are useful for
 CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
 CC acids are also useful for treating breast, ovarian, colorectal, lung,
 CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
 CC The sequences shown in ABZ62217 - ABZ64543, ABZ65532 - ABZ65519,
 CC ABZ66525 - ABZ66529, ABZ66586 - ABZ66658 represent human ribozymes of the
 CC invention.
 XX
 SQ Sequence 29 BP; 6 A; 9 C; 6 G; 2 T; 6 U; 0 other;
 XX
 Query Match 92.5%; Score 14.8; DB 25; Length 29;
 Best Local Similarity 87.5%; Pred. No. 93;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 RGGCTAGCHACACGA 16
 :|||||:|||||
 Db 7 AGGCTAGCTACACGA 22
 XX
 RESULT 23
 ABZ66652
 ID ABZ66652 standard; RNA; 29 BP.
 AC ABZ66652;
 XX
 DT 21-MAR-2003 (first entry)
 XX
 DE Human HIV enzymatic nucleic acid #4.
 XX
 KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
 KW anti-rheumatic; cancer; AIDS; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200297114-A2.
 XX
 PD 05-DEC-2002.
 XX
 PF 29-MAY-2002; 2002WO-US16840.
 XX
 PR 29-MAY-2001; 2001US-294140P.
 PR 06-JUN-2001; 2001US-296249P.
 PR 10-SEP-2001; 2001US-318471P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Mcswiggen J;
 XX
 DR WPI; 2003-140484/13.
 XX

PT Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
 PS Claim 122; Page 159; 185pp; English.
 CC
 CC The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytosstatic, anti-HIV, and
 CC anti-rheumatic activity. The nucleic acid molecules are useful for
 CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
 CC acids are also useful for treating breast, ovarian, colorectal, lung,
 CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
 CC The sequences shown in ABZ62217 - ABZ64543, ABZ65532 - ABZ65519,
 CC ABZ66525 - ABZ66529, ABZ66586 - ABZ66658 represent human ribozymes of the
 CC invention.
 XX
 SQ Sequence 29 BP; 8 A; 6 C; 8 G; 2 T; 5 U; 0 other;
 XX
 Query Match 92.5%; Score 14.8; DB 25; Length 29;
 Best Local Similarity 87.5%; Pred. No. 93;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 RGGCTAGCHACACGA 16
 :|||||:|||||
 Db 7 AGGCTAGCTACACGA 22
 XX
 RESULT 24
 ABZ66653
 ID ABZ66653 standard; RNA; 29 BP.
 AC ABZ66653;
 XX
 DT 21-MAR-2003 (first entry)
 XX
 DE Human HIV enzymatic nucleic acid #5.
 XX
 KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
 KW anti-rheumatic; cancer; AIDS; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200297114-A2.
 XX
 PD 05-DEC-2002.
 XX
 PF 29-MAY-2002; 2002WO-US16840.
 XX
 PR 29-MAY-2001; 2001US-294140P.
 PR 06-JUN-2001; 2001US-296249P.
 PR 10-SEP-2001; 2001US-318471P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Mcswiggen J;
 XX
 DR WPI; 2003-140484/13.
 XX
 PT Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
 PS Claim 122; Page 159; 185pp; English.
 CC
 CC The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytosstatic, anti-HIV, and

CC anti-rheumatic activity. The nucleic acid molecules are useful for
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
CC acids are also useful for treating breast, ovarian, colorectal, lung,
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
CC The sequences shown in AB262217 - AB264543, AB265532 - AB265519,
CC AB265525 - AB265529, AB265586 - AB266558 represent human ribozymes of the
CC invention.
XX
SQ Sequence 29 BP; 7 A; 12 C; 5 G; 2 T; 3 U; 0 other;
Query Match 92.5%; Score 14.8; DB 25; Length 29;
Best Local Similarity 87.5%; Pred. No. 93;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 RGCTAGCHACACGA 16
:|||||:|||||
7 AGGCTAGCTACACGA 22
Db
RESULT 25
ABX13988 standard; DNA; 29 BP.
XX
AC ABX13988;
XX
DT 25-FEB-2003 (first entry)
XX
DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1594.
XX
XX Catalytic DNA; catalytic RNA; hairless protein; ss;
KM hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;
KM ribozyme; DNazyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;
KM catalytic core; cleavage site; pharmaceutical; hair production;
KM hair follicle; anagen phase; catagen phase; hair removal product;
KM depilatory.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 8..22
FT /*tag= a
FT /note= "Catalytic domain"
XX
XX WO200283891-A2.
XX
XX 24-OCT-2002.
XX
XX 12-APR-2002; 2002WO-US11683.
XX
XX 13-APR-2001; 2001US-283618P.
XX
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX Christiano AM;
XX
XX WPI; 2003-093020/08.
XX
XX New catalytic nucleic acid molecule that specifically cleaves Hairless
XX Protein mRNA, useful for inhibiting hair production by a hair-producing
XX cell, or for inhibiting transition of a hair follicle from anagen phase
XX to catagen phase -
XX
XX Claim 3; Page 34; 65pp; English.
XX
XX The invention discloses a new catalytic DNA or RNA molecule that
XX specifically cleaves, or inhibits expression of, Hairless Protein mRNA
XX which comprises a catalytic domain that cleaves mRNA at a defined
XX consensus sequence and binding domains contiguous with the 5' and 3' ends
XX of the catalytic domain. Lack of expression of the hairless gene due to
XX inherited mutations leads to the complete loss of hair, known as
XX atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting
XX the genes promoting hair growth, and one way to get targeted, transient

CC gene suppression is through the use of catalytic nucleic acid technology,
CC including ribozymes and DNazymes. Ribozymes are RNA structures which have
CC a self-catalytic enzymatic function and sequence specific RNA binding
CC ability. Small DNA oligonucleotides that have a similar structure to the
CC hammerhead ribozyme, called deoxy-ribozymes or DNazymes, having a
CC catalytic core and two sequence specific arms. The deoxy-ribozymes have
CC more lenient consensus cleavage site requirements and are less likely to
CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids
CC are useful in pharmaceutical compositions for inhibiting hair production
CC by a hair-producing cell, for inhibiting hair growth and for inhibiting
CC the transition of a hair follicle from the anagen phase to the catagen
CC phase. A non-human transgenic mammal is useful as a model for testing
CC hair removal products which function by inhibiting hairless protein
CC expression. The sequence presented is the deoxy-ribozyme that cleaves the
CC human hairless protein mRNA immediately after nucleotide 1594.
XX
XX
SQ Sequence 29 BP; 7 A; 10 C; 8 G; 4 T; 0 other;
Query Match 92.5%; Score 14.8; DB 25; Length 29;
Best Local Similarity 87.5%; Pred. No. 93;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 RGCTAGCHACACGA 16
:|||||:|||||
7 GGGCTAGCTACACGA 22
Db
RESULT 26
ABX13989 standard; DNA; 29 BP.
XX
AC ABX13989;
XX
DT 25-FEB-2003 (first entry)
XX
DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1597.
XX
XX Catalytic DNA; catalytic RNA; hairless protein; ss;
KM hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;
KM ribozyme; DNazyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;
KM catalytic core; cleavage site; pharmaceutical; hair production;
KM hair follicle; anagen phase; catagen phase; hair removal product;
KM depilatory.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 8..22
FT /*tag= a
FT /note= "Catalytic domain"
XX
XX WO200283891-A2.
XX
XX 24-OCT-2002.
XX
XX 12-APR-2002; 2002WO-US11683.
XX
XX 13-APR-2001; 2001US-283618P.
XX
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX Christiano AM;
XX
XX WPI; 2003-093020/08.
XX
XX New catalytic nucleic acid molecule that specifically cleaves Hairless
XX Protein mRNA, useful for inhibiting hair production by a hair-producing
XX cell, or for inhibiting transition of a hair follicle from anagen phase
XX to catagen phase -
XX
XX Claim 3; Page 34; 65pp; English.
XX

CC The invention discloses a new catalytic DNA or RNA molecule that
 CC specifically cleaves, or inhibits expression of, Hairless protein mRNA
 CC which comprises a catalytic domain that cleaves mRNA at a defined
 CC consensus sequence and binding domains contiguous with the 5' and 3' ends
 CC of the catalytic domain. Lack of expression of the hairless gene due to
 CC inherited mutations leads to the complete loss of hair, known as
 CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting
 CC the genes promoting hair growth, and one way to get targeted, transient
 CC gene suppression is through the use of catalytic nucleic acid technology,
 CC including ribozymes and DNazymes. Ribozymes are RNA structures which have
 CC a self-catalytic enzymatic function and sequence specific RNA binding
 CC ability. Small DNA oligonucleotides that have a similar structure to the
 CC hammerhead ribozyme, called deoxy-ribozymes or DNazymes, having a
 CC catalytic core and two sequence specific arms. The deoxy-ribozymes have
 CC more lenient consensus cleavage site requirements and are less likely to
 CC degrade, *in vivo*, that hammerhead ribozymes. The catalytic nucleic acids
 CC are useful in pharmaceutical compositions for inhibiting hair production
 CC by a hair-producing cell, for inhibiting hair growth and for inhibiting
 CC the transition of a hair follicle from the anagen phase to the catagen
 CC phase. A non-human transgenic mammal is useful as a model for testing
 CC hair removal products which function by inhibiting hairless protein
 CC expression. The sequence presented is the deoxy-ribozyme that cleaves the
 CC human hairless protein mRNA immediately after nucleotide 1597.

CC Sequence 29 BP, 7 A, 9 C, 10 G, 3 T, 0 other;

Query Match 92.5%; Score 14.8; DB 25; Length 29;
 Best Local Similarity 87.5%; Pred. No. 93;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGGCHACACGA 16
 Db 7 AGGCTAGGCTACACGA 22

RESULT 27
 ABX13990
 ID ABX13990 standard; DNA; 29 BP.

AC ABX13990;

DT 25-FEB-2003 (first entry)

DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1641.

KM Catalytic DNA; catalytic RNA; hairless protein; ss;

KM hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;

KM ribozyme; DNazyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;

KM catalytic core; cleavage site; pharmaceutical; hair production;

KM hair follicle; anagen phase; catagen phase; hair removal product;

KM depilatory.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT misc_feature 8..22

FT /*tag= a

FT /note= "Catalytic domain"

XX WO200283891-A2.

XX 24-OCT-2002.

XX 12-APR-2002; 2002WO-US11683.

XX 13-APR-2001; 2001US-283618P.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Christiano AM;

XX WPI; 2003-093020/08.

XX New catalytic nucleic acid molecule that specifically cleaves Hairless
 PT protein mRNA, useful for inhibiting hair production by a hair-producing
 PT cell, or for inhibiting transition of a hair follicle from anagen phase
 PT to catagen phase
 XX Claim 3; Page 34; 65pp; English.

CC The invention discloses a new catalytic DNA or RNA molecule that
 CC specifically cleaves, or inhibits expression of, Hairless protein mRNA
 CC which comprises a catalytic domain that cleaves mRNA at a defined
 CC consensus sequence and binding domains contiguous with the 5' and 3' ends
 CC of the catalytic domain. Lack of expression of the hairless gene due to
 CC inherited mutations leads to the complete loss of hair, known as
 CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting
 CC the genes promoting hair growth, and one way to get targeted, transient
 CC gene suppression is through the use of catalytic nucleic acid technology,
 CC including ribozymes and DNazymes. Ribozymes are RNA structures which have
 CC a self-catalytic enzymatic function and sequence specific RNA binding
 CC ability. Small DNA oligonucleotides that have a similar structure to the
 CC hammerhead ribozyme, called deoxy-ribozymes or DNazymes, having a
 CC catalytic core and two sequence specific arms. The deoxy-ribozymes have
 CC more lenient consensus cleavage site requirements and are less likely to
 CC degrade, *in vivo*, that hammerhead ribozymes. The catalytic nucleic acids
 CC are useful in pharmaceutical compositions for inhibiting hair production
 CC by a hair-producing cell, for inhibiting hair growth and for inhibiting
 CC the transition of a hair follicle from the anagen phase to the catagen
 CC phase. A non-human transgenic mammal is useful as a model for testing
 CC hair removal products which function by inhibiting hairless protein
 CC expression. The sequence presented is the deoxy-ribozyme that cleaves the
 CC human hairless protein mRNA immediately after nucleotide 1641.

CC Sequence 29 BP, 7 A, 11 C, 7 G, 4 T, 0 other;

Query Match 92.5%; Score 14.8; DB 25; Length 29;
 Best Local Similarity 87.5%; Pred. No. 93;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGGCHACACGA 16
 Db 7 AGGCTAGGCTACACGA 22

RESULT 28
 ABX13991

ID ABX13991 standard; DNA; 29 BP.

AC ABX13991;

DT 25-FEB-2003 (first entry)

DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1698.

KM Catalytic DNA; catalytic RNA; hairless protein; ss;

KM hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;

KM ribozyme; DNazyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;

KM catalytic core; cleavage site; pharmaceutical; hair production;

KM hair follicle; anagen phase; catagen phase; hair removal product;

KM depilatory.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT misc_feature 8..22

FT /*tag= a

FT /note= "Catalytic domain"

XX WO200283891-A2.

XX 24-OCT-2002.

XX 12-APR-2002; 2002WO-US11683.

```

XX PR 13-APR-2001; 2001US-283618P.
XX PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX PI Cristiano AM;
XX DR WPI; 2003-093020/08.
XX
XX PT New catalytic nucleic acid molecule that specifically cleaves Hairless
XX PT Protein mRNA, useful for inhibiting hair production by a hair-producing
XX PT cell, or for inhibiting transition of a hair follicle from anagen phase
XX PT to catagen phase
XX
XX PS Claim 3; Page 34; 65pp; English.
XX
XX CC The invention discloses a new catalytic DNA or RNA molecule that
XX CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA
XX CC which comprises a catalytic domain that cleaves mRNA at a defined
XX CC consensus sequence and binding domains contiguous with the 5' and 3' ends
XX CC of the catalytic domain. Lack of expression of the hairless gene due to
XX CC inherited mutations leads to the complete loss of hair, known as
XX CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting
XX CC the genes promoting hair growth, and one way to get targeted, transient
XX CC gene suppression is through the use of catalytic nucleic acid technology,
XX CC including ribozymes and DNazymes. Ribozymes are RNA structures which have
XX CC a self-catalytic enzymatic function and sequence specific RNA binding
XX CC ability. Small DNA oligonucleotides that have a similar structure to the
XX CC hammerhead ribozyme, called deoxy-ribozymes or DNazymes, having a
XX CC catalytic core and two sequence specific arms. The deoxy-ribozymes have
XX CC more lenient consensus cleavage site requirements and are less likely to
XX CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids
XX CC are useful in pharmaceutical compositions for inhibiting hair production
XX CC by a hair-producing cell, for inhibiting hair growth and for inhibiting
XX CC the transition of a hair follicle from the anagen phase to the catagen
XX CC phase. A non-human transgenic mammal is useful as a model for testing
XX CC hair removal products which function by inhibiting hairless protein
XX CC expression. The sequence presented is the deoxy-ribozyme that cleaves the
XX CC human hairless protein mRNA immediately after nucleotide 1698.
XX
XX SQ Sequence 29 BP; 7 A; 7 C; 10 G; 5 T; 0 other;
XX
XX Query Match 92.5%; Score 14.8; DB 25; Length 29;
XX Best Local Similarity 87.5%; Pred. No. 93;
XX Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 RGGCTAGCHACACGA 16
Db 7 AGGCTAGCTACACGA 22
XX
XX RESULT 29
XX ABX13992
XX ID ABX13992 standard; DNA; 29 BP.
XX AC ABX13992;
XX XX
XX DT 25-FEB-2003 (first entry)
XX
XX DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1732.
XX
XX KW Catalytic DNA; catalytic RNA; hairless protein; ss;
XX KW hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;
XX KW ribozyme; DNazyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;
XX KW catalytic core; cleavage site; pharmaceutical; hair production;
XX KW hair follicle; anagen phase; catagen phase; hair removal product;
XX KW depilatory.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX misc_feature 8..22

```

```

FT FT /*tag= a
FT FT /note= "Catalytic domain"
XX XX
XX XX W0200283891-A2.
XX XX
XX XX 24-OCT-2002.
XX XX
XX XX 12-APR-2002; 2002WO-US11663.
XX XX
XX XX 13-APR-2001; 2001US-283618P.
XX XX
XX XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX XX
XX PI Cristiano AM;
XX XX
XX DR WPI; 2003-093020/08.
XX
XX PT New catalytic nucleic acid molecule that specifically cleaves Hairless
XX PT Protein mRNA, useful for inhibiting hair production by a hair-producing
XX PT cell, or for inhibiting transition of a hair follicle from anagen phase
XX PT to catagen phase
XX
XX PS Claim 3; Page 34; 65pp; English.
XX
XX CC The invention discloses a new catalytic DNA or RNA molecule that
XX CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA
XX CC which comprises a catalytic domain that cleaves mRNA at a defined
XX CC consensus sequence and binding domains contiguous with the 5' and 3' ends
XX CC of the catalytic domain. Lack of expression of the hairless gene due to
XX CC inherited mutations leads to the complete loss of hair, known as
XX CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting
XX CC the genes promoting hair growth, and one way to get targeted, transient
XX CC gene suppression is through the use of catalytic nucleic acid technology,
XX CC including ribozymes and DNazymes. Ribozymes are RNA structures which have
XX CC a self-catalytic enzymatic function and sequence specific RNA binding
XX CC ability. Small DNA oligonucleotides that have a similar structure to the
XX CC hammerhead ribozyme, called deoxy-ribozymes or DNazymes, having a
XX CC catalytic core and two sequence specific arms. The deoxy-ribozymes have
XX CC more lenient consensus cleavage site requirements and are less likely to
XX CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids
XX CC are useful in pharmaceutical compositions for inhibiting hair production
XX CC by a hair-producing cell, for inhibiting hair growth and for inhibiting
XX CC the transition of a hair follicle from the anagen phase to the catagen
XX CC phase. A non-human transgenic mammal is useful as a model for testing
XX CC hair removal products which function by inhibiting hairless protein
XX CC expression. The sequence presented is the deoxy-ribozyme that cleaves the
XX CC human hairless protein mRNA immediately after nucleotide 1732.
XX
XX SQ Sequence 29 BP; 6 A; 10 C; 8 G; 5 T; 0 other;
XX
XX Query Match 92.5%; Score 14.8; DB 25; Length 29;
XX Best Local Similarity 87.5%; Pred. No. 93;
XX Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 RGGCTAGCHACACGA 16
Db 7 AGGCTAGCTACACGA 22
XX
XX RESULT 30
XX ABX13993
XX ID ABX13993 standard; DNA; 29 BP.
XX AC ABX13993;
XX XX
XX DT 25-FEB-2003 (first entry)
XX
XX DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1750.
XX
XX KW Catalytic DNA; catalytic RNA; hairless protein; ss;
XX KW hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;
XX KW ribozyme; DNazyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;
XX KW catalytic core; cleavage site; pharmaceutical; hair production;
XX KW

```

KW	hair follicle; anagen phase; catagen phase; hair removal product;
KW	depilatory.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Key
FT	misc_feature
FT	8..22
FT	/tag=^
XX	/note= "Catalytic domain"
PN	
MO	WO200283891-A2.
XX	
PD	24-OCT-2002.
XX	
PF	12-APR-2002; 2002WO-US11683.
XX	
PR	13-APR-2001; 2001US-283618P.
XX	
PA	(UYCO) UNIV COLUMBIA NEW YORK.
XX	
PI	Christiano AM;
XX	
DR	WPI; 2003-093020/08.
XX	
PT	New catalytic nucleic acid molecule that specifically cleaves Hairless
PT	Protein mRNA, useful for inhibiting hair production by a hair-producing
PT	cell, or for inhibiting transition of a hair follicle from anagen phase
PT	to catagen phase -
XX	
PS	Claim 3; Page 34; 65pp; English.

The invention discloses a new catalytic DNA or RNA molecule that specifically cleaves, or inhibits expression of, hairless protein mRNA which comprises a catalytic domain that cleaves mRNA at a defined consensus sequence and binding domains continuous with the 5' and 3' ends of the catalytic domain. Lack of expression of the hairless gene due to inherited mutations leads to the complete loss of hair, known as atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting the genes promoting hair growth, and one way to get targeted, transient gene suppression is through the use of catalytic nucleic acid technology, including ribozymes and DNAzymes. Ribozymes are RNA structures which have a self-catalytic enzymatic function and sequence specific RNA binding ability. Small DNA oligonucleotides that have a similar structure to the hammerhead ribozyme, called deoxy-ribozymes or DNAzymes, having a catalytic core and two sequence specific arms. The deoxy-ribozymes have more lenient consensus cleavage site requirements and are less likely to degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids are useful in pharmaceutical compositions for inhibiting hair production by a hair-producing cell, for inhibiting hair growth and for inhibiting the transition of a hair follicle from the anagen phase to the catagen phase. A non-human transgenic mammal is useful as a model for testing hair removal products which function by inhibiting hairless protein expression. The sequence presented is the deoxy-ribozyme that cleaves the human hairless protein mRNA immediately after nucleotide 1750.

```

Query Match          92.5%;   Score 14.8;   DB 25;   Length 29;
Best Local Similarity 87.5%;   Pred. No. 9;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGGCTAGCHACAACGA 16
       : ||||| : |||||
       7 GGGCTAGGCTACAACGA 22
       : ||||| : |||||
       db      7 GGGCTAGGCTACAACGA 22
       : ||||| : |||||

```

RESULT 31	
ABX13994	
ID	ABX13994 standard; DNA; 29 BP.
XX	
AC	ABX13994;
XX	

DJ		25-FEB-2003	(first entry)
DE	XX	Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1801.	
KM	XX	Catalytic DNA; catalytic RNA; hairless protein; ss;	
KW	XX	hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;	
KV	XX	ribozyme; DNazymes; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;	
KW	XX	catalytic core; cleavage site; pharmaceutical; hair production;	
KW	XX	hair follicle; anagen phase; catagen phase; hair removal product;	
KL	XX	deplatory.	
OS	XX	Homo sapiens.	
OS	XX	Synthetic.	
FH	XX	Location/Qualifiers	
FT	XX	Key	misc_feature
FT	XX	8..22	/+tag= a
FT	XX	"Catalytic domain"	/note= "Catalytic domain"
PN	XX	WO200283691-A2.	
PD	XX	24-OCT-2002.	
PF	XX	12-APR-2002; 2002MO-US11683.	
PR	XX	13-APR-2001; 2001US-283618P.	
PA	XX	(UYCO) UNIV COLUMBIA NEW YORK.	
PI	XX	Christiano AM;	
DX	XX	WFI; 2003-093020/08.	
PT	XX	New catalytic nucleic acid molecule that specifically cleaves Hairless	
PT	XX	protein mRNA, useful for inhibiting hair production by a hair-producing	
PT	XX	cell, or for inhibiting transition of a hair follicle from anagen phase	
PT	XX	to catagen phase -	
PS	XX	Claim 3; Page 34; 65pp; English.	
CC	XX	The invention discloses a new catalytic DNA or RNA molecule that	
CC	XX	specifically cleaves, or inhibits expression of, Hairless Protein mRNA	
CC	XX	which comprises a catalytic domain that cleaves mRNA at a defined	
CC	XX	consensus sequence and binding domains contiguous with the 5' and 3' ends	
CC	XX	of the catalytic domain. Lack of expression of the hairless gene due to	
CC	XX	inherited mutations leads to the complete loss of hair, known as	
CC	XX	atrachia. Abundant hair growth, hirsutism, can be improved by inhibiting	
CC	XX	the genes promoting hair growth, and one way to get targeted, transint	
CC	XX	gene suppression is through the use of catalytic nucleic acid technology,	
CC	XX	including ribozymes and DNazymes. Ribozymes are RNA structures which have	
CC	XX	a self-catalytic enzymatic function and sequence specific RNA binding	
CC	XX	ability. Small DNA oligonucleotides that have a similar structure to the	
CC	XX	hammerhead ribozyme, called deoxy-ribozymes or DNazymes, having a	
CC	XX	catalytic core and two sequence specific arms. The deoxy-ribozymes have	
CC	XX	more lenient consensus cleavage site requirements and are less likely to	
CC	XX	degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids	
CC	XX	are useful in pharmaceutical compositions for inhibiting hair production	
CC	XX	by a hair-producing cell, for inhibiting hair growth and for inhibiting	
CC	XX	the transition of a hair follicle from the anagen phase to the catagen	
CC	XX	phase. A non-human transgenic mammal is useful as a model for testing	
CC	XX	hair removal products which function by inhibiting hairless protein	
CC	XX	expression. The sequence presented is the deoxy-ribozyme that cleaves the	
CC	XX	human hairless protein mRNA immediately after nucleotide 1801.	
SQ	XX	Sequence 29 BP; 9 A; 6 G; 11 C; 3 T; 0 other;	
Query Match		92.5%; Score 14.8; DB 25; Length 29;	
Best Local Similarity		87.5%; Pred. No. 93;	
Matches 14; Conservative		2; Mismatches 0; Indels 0; Gaps 0	
GZ		1 RGGCTAGCHACAAACA 16	
:		: :	
DB		7 AGGCTAGCTTCAACGA 22	

PS Claim 3, Page 34, 65pp; English.

XX
XX
XX The invention discloses a new catalytic DNA or RNA molecule that
CC specifically cleaves, or inhibits expression of, Hairless protein mRNA
CC which comprises a catalytic domain that cleaves mRNA at the defined
CC consensus sequence and binding domains contiguous with the 5' and 3' ends
CC of the catalytic domain. Lack of expression of the hairless gene due to
CC inherited mutations leads to the complete loss of hair, known as
CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting
CC the genes promoting hair growth, and one way to get targeted, transient
CC gene suppression is through the use of catalytic nucleic acid technology,
CC including ribozymes and DNAzymes. Ribozymes are RNA structures which have
CC a self-catalytic enzymatic function and sequence specific RNA binding
CC ability. Small DNA oligonucleotides that have a similar structure to the
CC hammerhead ribozyme, called deoxy-ribozymes or DNAzymes, having a
CC catalytic core and two sequence specific arms. The deoxy-ribozymes have
CC more lenient consensus cleavage site requirements and are less likely to
CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids
CC are useful in pharmaceutical compositions for inhibiting hair production
CC by a hair-producing cell, for inhibiting hair growth and for inhibiting
CC the transition of a hair follicle from the anagen phase to the catagen
CC phase. A non-human transgenic mammal is useful as a model for testing
CC hair removal products which function by inhibiting hairless protein
CC expression. The sequence presented is the deoxy-ribozyme that cleaves the
CC human hairless protein mRNA immediately after nucleotide 1801.

XX
XX
XX Sequence 29 BP; 9 A; 6 C; 11 G; 3 T; 0 other;

```

Query Match      92.5%; Score 14.8; DB 25; Length 29;
Best Local Similarity 87.5%; Pred. No. 93;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps
OY      1 RGGCTAGCHACAAACA 16
      :|||||:|||||
db       7 AGGCTAGCTACAAACA 22

```

RESULT 32
ABX13995
ID ABX13995 standard; DNA; 29 BP.
XX
AC ABX13995;
XX
XX 25-FEB-2003 (first entry)
XX
XX Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1811.
XX
XX Catalytic DNA; catalytic RNA; hairless protein; ss;
KW hair loss; atichia; hair growth; hirsutism; catalytic nucleic acid;
KW ribozyme; DNzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;
KW catalytic core; cleavage site; pharmaceutical; hair production;
KW hair follicle; anagen phase; catagen phase; hair removal product;
KW deplatory.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH misc_feature 8..22
FT /tag= a
FT /note= "Catalytic domain"
XX
XX WO200283891-A2.
XX
XX 24-OCT-2002.
XX
XX 12-APR-2002; 2002WO-US11683.
XX
XX 13-APR-2001; 2001US-283618P.
XX
XX (UNCO) UNIV COLUMBIA NEW YORK.
XX
XX Cristiano AM;
XX
XX WPI; 2003-093020/08.
XX
XX New catalytic nucleic acid molecule that specifically cleaves Hairless
XX Protein mRNA, useful for inhibiting hair production by a hair-producing
XX cell, or for inhibiting transition of a hair follicle from anagen phase
XX to catagen phase -
XX
XX Claim 3; Page 35; 65pp; English.
XX
XX The invention discloses a new catalytic DNA or RNA molecule that
XX specifically cleaves, or inhibits expression of, Hairless Protein mRNA
XX which comprises a catalytic domain that cleaves mRNA at a defined
XX consensus sequence and binding domains contiguous with the 5' and 3' ends
XX of the catalytic domain. Lack of expression of the hairless gene due to
XX inherited mutations leads to the complete loss of hair, known as
XX atichia. Abundant hair growth, hirsutism, can be improved by inhibiting
XX the genes promoting hair growth, and one way to get targeted, transient
XX gene suppression is through the use of catalytic nucleic acid technology,
XX including ribozymes and DNzymes. Ribozymes are RNA structures which have
XX a self-catalytic enzymatic function and sequence specific RNA binding
XX ability. Small DNA oligonucleotides that have a similar structure to the
XX hammerhead ribozyme, called deoxy-ribozymes or DNzymes, having a
XX catalytic core and two sequence specific arms. The deoxy-ribozymes have
XX more lenient consensus cleavage site requirements and are less likely to
XX degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids
XX are useful in pharmaceutical compositions for inhibiting hair production
XX by a hair-producing cell, for inhibiting hair growth and for inhibiting
XX the transition of a hair follicle from the anagen phase to the catagen
XX phase. A non-human transgenic mammal is useful as a model for testing
XX hair removal products which function by inhibiting hairless protein
XX expression. The sequence presented is the deoxy-ribozyme that cleaves the
XX human hairless protein mRNA immediately after nucleotide 1811.
XX
XX Sequence 29 BP; 9 A; 9 C; 9 G; 2 T; 0 other;

Query Match 92.5%; Score 14.8; DB 25; Length 29;
Best Local Similarity 87.5%; Pred. No. 93;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RGGCTAGCGACACGA 16
:|||||:
Db 7 AGGCTAGCTACACGA 22
RESULT 33
ABX13996
ID ABX13996 standard; DNA; 29 BP.
XX
AC ABX13996;
XX
XX 25-FEB-2003 (first entry)
XX
XX Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 2028.
XX
XX Catalytic DNA; catalytic RNA; hairless protein; ss;
KW hair loss; atichia; hair growth; hirsutism; catalytic nucleic acid;
KW ribozyme; DNzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;
KW catalytic core; cleavage site; pharmaceutical; hair production;
KW hair follicle; anagen phase; catagen phase; hair removal product;
KW deplatory.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH misc_feature 8..22
FT /tag= a
FT /note= "Catalytic domain"
XX
XX WO200283891-A2.
XX
XX 24-OCT-2002.
XX
XX 12-APR-2002; 2002WO-US11683.
XX
XX 13-APR-2001; 2001US-283618P.
XX
XX (UNCO) UNIV COLUMBIA NEW YORK.
XX
XX Cristiano AM;
XX
XX WPI; 2003-093020/08.
XX
XX New catalytic nucleic acid molecule that specifically cleaves Hairless
XX Protein mRNA, useful for inhibiting hair production by a hair-producing
XX cell, or for inhibiting transition of a hair follicle from anagen phase
XX to catagen phase -
XX
XX Claim 3; Page 35; 65pp; English.
XX
XX The invention discloses a new catalytic DNA or RNA molecule that
XX specifically cleaves, or inhibits expression of, Hairless Protein mRNA
XX which comprises a catalytic domain that cleaves mRNA at a defined
XX consensus sequence and binding domains contiguous with the 5' and 3' ends
XX of the catalytic domain. Lack of expression of the hairless gene due to
XX inherited mutations leads to the complete loss of hair, known as
XX atichia. Abundant hair growth, hirsutism, can be improved by inhibiting
XX the genes promoting hair growth, and one way to get targeted, transient
XX gene suppression is through the use of catalytic nucleic acid technology,
XX including ribozymes and DNzymes. Ribozymes are RNA structures which have
XX a self-catalytic enzymatic function and sequence specific RNA binding
XX ability. Small DNA oligonucleotides that have a similar structure to the
XX hammerhead ribozyme, called deoxy-ribozymes or DNzymes, having a
XX catalytic core and two sequence specific arms. The deoxy-ribozymes have
XX more lenient consensus cleavage site requirements and are less likely to
XX degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids
XX are useful in pharmaceutical compositions for inhibiting hair production

CC by a hair-producing cell, for inhibiting hair growth and for inhibiting
CC the transition of a hair follicle from the anagen phase to the catagen
CC phase. A non-human transgenic mammal is useful as a model for testing
CC hair removal products which function by inhibiting hairless protein
CC expression. The sequence presented is the deoxy-ribozyme that cleaves the
CC human hairless protein mRNA immediately after nucleotide 2028.
CC
XX
SQ Sequence 29 BP; 6 A; 7 C; 13 G; 3 T; 0 other;
Query Match 92.5%; Score 14.8; DB 25; Length 29;
Best Local Similarity 87.5%; Pred. No. 93;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RGCGTAGCHACACGA 16
Db 7 GGCTAGCTACACGA 22
RESULT 34
ID ABX13997 standard; DNA; 29 BP.
AC ABX13997;
XX
XX 25-FEB-2003 (first entry)
DT
XX
XX Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 2033.
DE
XX
XX Catalytic DNA; catalytic RNA; hairless protein; ss;
KM hair loss; atichia; hair growth; hirsutism; catalytic nucleic acid;
KM ribozyme; DNazyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;
KM catalytic core; cleavage site; pharmaceutical; hair production;
KM hair follicle; anagen phase; catagen phase; hair removal product;
KM depilatory.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH 8..22
FT misc_feature /tag= a
FT /note= "Catalytic domain"
FT
XX
XX WO200283891-A2.
XX
XX 24-OCT-2002.
XX
XX 12-APR-2002; 2002WO-US11683.
XX
XX 13-APR-2001; 2001US-283618P.
XX
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX Christiano AM;
XX
XX MPI; 2003-093020/08.
XX
XX
XX New catalytic nucleic acid molecule that specifically cleaves Hairless
XX Protein mRNA, useful for inhibiting hair production by a hair-producing
XX cell, or for inhibiting transition of a hair follicle from anagen phase
XX to catagen phase -
XX
XX Claim 3; Page 35; 65pp; English.
XX
XX The invention discloses a new catalytic DNA or RNA molecule that
XX specifically cleaves, or inhibits expression of, Hairless Protein mRNA
XX which comprises a catalytic domain that cleaves mRNA at a defined
XX consensus sequence and binding domains contiguous with the 5' and 3' ends
XX of the catalytic domain. Lack of expression of the hairless gene due to
XX inherited mutations leads to the complete loss of hair, known as
XX atichia. Abundant hair growth, hirsutism, can be improved by inhibiting
XX the genes promoting hair growth, and one way to get targeted, transient
XX gene suppression is through the use of catalytic nucleic acid technology.

CC including ribozymes and DNazymes. Ribozymes are RNA structures which have
CC a self-catalytic enzymatic function and sequence specific RNA binding
CC ability. Small DNA oligonucleotides that have a similar structure to the
CC hammerhead ribozyme, called deoxy-ribozymes or DNazymes, having a
CC catalytic core and two sequence specific arms. The deoxy-ribozymes have
CC more lenient consensus cleavage site requirements and are less likely to
CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids
CC are useful in pharmaceutical compositions for inhibiting hair production
CC by a hair-producing cell, for inhibiting hair growth and for inhibiting
CC the transition of a hair follicle from the anagen phase to the catagen
CC phase. A non-human transgenic mammal is useful as a model for testing
CC hair removal products which function by inhibiting hairless protein
CC expression. The sequence presented is the deoxy-ribozyme that cleaves the
CC human hairless protein mRNA immediately after nucleotide 2033.
CC
XX
SQ Sequence 29 BP; 7 A; 5 C; 13 G; 4 T; 0 other;
Query Match 92.5%; Score 14.8; DB 25; Length 29;
Best Local Similarity 87.5%; Pred. No. 93;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RGCGTAGCHACACGA 16
Db 7 GGCTAGCTACACGA 22
RESULT 35
ID ABX13998 standard; DNA; 29 BP.
AC ABX13998;
XX
XX 25-FEB-2003 (first entry)
DT
XX
XX Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 2047.
DE
XX
XX Catalytic DNA; catalytic RNA; hairless protein; ss;
KM hair loss; atichia; hair growth; hirsutism; catalytic nucleic acid;
KM ribozyme; DNazyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;
KM catalytic core; cleavage site; pharmaceutical; hair production;
KM hair follicle; anagen phase; catagen phase; hair removal product;
KM depilatory.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH 8..22
FT misc_feature /tag= a
FT /note= "Catalytic domain"
FT
XX
XX WO200283891-A2.
XX
XX 24-OCT-2002.
XX
XX 12-APR-2002; 2002WO-US11683.
XX
XX 13-APR-2001; 2001US-283618P.
XX
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX Christiano AM;
XX
XX MPI; 2003-093020/08.
XX
XX
XX New catalytic nucleic acid molecule that specifically cleaves Hairless
XX Protein mRNA, useful for inhibiting hair production by a hair-producing
XX cell, or for inhibiting transition of a hair follicle from anagen phase
XX to catagen phase -
XX
XX Claim 3; Page 35; 65pp; English.
XX
XX The invention discloses a new catalytic DNA or RNA molecule that

CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA
 CC which comprises a catalytic domain that cleaves mRNA at a defined
 CC consensus sequence and binding domains contiguous with the 5' and 3' ends
 CC of the catalytic domain. Lack of expression of the hairless gene due to
 CC inherited mutations leads to the complete loss of hair, known as
 CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting
 CC the genes promoting hair growth, and one way to get targeted, transient
 CC gene suppression is through the use of catalytic nucleic acid technology,
 CC including ribozymes and DNAzymes. Ribozymes are RNA structures which have
 CC a self-catalytic enzymatic function and sequence specific RNA binding
 CC ability. Small DNA oligonucleotides that have a similar structure to the
 CC hammerhead ribozyme, called deoxy-ribozymes or DNAzymes, having a
 CC catalytic core and two sequence specific arms. The deoxy-ribozymes have
 CC more lenient consensus cleavage site requirements and are less likely to
 CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids
 CC are useful in pharmaceutical compositions for inhibiting hair production
 CC by a hair-producing cell, for inhibiting hair growth and for inhibiting
 CC the transition of a hair follicle from the anagen phase to the catagen
 CC phase. A non-human transgenic mammal is useful as a model for testing
 CC hair removal products which function by inhibiting hairless protein
 CC expression. The sequence presented is the deoxy-ribozyme that cleaves the
 CC human hairless protein mRNA immediately after nucleotide 2047.
 CC
 SQ Sequence 29 BP; 9 A; 10 C; 7 G; 3 T; 0 other;

Query Match 92.5%; Score 14.8; DB 25; Length 29;
 Best Local Similarity 87.5%; Pred. No. 93;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16
 :|||||:|||||
 Db 7 GGCTAGCTACACGA 22

RESULT 36
 ABX13999
 ID ABX13999 standard; DNA; 29 BP.

AC ABX13999;

DT 25-FEB-2003 (first entry)

DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 2083.

KW Catalytic DNA; catalytic RNA; hairless protein; ss;
 KW hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;
 KW ribozyme; DNAzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;
 KW catalytic core; cleavage site; pharmaceutical; hair production;
 KW hair follicle; anagen phase; catagen phase; hair removal product;
 KW depilatory.

OS Homo sapiens.
 OS Synthetic.

XX
 XX
 FT Key Location/Qualifiers
 FT misc_feature 8..22
 FT /*tag= a
 FT /note= "Catalytic domain"

PN WO200283891-A2.

PD 24-OCT-2002.

XX 12-APR-2002; 2002WO-US11683.

XX 13-APR-2001; 2001US-283618P.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Christiano AM;

XX PI
 XX DR WPI, 2003-093020/08.

PT New catalytic nucleic acid molecule that specifically cleaves Hairless
 PT Protein mRNA, useful for inhibiting hair production by a hair-producing
 PT cell, or for inhibiting transition of a hair follicle from anagen phase
 PT to catagen phase
 PT
 XX
 PS Claim 3; Page 35; 65pp; English.

CC The invention discloses a new catalytic DNA or RNA molecule that
 CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA
 CC which comprises a catalytic domain that cleaves mRNA at a defined
 CC consensus sequence and binding domains contiguous with the 5' and 3' ends
 CC of the catalytic domain. Lack of expression of the hairless gene due to
 CC inherited mutations leads to the complete loss of hair, known as
 CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting
 CC the genes promoting hair growth, and one way to get targeted, transient
 CC gene suppression is through the use of catalytic nucleic acid technology,
 CC including ribozymes and DNAzymes. Ribozymes are RNA structures which have
 CC a self-catalytic enzymatic function and sequence specific RNA binding
 CC ability. Small DNA oligonucleotides that have a similar structure to the
 CC hammerhead ribozyme, called deoxy-ribozymes or DNAzymes, having a
 CC catalytic core and two sequence specific arms. The deoxy-ribozymes have
 CC more lenient consensus cleavage site requirements and are less likely to
 CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids
 CC are useful in pharmaceutical compositions for inhibiting hair production
 CC by a hair-producing cell, for inhibiting hair growth and for inhibiting
 CC the transition of a hair follicle from the anagen phase to the catagen
 CC phase. A non-human transgenic mammal is useful as a model for testing
 CC hair removal products which function by inhibiting hairless protein
 CC expression. The sequence presented is the deoxy-ribozyme that cleaves the
 CC human hairless protein mRNA immediately after nucleotide 2083.
 CC
 SQ Sequence 29 BP; 9 A; 7 C; 9 G; 4 T; 0 other;

Query Match 92.5%; Score 14.8; DB 25; Length 29;
 Best Local Similarity 87.5%; Pred. No. 93;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCHACACGA 16
 :|||||:|||||
 Db 7 GGCTAGCTACACGA 22

RESULT 37
 ABX14001
 ID ABX14001 standard; DNA; 29 BP.

AC ABX14001;

DT 25-FEB-2003 (first entry)

DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 2380.

KW Catalytic DNA; catalytic RNA; hairless protein; ss;
 KW hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;
 KW ribozyme; DNAzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;
 KW catalytic core; cleavage site; pharmaceutical; hair production;
 KW hair follicle; anagen phase; catagen phase; hair removal product;
 KW depilatory.

OS Homo sapiens.
 OS Synthetic.

XX
 XX
 FT Key Location/Qualifiers
 FT misc_feature 8..22
 FT /*tag= a
 FT /note= "Catalytic domain"

PN WO200283891-A2.

PD 24-OCT-2002.

XX 12-APR-2002; 2002WO-US11683.

PR 13-APR-2001; 2001US-283618P.
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 PA
 XX
 XX
 PI Cristiano AM;
 XX
 DR WPI; 2003-093020/08.
 XX
 XX New catalytic nucleic acid molecule that specifically cleaves Hairless
 PT Protein mRNA, useful for inhibiting hair production by a hair-producing
 PT cell, or for inhibiting transition of a hair follicle from anagen phase
 PT to catagen phase -
 XX
 PS Claim 3; Page 35; 65pp; English.
 XX
 XX The invention discloses a new catalytic DNA or RNA molecule that
 CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA
 CC which comprises a catalytic domain that cleaves mRNA at a defined
 CC consensus sequence and binding domains contiguous with the 5' and 3' ends
 CC of the catalytic domain. Lack of expression of the hairless gene due to
 CC inherited mutations leads to the complete loss of hair, known as
 CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting
 CC the genes promoting hair growth, and one way to get targeted, transient
 CC gene suppression is through the use of catalytic nucleic acid technology,
 CC including ribozymes and DNazymes. Ribozymes are RNA structures which have
 CC a self-catalytic enzymatic function and sequence specific RNA binding
 CC ability. Small DNA oligonucleotides that have a similar structure to the
 CC hammerhead ribozyme, called deoxy-ribozymes or DNazymes, having a
 CC catalytic core and two sequence specific arms. The deoxy-ribozymes have
 CC more lenient consensus cleavage site requirements and are less likely to
 CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids
 CC are useful in pharmaceutical compositions for inhibiting hair production
 CC by a hair-producing cell, for inhibiting hair growth and for inhibiting
 CC the transition of a hair follicle from the anagen phase to the catagen
 CC phase. A non-human transgenic mammal is useful as a model for testing
 CC hair removal products which function by inhibiting hairless protein
 CC expression. The sequence presented is the deoxy-ribozyme that cleaves the
 CC human hairless protein mRNA immediately after nucleotide 2380.
 XX
 XX Sequence 29 BP; 6 A; 10 C; 8 G; 5 T; 0 other;
 SQ
 Query Match 92.5%; Score 14.8; DB 25; Length 29;
 Best Local Similarity 87.5%; Pred. No. 93;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGGCTAGCHCAACGA 16
 :|||||:|||||
 7 AGGCTAGCTACACGA 22
 DB
 RESULT 38
 ABX14002 standard; DNA; 29 BP.
 XX
 AC ABX14002;
 XX
 DT 25-FEB-2003 (first entry)
 XX
 DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 2395.
 XX
 XX Catalytic DNA; catalytic RNA; hairless protein; ss;
 KW hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;
 KW ribozyme; DNazyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;
 KW catalytic core; cleavage site; pharmaceutical; hair production;
 KW hair follicle; anagen phase; catagen phase; hair removal product;
 KW depilatory.
 XX
 XX Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH misc_feature 8..22
 FT
 FT *tag= a

FT /note= "Catalytic domain"
 XX
 XX WO200283891-A2.
 XX
 XX PD 24-OCT-2002.
 XX
 XX PF 12-APR-2002; 2002WO-US11683.
 XX
 XX PR 13-APR-2001; 2001US-283618P.
 XX
 XX PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 XX PI Cristiano AM;
 XX
 XX WPI; 2003-093020/08.
 DR
 XX
 XX New catalytic nucleic acid molecule that specifically cleaves Hairless
 PT Protein mRNA, useful for inhibiting hair production by a hair-producing
 PT cell, or for inhibiting transition of a hair follicle from anagen phase
 PT to catagen phase -
 XX
 PS Claim 3; Page 35; 65pp; English.
 XX
 XX The invention discloses a new catalytic DNA or RNA molecule that
 CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA
 CC which comprises a catalytic domain that cleaves mRNA at a defined
 CC consensus sequence and binding domains contiguous with the 5' and 3' ends
 CC of the catalytic domain. Lack of expression of the hairless gene due to
 CC inherited mutations leads to the complete loss of hair, known as
 CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting
 CC the genes promoting hair growth, and one way to get targeted, transient
 CC gene suppression is through the use of catalytic nucleic acid technology,
 CC including ribozymes and DNazymes. Ribozymes are RNA structures which have
 CC a self-catalytic enzymatic function and sequence specific RNA binding
 CC ability. Small DNA oligonucleotides that have a similar structure to the
 CC hammerhead ribozyme, called deoxy-ribozymes or DNazymes, having a
 CC catalytic core and two sequence specific arms. The deoxy-ribozymes have
 CC more lenient consensus cleavage site requirements and are less likely to
 CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids
 CC are useful in pharmaceutical compositions for inhibiting hair production
 CC by a hair-producing cell, for inhibiting hair growth and for inhibiting
 CC the transition of a hair follicle from the anagen phase to the catagen
 CC phase. A non-human transgenic mammal is useful as a model for testing
 CC hair removal products which function by inhibiting hairless protein
 CC expression. The sequence presented is the deoxy-ribozyme that cleaves the
 CC human hairless protein mRNA immediately after nucleotide 2395.
 XX
 XX Sequence 29 BP; 9 A; 9 C; 8 G; 3 T; 0 other;
 SQ
 Query Match 92.5%; Score 14.8; DB 25; Length 29;
 Best Local Similarity 87.5%; Pred. No. 93;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGGCTAGCHCAACGA 16
 :|||||:|||||
 7 GGGCTAGCTACACGA 22
 DB
 RESULT 39
 AAA14525/c
 ID AAA14525 standard; DNA; 30 BP.
 XX
 AC AAA14525;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Oligonucleotide 5'-polym-gaglink-(pleio)-DNase-1023-B/P.
 XX
 XX Reverse transcriptase; RNase H; stem-loop structure; genetic element;
 KW inverted tandem repeat; vector; inhibitory nucleic acid;
 KW antisense sequence; aptamer; gene expression; ss.
 XX
 OS Synthetic.

XX PN WO200022114-A1.
 XX PD 20-APR-2000.
 XX PF 12-OCT-1999; 99WO-US23936.
 XX PR 09-OCT-1998; 98US-0169793.
 XX PR 16-SEP-1999; 99US-0397782.
 XX PR 04-OCT-1999; 99US-0169793.
 XX PA (INGE-) INGENE INC.
 XX PI Conrad CA;
 XX DR WPI; 2000-317974/27.
 XX PT Genetic element for producing and delivering single-stranded DNA,
 PT comprises a gene encoding reverse transcriptase and a sequence of
 PT interest flanked by an inverted tandem repeat and primer binding site
 PT -
 XX PS Disclosure; Page 45; 77pp; English.
 XX CC The specification describes methods for producing single-stranded cDNA
 CC (sscDNA) in eukaryotic cells. They use a DNA cassette that produces
 CC sscDNA in vivo. The cassette contains the Moloney murine leukemia virus
 CC reverse transcriptase/RNase H, a bacterial restriction endonuclease
 CC gene, and a sequence of interest which produces a RNA template from
 CC which the reverse transcriptase synthesizes cDNA of a specified sequence.
 CC The sscDNA is then modified to remove all flanking vector sequences by
 CC taking advantage of the stem-loop structure of the cDNA, which forms as
 CC a result of the inclusion of an inverted tandem repeat that allows the
 CC sscDNA to fold back on itself, forming a double stranded DNA stem, in
 CC the sequence of interest. The double-stranded stem contains one or more
 CC functional genetic elements (GE), adapted for incorporation into a vector
 CC for delivery to a cell. The vectors are is useful for producing a sscDNA
 CC sequence of interest, particularly a cDNA transcript, an inhibitory
 CC nucleic acid molecule which is an antisense sequence or aptamer, an mRNA
 CC transcript and a heteroduplex molecule. Inhibitory nucleic acid molecules
 CC to a target cell are useful for alleviating pathological conditions by
 CC regulating gene expression. The present oligonucleotide was used to
 CC produce a vector for use in the course of the invention.
 XX SQ Sequence 30 BP; 5 A; 8 C; 8 G; 9 T; 0 other;
 Query Match 92.5%; Score 14.8; DB 21; Length 30;
 Best Local Similarity 87.5%; Pred. No. 93;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGCTAGCHACACGA 16
 : |||||: |||||
 Db 24 AGGCTAGCTACACGA 9
 RESULT 40
 AA287648
 ID AA287648 standard; DNA; 30 BP.
 XX AC AA287648;
 XX DT 09-MAY-2000 (first entry)
 XX DE Human short protein kinase C (PKC)alpha DNA ribozyme.
 XX KW Ribozyme; hammerhead: RNAase degradation; catalytic: PKCalpha; VEGF;
 KW protein kinase C alpha; tumour necrosis factor alpha; TNFalpha; cancer;
 KW vascular epithelial growth factor; gene expression; malignant glioma;
 XX cell proliferation; cytostatic; human; ss.
 XX OS Homo sapiens.
 XX PN WO9963066-A2.

XX PD 09-DEC-1999.
 XX PF 28-MAY-1999; 99WO-GB01706.
 XX PR 01-JUN-1998; 98GB-0011750.
 XX PA (NOR-) NORWEGIAN RADIIUM HOSPITAL RES FOUND.
 XX PA (DZIE/) DZIEGLSKA H E.
 XX PI Sloud M;
 XX DR WPI; 2000-147046/13.
 XX PT Novel ribozymes, used for inhibiting the proliferation of cells, e.g.
 PT for treating or preventing cancers -
 XX PS Disclosure; Page 9; 93pp; English.
 XX CC The invention provides novel modified ribozymes that have 3 or more
 CC pyrimidine nucleotides (PMN) in the ribozyme modified at the 2'-position,
 CC where the PMNs are modified to 2'-amino PMNs and the ribozymes exhibit
 CC improved stability to RNAase degradation and exhibits 85% or more
 CC catalytic activity of the unmodified ribozymes. The ribozymes of the
 CC invention are selected from rat and human protein kinase C (PKC)alpha
 CC ribozymes, tumour necrosis factor (TNF)alpha ribozyme, rat and human
 CC vascular epithelial growth factor (VEGF) ribozymes. These ribozymes can
 CC be used for treating or preventing a disease or condition responsive to
 CC an alteration in the expression of a gene, where the ribozyme is capable
 CC of cleaving the RNA transcribed from the gene. They can be used for
 CC treating or preventing a disease or condition associated with the
 CC proliferation of rapidly dividing cells, e.g. cancer such as malignant
 CC glioma. They can also be used for inhibiting the proliferation of cells.
 CC The use of 2'-amino modified pyrimidine can provide ribozymes of improved
 CC stability which retain the activity of the unmodified ribozyme. The
 CC present sequence represents a human short PKCalpha DNA ribozyme.
 XX SQ Sequence 30 BP; 7 A; 11 C; 8 G; 4 T; 0 other;
 Query Match 92.5%; Score 14.8; DB 21; Length 30;
 Best Local Similarity 87.5%; Pred. No. 93;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGCTAGCHACACGA 16
 : |||||: |||||
 Db 8 AGGCTAGCTACACGA 23
 Search completed: January 21, 2004, 06:52:50
 Job time : 153.5 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 05:19:13 ; Search time 1004.5 Seconds
(without alignments)
651.622 Million cell updates/sec

Title: US-09-423-035B-122
Perfect score: 16
Sequence: 1 rgcctagchacaaga 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 205481386 residues
Total number of hits satisfying chosen parameters: 1520254

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_ov: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vt: *
15: em_da: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vt: *
30: em_htg_hum: *
31: em_htg_inv: *
32: em_htg_other: *
33: em_htg_mus: *
34: em_htg_pln: *
35: em_htg_rtd: *
36: em_htg_mam: *
37: em_htg_vrt: *
38: em_sy: *
39: em_htgo_hum: *
40: em_htgo_mus: *
41: em_htgo_other: *

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.8	92.5	16	6	AX036342 Sequence
2	14.8	92.5	16	6	AX223826 Sequence
3	14.8	92.5	16	6	AX229619 Sequence
4	14.8	92.5	16	6	AX274735 Sequence
5	14.8	92.5	16	6	AX282449 Sequence
6	14.8	92.5	16	6	AX427010 Sequence
7	14.8	92.5	16	6	AX583609 Sequence
8	14.8	92.5	29	6	AR201808 Sequence
9	14.8	92.5	29	6	AR201810 Sequence
10	14.8	92.5	30	6	AR201840 Sequence
11	14.8	92.5	30	6	AX009377 Sequence
12	14.8	92.5	30	6	AX111628 Sequence
13	14.8	92.5	30	6	AX274718 Sequence
14	14.8	92.5	30	6	AX274719 Sequence
15	14.8	92.5	30	6	AX274720 Sequence
16	14.8	92.5	30	6	AX274721 Sequence
17	14.8	92.5	30	6	AX274722 Sequence
18	14.8	92.5	31	6	AR116975 Sequence
19	14.8	92.5	31	6	AR201827 Sequence
20	14.8	92.5	31	6	AR201830 Sequence
21	14.8	92.5	31	6	AR201833 Sequence
22	14.8	92.5	31	6	AR201836 Sequence
23	14.8	92.5	31	6	AR204371 Sequence
24	14.8	92.5	31	6	AX220546 Sequence
25	14.8	92.5	31	6	AX220547 Sequence
26	14.8	92.5	31	6	AX220548 Sequence
27	14.8	92.5	31	6	AX220549 Sequence
28	14.8	92.5	31	6	AX220550 Sequence
29	14.8	92.5	31	6	AX220551 Sequence
30	14.8	92.5	31	6	AX220552 Sequence
31	14.8	92.5	31	6	AX220553 Sequence
32	14.8	92.5	31	6	AX220554 Sequence
33	14.8	92.5	31	6	AX220555 Sequence
34	14.8	92.5	31	6	AX220556 Sequence
35	14.8	92.5	31	6	AX220557 Sequence
36	14.8	92.5	31	6	AX220558 Sequence
37	14.8	92.5	31	6	AX220559 Sequence
38	14.8	92.5	31	6	AX220560 Sequence
39	14.8	92.5	31	6	AX220561 Sequence
40	14.8	92.5	31	6	AX220562 Sequence
41	14.8	92.5	31	6	AX220563 Sequence
42	14.8	92.5	31	6	AX220564 Sequence
43	14.8	92.5	31	6	AX220565 Sequence
44	14.8	92.5	31	6	AX220566 Sequence
45	14.8	92.5	31	6	AX220567 Sequence
46	14.8	92.5	31	6	AX220568 Sequence
47	14.8	92.5	31	6	AX220569 Sequence
48	14.8	92.5	31	6	AX220570 Sequence
49	14.8	92.5	31	6	AX220571 Sequence
50	14.8	92.5	31	6	AX220572 Sequence
51	14.8	92.5	31	6	AX220573 Sequence
52	14.8	92.5	31	6	AX220574 Sequence
53	14.8	92.5	31	6	AX220575 Sequence
54	14.8	92.5	31	6	AX220576 Sequence
55	14.8	92.5	31	6	AX220577 Sequence
56	14.8	92.5	31	6	AX220578 Sequence
57	14.8	92.5	31	6	AX220579 Sequence
58	14.8	92.5	31	6	AX220580 Sequence
59	14.8	92.5	31	6	AX220581 Sequence
60	14.8	92.5	31	6	AX220582 Sequence
61	14.8	92.5	31	6	AX220583 Sequence
62	14.8	92.5	31	6	AX220584 Sequence
63	14.8	92.5	31	6	AX220585 Sequence
64	14.8	92.5	31	6	AX220586 Sequence
65	14.8	92.5	31	6	AX220587 Sequence

Pred. No. is the number of results predicted by chance to have a

212	14.8	92.5	31	6	AX220734	Sequence	285	14.8	92.5	31	6	AX220807	Sequence
213	14.8	92.5	31	6	AX220735	Sequence	286	14.8	92.5	31	6	AX220808	Sequence
214	14.8	92.5	31	6	AX220736	Sequence	287	14.8	92.5	31	6	AX220809	Sequence
215	14.8	92.5	31	6	AX220737	Sequence	288	14.8	92.5	31	6	AX220810	Sequence
216	14.8	92.5	31	6	AX220738	Sequence	289	14.8	92.5	31	6	AX220811	Sequence
217	14.8	92.5	31	6	AX220739	Sequence	290	14.8	92.5	31	6	AX220812	Sequence
218	14.8	92.5	31	6	AX220740	Sequence	291	14.8	92.5	31	6	AX220813	Sequence
219	14.8	92.5	31	6	AX220741	Sequence	292	14.8	92.5	31	6	AX220814	Sequence
220	14.8	92.5	31	6	AX220742	Sequence	293	14.8	92.5	31	6	AX220815	Sequence
221	14.8	92.5	31	6	AX220743	Sequence	294	14.8	92.5	31	6	AX220816	Sequence
222	14.8	92.5	31	6	AX220744	Sequence	295	14.8	92.5	31	6	AX220817	Sequence
223	14.8	92.5	31	6	AX220745	Sequence	296	14.8	92.5	31	6	AX220818	Sequence
224	14.8	92.5	31	6	AX220746	Sequence	297	14.8	92.5	31	6	AX220819	Sequence
225	14.8	92.5	31	6	AX220747	Sequence	298	14.8	92.5	31	6	AX220820	Sequence
226	14.8	92.5	31	6	AX220748	Sequence	299	14.8	92.5	31	6	AX220821	Sequence
227	14.8	92.5	31	6	AX220749	Sequence	300	14.8	92.5	31	6	AX220822	Sequence
228	14.8	92.5	31	6	AX220750	Sequence	301	14.8	92.5	31	6	AX220823	Sequence
229	14.8	92.5	31	6	AX220751	Sequence	302	14.8	92.5	31	6	AX220824	Sequence
230	14.8	92.5	31	6	AX220752	Sequence	303	14.8	92.5	31	6	AX220825	Sequence
231	14.8	92.5	31	6	AX220753	Sequence	304	14.8	92.5	31	6	AX220826	Sequence
232	14.8	92.5	31	6	AX220754	Sequence	305	14.8	92.5	31	6	AX220827	Sequence
233	14.8	92.5	31	6	AX220755	Sequence	306	14.8	92.5	31	6	AX220828	Sequence
234	14.8	92.5	31	6	AX220756	Sequence	307	14.8	92.5	31	6	AX220829	Sequence
235	14.8	92.5	31	6	AX220757	Sequence	308	14.8	92.5	31	6	AX220830	Sequence
236	14.8	92.5	31	6	AX220758	Sequence	309	14.8	92.5	31	6	AX220831	Sequence
237	14.8	92.5	31	6	AX220759	Sequence	310	14.8	92.5	31	6	AX220832	Sequence
238	14.8	92.5	31	6	AX220760	Sequence	311	14.8	92.5	31	6	AX220833	Sequence
239	14.8	92.5	31	6	AX220761	Sequence	312	14.8	92.5	31	6	AX220834	Sequence
240	14.8	92.5	31	6	AX220762	Sequence	313	14.8	92.5	31	6	AX220835	Sequence
241	14.8	92.5	31	6	AX220763	Sequence	314	14.8	92.5	31	6	AX220836	Sequence
242	14.8	92.5	31	6	AX220764	Sequence	315	14.8	92.5	31	6	AX220837	Sequence
243	14.8	92.5	31	6	AX220765	Sequence	316	14.8	92.5	31	6	AX220838	Sequence
244	14.8	92.5	31	6	AX220766	Sequence	317	14.8	92.5	31	6	AX220839	Sequence
245	14.8	92.5	31	6	AX220767	Sequence	318	14.8	92.5	31	6	AX220840	Sequence
246	14.8	92.5	31	6	AX220768	Sequence	319	14.8	92.5	31	6	AX220841	Sequence
247	14.8	92.5	31	6	AX220769	Sequence	320	14.8	92.5	31	6	AX220842	Sequence
248	14.8	92.5	31	6	AX220770	Sequence	321	14.8	92.5	31	6	AX220843	Sequence
249	14.8	92.5	31	6	AX220771	Sequence	322	14.8	92.5	31	6	AX220844	Sequence
250	14.8	92.5	31	6	AX220772	Sequence	323	14.8	92.5	31	6	AX220845	Sequence
251	14.8	92.5	31	6	AX220773	Sequence	324	14.8	92.5	31	6	AX220846	Sequence
252	14.8	92.5	31	6	AX220774	Sequence	325	14.8	92.5	31	6	AX220847	Sequence
253	14.8	92.5	31	6	AX220775	Sequence	326	14.8	92.5	31	6	AX220848	Sequence
254	14.8	92.5	31	6	AX220776	Sequence	327	14.8	92.5	31	6	AX220849	Sequence
255	14.8	92.5	31	6	AX220777	Sequence	328	14.8	92.5	31	6	AX220850	Sequence
256	14.8	92.5	31	6	AX220778	Sequence	329	14.8	92.5	31	6	AX220851	Sequence
257	14.8	92.5	31	6	AX220779	Sequence	330	14.8	92.5	31	6	AX220852	Sequence
258	14.8	92.5	31	6	AX220780	Sequence	331	14.8	92.5	31	6	AX220853	Sequence
259	14.8	92.5	31	6	AX220781	Sequence	332	14.8	92.5	31	6	AX220854	Sequence
260	14.8	92.5	31	6	AX220782	Sequence	333	14.8	92.5	31	6	AX220855	Sequence
261	14.8	92.5	31	6	AX220783	Sequence	334	14.8	92.5	31	6	AX220856	Sequence
262	14.8	92.5	31	6	AX220784	Sequence	335	14.8	92.5	31	6	AX220857	Sequence
263	14.8	92.5	31	6	AX220785	Sequence	336	14.8	92.5	31	6	AX220858	Sequence
264	14.8	92.5	31	6	AX220786	Sequence	337	14.8	92.5	31	6	AX220859	Sequence
265	14.8	92.5	31	6	AX220787	Sequence	338	14.8	92.5	31	6	AX220860	Sequence
266	14.8	92.5	31	6	AX220788	Sequence	339	14.8	92.5	31	6	AX220861	Sequence
267	14.8	92.5	31	6	AX220789	Sequence	340	14.8	92.5	31	6	AX220862	Sequence
268	14.8	92.5	31	6	AX220790	Sequence	341	14.8	92.5	31	6	AX220863	Sequence
269	14.8	92.5	31	6	AX220791	Sequence	342	14.8	92.5	31	6	AX220864	Sequence
270	14.8	92.5	31	6	AX220792	Sequence	343	14.8	92.5	31	6	AX220865	Sequence
271	14.8	92.5	31	6	AX220793	Sequence	344	14.8	92.5	31	6	AX220866	Sequence
272	14.8	92.5	31	6	AX220794	Sequence	345	14.8	92.5	31	6	AX220867	Sequence
273	14.8	92.5	31	6	AX220795	Sequence	346	14.8	92.5	31	6	AX220868	Sequence
274	14.8	92.5	31	6	AX220796	Sequence	347	14.8	92.5	31	6	AX220869	Sequence
275	14.8	92.5	31	6	AX220797	Sequence	348	14.8	92.5	31	6	AX220870	Sequence
276	14.8	92.5	31	6	AX220798	Sequence	349	14.8	92.5	31	6	AX220871	Sequence
277	14.8	92.5	31	6	AX220799	Sequence	350	14.8	92.5	31	6	AX220872	Sequence
278	14.8	92.5	31	6	AX220800	Sequence	351	14.8	92.5	31	6	AX220873	Sequence
279	14.8	92.5	31	6	AX220801	Sequence	352	14.8	92.5	31	6	AX220874	Sequence
280	14.8	92.5	31	6	AX220802	Sequence	353	14.8	92.5	31	6	AX220875	Sequence
281	14.8	92.5	31	6	AX220803	Sequence	354	14.8	92.5	31	6	AX220876	Sequence
282	14.8	92.5	31	6	AX220804	Sequence	355	14.8	92.5	31	6	AX220877	Sequence
283	14.8	92.5	31	6	AX220805	Sequence	356	14.8	92.5	31	6	AX220878	Sequence
284	14.8	92.5	31	6	AX220806	Sequence	357	14.8	92.5	31	6	AX220879	Sequence

504	14.8	92.5	31	6	AX221026	Sequence	577	14.8	92.5	31	6	AX221099	Sequence	AX221099
505	14.8	92.5	31	6	AX221027	Sequence	578	14.8	92.5	31	6	AX221100	Sequence	AX221100
506	14.8	92.5	31	6	AX221028	Sequence	579	14.8	92.5	31	6	AX221101	Sequence	AX221101
507	14.8	92.5	31	6	AX221029	Sequence	580	14.8	92.5	31	6	AX221102	Sequence	AX221102
508	14.8	92.5	31	6	AX221030	Sequence	581	14.8	92.5	31	6	AX221103	Sequence	AX221103
509	14.8	92.5	31	6	AX221031	Sequence	582	14.8	92.5	31	6	AX221104	Sequence	AX221104
510	14.8	92.5	31	6	AX221032	Sequence	583	14.8	92.5	31	6	AX221105	Sequence	AX221105
511	14.8	92.5	31	6	AX221033	Sequence	584	14.8	92.5	31	6	AX221106	Sequence	AX221106
512	14.8	92.5	31	6	AX221034	Sequence	585	14.8	92.5	31	6	AX221107	Sequence	AX221107
513	14.8	92.5	31	6	AX221035	Sequence	586	14.8	92.5	31	6	AX221108	Sequence	AX221108
514	14.8	92.5	31	6	AX221036	Sequence	587	14.8	92.5	31	6	AX221109	Sequence	AX221109
515	14.8	92.5	31	6	AX221037	Sequence	588	14.8	92.5	31	6	AX221110	Sequence	AX221110
516	14.8	92.5	31	6	AX221038	Sequence	589	14.8	92.5	31	6	AX221111	Sequence	AX221111
517	14.8	92.5	31	6	AX221039	Sequence	590	14.8	92.5	31	6	AX221112	Sequence	AX221112
518	14.8	92.5	31	6	AX221040	Sequence	591	14.8	92.5	31	6	AX221113	Sequence	AX221113
519	14.8	92.5	31	6	AX221041	Sequence	592	14.8	92.5	31	6	AX221114	Sequence	AX221114
520	14.8	92.5	31	6	AX221042	Sequence	593	14.8	92.5	31	6	AX221115	Sequence	AX221115
521	14.8	92.5	31	6	AX221043	Sequence	594	14.8	92.5	31	6	AX221116	Sequence	AX221116
522	14.8	92.5	31	6	AX221044	Sequence	595	14.8	92.5	31	6	AX221117	Sequence	AX221117
523	14.8	92.5	31	6	AX221045	Sequence	596	14.8	92.5	31	6	AX221118	Sequence	AX221118
524	14.8	92.5	31	6	AX221046	Sequence	597	14.8	92.5	31	6	AX221119	Sequence	AX221119
525	14.8	92.5	31	6	AX221047	Sequence	598	14.8	92.5	31	6	AX221120	Sequence	AX221120
526	14.8	92.5	31	6	AX221048	Sequence	599	14.8	92.5	31	6	AX221121	Sequence	AX221121
527	14.8	92.5	31	6	AX221049	Sequence	600	14.8	92.5	31	6	AX221122	Sequence	AX221122
528	14.8	92.5	31	6	AX221050	Sequence	601	14.8	92.5	31	6	AX221123	Sequence	AX221123
529	14.8	92.5	31	6	AX221051	Sequence	602	14.8	92.5	31	6	AX221124	Sequence	AX221124
530	14.8	92.5	31	6	AX221052	Sequence	603	14.8	92.5	31	6	AX221125	Sequence	AX221125
531	14.8	92.5	31	6	AX221053	Sequence	604	14.8	92.5	31	6	AX221126	Sequence	AX221126
532	14.8	92.5	31	6	AX221054	Sequence	605	14.8	92.5	31	6	AX221127	Sequence	AX221127
533	14.8	92.5	31	6	AX221055	Sequence	606	14.8	92.5	31	6	AX221128	Sequence	AX221128
534	14.8	92.5	31	6	AX221056	Sequence	607	14.8	92.5	31	6	AX221129	Sequence	AX221129
535	14.8	92.5	31	6	AX221057	Sequence	608	14.8	92.5	31	6	AX221130	Sequence	AX221130
536	14.8	92.5	31	6	AX221058	Sequence	609	14.8	92.5	31	6	AX221131	Sequence	AX221131
537	14.8	92.5	31	6	AX221059	Sequence	610	14.8	92.5	31	6	AX221132	Sequence	AX221132
538	14.8	92.5	31	6	AX221060	Sequence	611	14.8	92.5	31	6	AX221133	Sequence	AX221133
539	14.8	92.5	31	6	AX221061	Sequence	612	14.8	92.5	31	6	AX221134	Sequence	AX221134
540	14.8	92.5	31	6	AX221062	Sequence	613	14.8	92.5	31	6	AX221135	Sequence	AX221135
541	14.8	92.5	31	6	AX221063	Sequence	614	14.8	92.5	31	6	AX221136	Sequence	AX221136
542	14.8	92.5	31	6	AX221064	Sequence	615	14.8	92.5	31	6	AX221137	Sequence	AX221137
543	14.8	92.5	31	6	AX221065	Sequence	616	14.8	92.5	31	6	AX221138	Sequence	AX221138
544	14.8	92.5	31	6	AX221066	Sequence	617	14.8	92.5	31	6	AX221139	Sequence	AX221139
545	14.8	92.5	31	6	AX221067	Sequence	618	14.8	92.5	31	6	AX221140	Sequence	AX221140
546	14.8	92.5	31	6	AX221068	Sequence	619	14.8	92.5	31	6	AX221141	Sequence	AX221141
547	14.8	92.5	31	6	AX221069	Sequence	620	14.8	92.5	31	6	AX221142	Sequence	AX221142
548	14.8	92.5	31	6	AX221070	Sequence	621	14.8	92.5	31	6	AX221143	Sequence	AX221143
549	14.8	92.5	31	6	AX221071	Sequence	622	14.8	92.5	31	6	AX221144	Sequence	AX221144
550	14.8	92.5	31	6	AX221072	Sequence	623	14.8	92.5	31	6	AX221145	Sequence	AX221145
551	14.8	92.5	31	6	AX221073	Sequence	624	14.8	92.5	31	6	AX221146	Sequence	AX221146
552	14.8	92.5	31	6	AX221074	Sequence	625	14.8	92.5	31	6	AX221147	Sequence	AX221147
553	14.8	92.5	31	6	AX221075	Sequence	626	14.8	92.5	31	6	AX221148	Sequence	AX221148
554	14.8	92.5	31	6	AX221076	Sequence	627	14.8	92.5	31	6	AX221149	Sequence	AX221149
555	14.8	92.5	31	6	AX221077	Sequence	628	14.8	92.5	31	6	AX221150	Sequence	AX221150
556	14.8	92.5	31	6	AX221078	Sequence	629	14.8	92.5	31	6	AX221151	Sequence	AX221151
557	14.8	92.5	31	6	AX221079	Sequence	630	14.8	92.5	31	6	AX221152	Sequence	AX221152
558	14.8	92.5	31	6	AX221080	Sequence	631	14.8	92.5	31	6	AX221153	Sequence	AX221153
559	14.8	92.5	31	6	AX221081	Sequence	632	14.8	92.5	31	6	AX221154	Sequence	AX221154
560	14.8	92.5	31	6	AX221082	Sequence	633	14.8	92.5	31	6	AX221155	Sequence	AX221155
561	14.8	92.5	31	6	AX221083	Sequence	634	14.8	92.5	31	6	AX221156	Sequence	AX221156
562	14.8	92.5	31	6	AX221084	Sequence	635	14.8	92.5	31	6	AX221157	Sequence	AX221157
563	14.8	92.5	31	6	AX221085	Sequence	636	14.8	92.5	31	6	AX221158	Sequence	AX221158
564	14.8	92.5	31	6	AX221086	Sequence	637	14.8	92.5	31	6	AX221159	Sequence	AX221159
565	14.8	92.5	31	6	AX221087	Sequence	638	14.8	92.5	31	6	AX221160	Sequence	AX221160
566	14.8	92.5	31	6	AX221088	Sequence	639	14.8	92.5	31	6	AX221161	Sequence	AX221161
567	14.8	92.5	31	6	AX221089	Sequence	640	14.8	92.5	31	6	AX221162	Sequence	AX221162
568	14.8	92.5	31	6	AX221090	Sequence	641	14.8	92.5	31	6	AX221163	Sequence	AX221163
569	14.8	92.5	31	6	AX221091	Sequence	642	14.8	92.5	31	6	AX221164	Sequence	AX221164
570	14.8	92.5	31	6	AX221092	Sequence	643	14.8	92.5	31	6	AX221165	Sequence	AX221165
571	14.8	92.5	31	6	AX221093	Sequence	644	14.8	92.5	31	6	AX221166	Sequence	AX221166
572	14.8	92.5	31	6	AX221094	Sequence	645	14.8	92.5	31	6	AX221167	Sequence	AX221167
573	14.8	92.5	31	6	AX221095	Sequence	646	14.8	92.5	31	6	AX221168	Sequence	AX221168
574	14.8	92.5	31	6	AX221096	Sequence	647	14.8	92.5	31	6	AX221169	Sequence	AX221169
575	14.8	92.5	31	6	AX221097	Sequence	648	14.8	92.5	31	6	AX221170	Sequence	AX221170
576	14.8	92.5	31	6	AX221098	Sequence	649	14.8	92.5	31	6	AX221171	Sequence	AX221171
577	14.8	92.5	31	6	AX221099	Sequence	650	14.8	92.5	31	6	AX221172	Sequence	AX221172

650	14.8	92.5	31	6	AX221172	Sequence	723	14.8	92.5	31	6	AX221245	Sequence
651	14.8	92.5	31	6	AX221173	Sequence	724	14.8	92.5	31	6	AX221246	Sequence
652	14.8	92.5	31	6	AX221174	Sequence	725	14.8	92.5	31	6	AX221247	Sequence
653	14.8	92.5	31	6	AX221175	Sequence	726	14.8	92.5	31	6	AX221248	Sequence
654	14.8	92.5	31	6	AX221176	Sequence	727	14.8	92.5	31	6	AX221249	Sequence
655	14.8	92.5	31	6	AX221177	Sequence	728	14.8	92.5	31	6	AX221250	Sequence
656	14.8	92.5	31	6	AX221178	Sequence	729	14.8	92.5	31	6	AX221251	Sequence
657	14.8	92.5	31	6	AX221179	Sequence	730	14.8	92.5	31	6	AX221252	Sequence
658	14.8	92.5	31	6	AX221180	Sequence	731	14.8	92.5	31	6	AX221253	Sequence
659	14.8	92.5	31	6	AX221181	Sequence	732	14.8	92.5	31	6	AX221254	Sequence
660	14.8	92.5	31	6	AX221182	Sequence	733	14.8	92.5	31	6	AX221255	Sequence
661	14.8	92.5	31	6	AX221183	Sequence	734	14.8	92.5	31	6	AX221256	Sequence
662	14.8	92.5	31	6	AX221184	Sequence	735	14.8	92.5	31	6	AX221257	Sequence
663	14.8	92.5	31	6	AX221185	Sequence	736	14.8	92.5	31	6	AX221258	Sequence
664	14.8	92.5	31	6	AX221186	Sequence	737	14.8	92.5	31	6	AX221259	Sequence
665	14.8	92.5	31	6	AX221187	Sequence	738	14.8	92.5	31	6	AX221260	Sequence
666	14.8	92.5	31	6	AX221188	Sequence	739	14.8	92.5	31	6	AX221261	Sequence
667	14.8	92.5	31	6	AX221189	Sequence	740	14.8	92.5	31	6	AX221262	Sequence
668	14.8	92.5	31	6	AX221190	Sequence	741	14.8	92.5	31	6	AX221263	Sequence
669	14.8	92.5	31	6	AX221191	Sequence	742	14.8	92.5	31	6	AX221264	Sequence
670	14.8	92.5	31	6	AX221192	Sequence	743	14.8	92.5	31	6	AX221265	Sequence
671	14.8	92.5	31	6	AX221193	Sequence	744	14.8	92.5	31	6	AX221266	Sequence
672	14.8	92.5	31	6	AX221194	Sequence	745	14.8	92.5	31	6	AX221267	Sequence
673	14.8	92.5	31	6	AX221195	Sequence	746	14.8	92.5	31	6	AX221268	Sequence
674	14.8	92.5	31	6	AX221196	Sequence	747	14.8	92.5	31	6	AX221269	Sequence
675	14.8	92.5	31	6	AX221197	Sequence	748	14.8	92.5	31	6	AX221270	Sequence
676	14.8	92.5	31	6	AX221198	Sequence	749	14.8	92.5	31	6	AX221271	Sequence
677	14.8	92.5	31	6	AX221199	Sequence	750	14.8	92.5	31	6	AX221272	Sequence
678	14.8	92.5	31	6	AX221200	Sequence	751	14.8	92.5	31	6	AX221273	Sequence
679	14.8	92.5	31	6	AX221201	Sequence	752	14.8	92.5	31	6	AX221274	Sequence
680	14.8	92.5	31	6	AX221202	Sequence	753	14.8	92.5	31	6	AX221275	Sequence
681	14.8	92.5	31	6	AX221203	Sequence	754	14.8	92.5	31	6	AX221276	Sequence
682	14.8	92.5	31	6	AX221204	Sequence	755	14.8	92.5	31	6	AX221277	Sequence
683	14.8	92.5	31	6	AX221205	Sequence	756	14.8	92.5	31	6	AX221278	Sequence
684	14.8	92.5	31	6	AX221206	Sequence	757	14.8	92.5	31	6	AX221279	Sequence
685	14.8	92.5	31	6	AX221207	Sequence	758	14.8	92.5	31	6	AX221280	Sequence
686	14.8	92.5	31	6	AX221208	Sequence	759	14.8	92.5	31	6	AX221281	Sequence
687	14.8	92.5	31	6	AX221209	Sequence	760	14.8	92.5	31	6	AX221282	Sequence
688	14.8	92.5	31	6	AX221210	Sequence	761	14.8	92.5	31	6	AX221283	Sequence
689	14.8	92.5	31	6	AX221211	Sequence	762	14.8	92.5	31	6	AX221284	Sequence
690	14.8	92.5	31	6	AX221212	Sequence	763	14.8	92.5	31	6	AX221285	Sequence
691	14.8	92.5	31	6	AX221213	Sequence	764	14.8	92.5	31	6	AX221286	Sequence
692	14.8	92.5	31	6	AX221214	Sequence	765	14.8	92.5	31	6	AX221287	Sequence
693	14.8	92.5	31	6	AX221215	Sequence	766	14.8	92.5	31	6	AX221288	Sequence
694	14.8	92.5	31	6	AX221216	Sequence	767	14.8	92.5	31	6	AX221289	Sequence
695	14.8	92.5	31	6	AX221217	Sequence	768	14.8	92.5	31	6	AX221290	Sequence
696	14.8	92.5	31	6	AX221218	Sequence	769	14.8	92.5	31	6	AX221291	Sequence
697	14.8	92.5	31	6	AX221219	Sequence	770	14.8	92.5	31	6	AX221292	Sequence
698	14.8	92.5	31	6	AX221220	Sequence	771	14.8	92.5	31	6	AX221293	Sequence
699	14.8	92.5	31	6	AX221221	Sequence	772	14.8	92.5	31	6	AX221294	Sequence
700	14.8	92.5	31	6	AX221222	Sequence	773	14.8	92.5	31	6	AX221295	Sequence
701	14.8	92.5	31	6	AX221223	Sequence	774	14.8	92.5	31	6	AX221296	Sequence
702	14.8	92.5	31	6	AX221224	Sequence	775	14.8	92.5	31	6	AX221297	Sequence
703	14.8	92.5	31	6	AX221225	Sequence	776	14.8	92.5	31	6	AX221298	Sequence
704	14.8	92.5	31	6	AX221226	Sequence	777	14.8	92.5	31	6	AX221299	Sequence
705	14.8	92.5	31	6	AX221227	Sequence	778	14.8	92.5	31	6	AX221300	Sequence
706	14.8	92.5	31	6	AX221228	Sequence	779	14.8	92.5	31	6	AX221301	Sequence
707	14.8	92.5	31	6	AX221229	Sequence	780	14.8	92.5	31	6	AX221302	Sequence
708	14.8	92.5	31	6	AX221230	Sequence	781	14.8	92.5	31	6	AX221303	Sequence
709	14.8	92.5	31	6	AX221231	Sequence	782	14.8	92.5	31	6	AX221304	Sequence
710	14.8	92.5	31	6	AX221232	Sequence	783	14.8	92.5	31	6	AX221305	Sequence
711	14.8	92.5	31	6	AX221233	Sequence	784	14.8	92.5	31	6	AX221306	Sequence
712	14.8	92.5	31	6	AX221234	Sequence	785	14.8	92.5	31	6	AX221307	Sequence
713	14.8	92.5	31	6	AX221235	Sequence	786	14.8	92.5	31	6	AX221308	Sequence
714	14.8	92.5	31	6	AX221236	Sequence	787	14.8	92.5	31	6	AX221309	Sequence
715	14.8	92.5	31	6	AX221237	Sequence	788	14.8	92.5	31	6	AX221310	Sequence
716	14.8	92.5	31	6	AX221238	Sequence	789	14.8	92.5	31	6	AX221311	Sequence
717	14.8	92.5	31	6	AX221239	Sequence	790	14.8	92.5	31	6	AX221312	Sequence
718	14.8	92.5	31	6	AX221240	Sequence	791	14.8	92.5	31	6	AX221313	Sequence
719	14.8	92.5	31	6	AX221241	Sequence	792	14.8	92.5	31	6	AX221314	Sequence
720	14.8	92.5	31	6	AX221242	Sequence	793	14.8	92.5	31	6	AX221315	Sequence
721	14.8	92.5	31	6	AX221243	Sequence	794	14.8	92.5	31	6	AX221316	Sequence
722	14.8	92.5	31	6	AX221244	Sequence	795	14.8	92.5	31	6	AX221317	Sequence

796	14.8	92.5	31	6	AX221318	Sequence	869	14.8	92.5	31	6	AX221391	Sequence	AX221391
797	14.8	92.5	31	6	AX221319	Sequence	870	14.8	92.5	31	6	AX221392	Sequence	AX221392
798	14.8	92.5	31	6	AX221320	Sequence	871	14.8	92.5	31	6	AX221393	Sequence	AX221393
799	14.8	92.5	31	6	AX221321	Sequence	872	14.8	92.5	31	6	AX221394	Sequence	AX221394
800	14.8	92.5	31	6	AX221322	Sequence	873	14.8	92.5	31	6	AX221395	Sequence	AX221395
801	14.8	92.5	31	6	AX221323	Sequence	874	14.8	92.5	31	6	AX221396	Sequence	AX221396
802	14.8	92.5	31	6	AX221324	Sequence	875	14.8	92.5	31	6	AX221397	Sequence	AX221397
803	14.8	92.5	31	6	AX221325	Sequence	876	14.8	92.5	31	6	AX221398	Sequence	AX221398
804	14.8	92.5	31	6	AX221326	Sequence	877	14.8	92.5	31	6	AX221382	Sequence	AX221382
805	14.8	92.5	31	6	AX221327	Sequence	878	14.8	92.5	31	6	AX221383	Sequence	AX221383
806	14.8	92.5	31	6	AX221328	Sequence	879	14.8	92.5	31	6	AX221384	Sequence	AX221384
807	14.8	92.5	31	6	AX221329	Sequence	880	14.8	92.5	31	6	AX221385	Sequence	AX221385
808	14.8	92.5	31	6	AX221330	Sequence	881	14.8	92.5	31	6	AX221386	Sequence	AX221386
809	14.8	92.5	31	6	AX221331	Sequence	882	14.8	92.5	31	6	AX221387	Sequence	AX221387
810	14.8	92.5	31	6	AX221332	Sequence	883	14.8	92.5	31	6	AX221388	Sequence	AX221388
811	14.8	92.5	31	6	AX221333	Sequence	884	14.8	92.5	31	6	AX221389	Sequence	AX221389
812	14.8	92.5	31	6	AX221334	Sequence	885	14.8	92.5	31	6	AX221390	Sequence	AX221390
813	14.8	92.5	31	6	AX221335	Sequence	886	14.8	92.5	31	6	AX221391	Sequence	AX221391
814	14.8	92.5	31	6	AX221336	Sequence	887	14.8	92.5	31	6	AX221392	Sequence	AX221392
815	14.8	92.5	31	6	AX221337	Sequence	888	14.8	92.5	31	6	AX221393	Sequence	AX221393
816	14.8	92.5	31	6	AX221338	Sequence	889	14.8	92.5	31	6	AX221394	Sequence	AX221394
817	14.8	92.5	31	6	AX221339	Sequence	890	14.8	92.5	31	6	AX221395	Sequence	AX221395
818	14.8	92.5	31	6	AX221340	Sequence	891	14.8	92.5	31	6	AX221396	Sequence	AX221396
819	14.8	92.5	31	6	AX221341	Sequence	892	14.8	92.5	31	6	AX221397	Sequence	AX221397
820	14.8	92.5	31	6	AX221342	Sequence	893	14.8	92.5	31	6	AX221398	Sequence	AX221398
821	14.8	92.5	31	6	AX221343	Sequence	894	14.8	92.5	31	6	AX221399	Sequence	AX221399
822	14.8	92.5	31	6	AX221344	Sequence	895	14.8	92.5	31	6	AX221400	Sequence	AX221400
823	14.8	92.5	31	6	AX221345	Sequence	896	14.8	92.5	31	6	AX221401	Sequence	AX221401
824	14.8	92.5	31	6	AX221346	Sequence	897	14.8	92.5	31	6	AX221402	Sequence	AX221402
825	14.8	92.5	31	6	AX221347	Sequence	898	14.8	92.5	31	6	AX221403	Sequence	AX221403
826	14.8	92.5	31	6	AX221348	Sequence	899	14.8	92.5	31	6	AX221404	Sequence	AX221404
827	14.8	92.5	31	6	AX221349	Sequence	900	14.8	92.5	31	6	AX221405	Sequence	AX221405
828	14.8	92.5	31	6	AX221350	Sequence	901	14.8	92.5	31	6	AX221406	Sequence	AX221406
829	14.8	92.5	31	6	AX221351	Sequence	902	14.8	92.5	31	6	AX221407	Sequence	AX221407
830	14.8	92.5	31	6	AX221352	Sequence	903	14.8	92.5	31	6	AX221408	Sequence	AX221408
831	14.8	92.5	31	6	AX221353	Sequence	904	14.8	92.5	31	6	AX221409	Sequence	AX221409
832	14.8	92.5	31	6	AX221354	Sequence	905	14.8	92.5	31	6	AX221410	Sequence	AX221410
833	14.8	92.5	31	6	AX221355	Sequence	906	14.8	92.5	31	6	AX221411	Sequence	AX221411
834	14.8	92.5	31	6	AX221356	Sequence	907	14.8	92.5	31	6	AX221412	Sequence	AX221412
835	14.8	92.5	31	6	AX221357	Sequence	908	14.8	92.5	31	6	AX221413	Sequence	AX221413
836	14.8	92.5	31	6	AX221358	Sequence	909	14.8	92.5	31	6	AX221414	Sequence	AX221414
837	14.8	92.5	31	6	AX221359	Sequence	910	14.8	92.5	31	6	AX221415	Sequence	AX221415
838	14.8	92.5	31	6	AX221360	Sequence	911	14.8	92.5	31	6	AX221416	Sequence	AX221416
839	14.8	92.5	31	6	AX221361	Sequence	912	14.8	92.5	31	6	AX221417	Sequence	AX221417
840	14.8	92.5	31	6	AX221362	Sequence	913	14.8	92.5	31	6	AX221418	Sequence	AX221418
841	14.8	92.5	31	6	AX221363	Sequence	914	14.8	92.5	31	6	AX221419	Sequence	AX221419
842	14.8	92.5	31	6	AX221364	Sequence	915	14.8	92.5	31	6	AX221420	Sequence	AX221420
843	14.8	92.5	31	6	AX221365	Sequence	916	14.8	92.5	31	6	AX221421	Sequence	AX221421
844	14.8	92.5	31	6	AX221366	Sequence	917	14.8	92.5	31	6	AX221422	Sequence	AX221422
845	14.8	92.5	31	6	AX221367	Sequence	918	14.8	92.5	31	6	AX221423	Sequence	AX221423
846	14.8	92.5	31	6	AX221368	Sequence	919	14.8	92.5	31	6	AX221424	Sequence	AX221424
847	14.8	92.5	31	6	AX221369	Sequence	920	14.8	92.5	31	6	AX221425	Sequence	AX221425
848	14.8	92.5	31	6	AX221370	Sequence	921	14.8	92.5	31	6	AX221426	Sequence	AX221426
849	14.8	92.5	31	6	AX221371	Sequence	922	14.8	92.5	31	6	AX221427	Sequence	AX221427
850	14.8	92.5	31	6	AX221372	Sequence	923	14.8	92.5	31	6	AX221428	Sequence	AX221428
851	14.8	92.5	31	6	AX221373	Sequence	924	14.8	92.5	31	6	AX221429	Sequence	AX221429
852	14.8	92.5	31	6	AX221374	Sequence	925	14.8	92.5	31	6	AX221430	Sequence	AX221430
853	14.8	92.5	31	6	AX221375	Sequence	926	14.8	92.5	31	6	AX221431	Sequence	AX221431
854	14.8	92.5	31	6	AX221376	Sequence	927	14.8	92.5	31	6	AX221432	Sequence	AX221432
855	14.8	92.5	31	6	AX221377	Sequence	928	14.8	92.5	31	6	AX221433	Sequence	AX221433
856	14.8	92.5	31	6	AX221378	Sequence	929	14.8	92.5	31	6	AX221434	Sequence	AX221434
857	14.8	92.5	31	6	AX221379	Sequence	930	14.8	92.5	31	6	AX221435	Sequence	AX221435
858	14.8	92.5	31	6	AX221380	Sequence	931	14.8	92.5	31	6	AX221436	Sequence	AX221436
859	14.8	92.5	31	6	AX221381	Sequence	932	14.8	92.5	31	6	AX221437	Sequence	AX221437
860	14.8	92.5	31	6	AX221382	Sequence	933	14.8	92.5	31	6	AX221438	Sequence	AX221438
861	14.8	92.5	31	6	AX221383	Sequence	934	14.8	92.5	31	6	AX221439	Sequence	AX221439
862	14.8	92.5	31	6	AX221384	Sequence	935	14.8	92.5	31	6	AX221440	Sequence	AX221440
863	14.8	92.5	31	6	AX221385	Sequence	936	14.8	92.5	31	6	AX221441	Sequence	AX221441
864	14.8	92.5	31	6	AX221386	Sequence	937	14.8	92.5	31	6	AX221442	Sequence	AX221442
865	14.8	92.5	31	6	AX221387	Sequence	938	14.8	92.5	31	6	AX221443	Sequence	AX221443
866	14.8	92.5	31	6	AX221388	Sequence	939	14.8	92.5	31	6	AX221444	Sequence	AX221444
867	14.8	92.5	31	6	AX221389	Sequence	940	14.8	92.5	31	6	AX221445	Sequence	AX221445
868	14.8	92.5	31	6	AX221390	Sequence	941	14.8	92.5	31	6	AX221446	Sequence	AX221446

942 14.8 92.5 31 6 AX223247 Sequence
 943 14.8 92.5 31 6 AX223248 Sequence
 944 14.8 92.5 31 6 AX223249 Sequence
 945 14.8 92.5 31 6 AX223250 Sequence
 946 14.8 92.5 31 6 AX223251 Sequence
 947 14.8 92.5 31 6 AX223252 Sequence
 948 14.8 92.5 31 6 AX223253 Sequence
 949 14.8 92.5 31 6 AX223254 Sequence
 950 14.8 92.5 31 6 AX223255 Sequence
 951 14.8 92.5 31 6 AX223256 Sequence
 952 14.8 92.5 31 6 AX223257 Sequence
 953 14.8 92.5 31 6 AX223258 Sequence
 954 14.8 92.5 31 6 AX223259 Sequence
 955 14.8 92.5 31 6 AX223260 Sequence
 956 14.8 92.5 31 6 AX223261 Sequence
 957 14.8 92.5 31 6 AX223262 Sequence
 958 14.8 92.5 31 6 AX223263 Sequence
 959 14.8 92.5 31 6 AX223264 Sequence
 960 14.8 92.5 31 6 AX223265 Sequence
 961 14.8 92.5 31 6 AX223266 Sequence
 962 14.8 92.5 31 6 AX223267 Sequence
 963 14.8 92.5 31 6 AX223268 Sequence
 964 14.8 92.5 31 6 AX223269 Sequence
 965 14.8 92.5 31 6 AX223270 Sequence
 966 14.8 92.5 31 6 AX223271 Sequence
 967 14.8 92.5 31 6 AX223272 Sequence
 968 14.8 92.5 31 6 AX223273 Sequence
 969 14.8 92.5 31 6 AX223274 Sequence
 970 14.8 92.5 31 6 AX223275 Sequence
 971 14.8 92.5 31 6 AX223276 Sequence
 972 14.8 92.5 31 6 AX223277 Sequence
 973 14.8 92.5 31 6 AX223278 Sequence
 974 14.8 92.5 31 6 AX223279 Sequence
 975 14.8 92.5 31 6 AX223280 Sequence
 976 14.8 92.5 31 6 AX223281 Sequence
 977 14.8 92.5 31 6 AX223282 Sequence
 978 14.8 92.5 31 6 AX223283 Sequence
 979 14.8 92.5 31 6 AX223284 Sequence
 980 14.8 92.5 31 6 AX223285 Sequence
 981 14.8 92.5 31 6 AX223286 Sequence
 982 14.8 92.5 31 6 AX223287 Sequence
 983 14.8 92.5 31 6 AX223288 Sequence
 984 14.8 92.5 31 6 AX223289 Sequence
 985 14.8 92.5 31 6 AX223290 Sequence
 986 14.8 92.5 31 6 AX223291 Sequence
 987 14.8 92.5 31 6 AX223292 Sequence
 988 14.8 92.5 31 6 AX223293 Sequence
 989 14.8 92.5 31 6 AX223294 Sequence
 990 14.8 92.5 31 6 AX223295 Sequence
 991 14.8 92.5 31 6 AX223296 Sequence
 992 14.8 92.5 31 6 AX223297 Sequence
 993 14.8 92.5 31 6 AX223298 Sequence
 994 14.8 92.5 31 6 AX223299 Sequence
 995 14.8 92.5 31 6 AX223300 Sequence
 996 14.8 92.5 31 6 AX223301 Sequence
 997 14.8 92.5 31 6 AX223302 Sequence
 998 14.8 92.5 31 6 AX223303 Sequence
 999 14.8 92.5 31 6 AX223304 Sequence
 1000 14.8 92.5 31 6 BD136890 Method of

ALIGNMENTS

RESULT 1
 LOCUS AX036342 16 bp DNA linear PAT 16-NOV-2000
 DEFINITION Sequence 4 from Patent DE19915141.
 ACCESSION AX036342
 VERSION AX036342.1 GI:11225952
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct

REFERENCE 1 artificial sequences.
 AUTHORS Krupp, G.
 JOURNAL Patent: DE 19915141-A 4 28-SEP-2000;
 ARTUS GES FUER MOLEKULARBIOLOG (DE)
 FEATURES
 source
 1. 16
 location/Qualifiers
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="Kuenstliche DNA-Sequenz"
 BASE COUNT 5 a 4 c 4 g 1 t 2 others
 ORIGIN
 Query Match 92.5%; Score 14.8; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16
 Db 1 RGGCTAGCHACACGA 16
 RESULT 2
 LOCUS AX223826 16 bp DNA linear PAT 07-SEP-2001
 DEFINITION Sequence 9268 from Patent WO0159103.
 ACCESSION AX223826
 VERSION AX223826.1 GI:15551550
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1
 AUTHORS Blatt, L., Meswigen, J. and Chowrira, B.M.
 TITLE Method and reagent for the modulation and diagnosis of cdk20 and
 JOUENAL nogo gene expression
 Patent: WO 0159103-A 9268 16-AUG-2001;
 RHOZOME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
 McSwigen, James (US); Chowrira, Bharat M. (US)
 FEATURES
 source
 1. 16
 location/Qualifiers
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="Nucleic Acid"

BASE COUNT 5 a 4 c 4 g 2 t 1 others
 ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 16;
 Best Local Similarity 93.8%; Pred. No. 3.1e+02;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16
 Db 1 RGGCTAGCHACACGA 16

RESULT 3
 LOCUS AX229619 16 bp DNA linear PAT 10-SEP-2001
 DEFINITION Sequence 2991 from Patent WO0157206.
 ACCESSION AX229619
 VERSION AX229619.1 GI:15558760
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1
 AUTHORS Fattaey, A.R., Jarvis, T., Meswigen, J., Bochner, R.N. and Holman, P.S.
 TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk
 1) enzyme
 Patent: WO 0157206-A 2991 09-AUG-2001;

FEATURES RIBOZYME PHARMACEUTICALS, INC. (US) ; Patraey, Ali R. (US)
SOURCE
1. .16
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 5 a 4 c 4 g 2 t 1 others
ORIGIN
Query Match 92.5%; Score 14.8; DB 6; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.1e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OR 1 RGCTAGCTACACGA 16
Db 1 RGCTAGCTACACGA 16
RESULT 4
LOCUS AX274735 16 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 2304 from Patent WO0162911.
ACCESSION AX274735
VERSION AX274735.1 GI:16547474
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Jarvis,T., von Carlwiltz,I., Mcswigen,J.A., Hamblin,P.A. and Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 2304 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
SOURCE 1. .16
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT 5 a 4 c 4 g 2 t 1 others
ORIGIN
Query Match 92.5%; Score 14.8; DB 6; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.1e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OR 1 RGCTAGCTACACGA 16
Db 1 RGCTAGCTACACGA 16
RESULT 5
LOCUS AX282449 16 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 21 from Patent WO0166721.
ACCESSION AX282449
VERSION AX282449.1 GI:16609580
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Uman,N., Mcswigen,J.A., Zinnen,S., Seiwert,S., Haeblerl,P., Chowrira,B. and Blatt,L.
TITLE Nucleic acid sensor molecules
JOURNAL Patent: WO 0166721-A 21 13-SEP-2001;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
SOURCE 1. .16
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

BASE COUNT 5 a 4 c 4 g 2 t 1 others
ORIGIN
Query Match 92.5%; Score 14.8; DB 6; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.1e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OR 1 RGCTAGCTACACGA 16
Db 1 RGCTAGCTACACGA 16
RESULT 6
LOCUS AX427010 16 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 5346 from Patent WO0188124.
ACCESSION AX427010
VERSION AX427010.1 GI:21530396
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Jarvis,T., von Carlwiltz,I., Mcswigen,J.A., McLaughlin,P.G. and Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 5346 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
SOURCE 1. .16
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"
BASE COUNT 5 a 4 c 4 g 2 t 1 others
ORIGIN
Query Match 92.5%; Score 14.8; DB 6; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.1e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OR 1 RGCTAGCTACACGA 16
Db 1 RGCTAGCTACACGA 16
RESULT 7
LOCUS AX583609 16 bp DNA linear PAT 10-JAN-2003
DEFINITION Sequence 5447 from Patent WO0211674.
ACCESSION AX583609
VERSION AX583609.1 GI:27655419
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Thompson,J., Mcswigen,J., McKenzie,T., Ayers,D., Szymkowski,D.E. and Grube,A.
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (Clca-1)
JOURNAL Patent: WO 0211674-A 5447 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)
FEATURES
SOURCE 1. .16
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"

Query Match 92.5%; Score 14.8; DB 6; Length 16;
 Best Local Similarity 93.8%; Pred. No. 3.1e+02;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16
 :|||||:|||||
 Db 1 RGGCTAGCTACACGA 16

RESULT 8
 AR201808 29 bp DNA linear PAT 20-APR-2002
 LOCUS AR201808
 DEFINITION Sequence 23 from patent US 6361941.
 ACCESSION AR201808
 VERSION AR201808.1 GI:20256347
 KEYWORDS
 SOURCE Unknown.
 ORGANISM
 REFERENCE
 1 (bases 1 to 29)
 AUTHORS Todd,A.V., Fuery,C.J. and Cairns,M.J.
 TITLE Catalytic nucleic acid-based diagnostic methods
 JOURNAL Patent: US 6361941-A 23 26-MAR-2002;
 FEATURES
 source location/Qualifiers
 1..29
 /organism="unknown"

BASE COUNT 10 a 5 c 10 g 3 t 1 others

ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 29;
 Best Local Similarity 87.5%; Pred. No. 3.1e+02;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16
 :|||||:|||||
 Db 8 AGGCTAGCTACACGA 23

RESULT 9
 AR201810 29 bp DNA linear PAT 20-APR-2002
 LOCUS AR201810
 DEFINITION Sequence 25 from patent US 6361941.
 ACCESSION AR201810
 VERSION AR201810.1 GI:20256349
 KEYWORDS
 SOURCE Unknown.
 ORGANISM
 REFERENCE
 1 (bases 1 to 29)
 AUTHORS Todd,A.V., Fuery,C.J. and Cairns,M.J.
 TITLE Catalytic nucleic acid-based diagnostic methods
 JOURNAL Patent: US 6361941-A 25 26-MAR-2002;
 FEATURES
 source location/Qualifiers
 1..29
 /organism="unknown"

BASE COUNT 7 a 10 c 5 g 7 t

ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 29;
 Best Local Similarity 87.5%; Pred. No. 3.1e+02;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16
 :|||||:|||||
 Db 9 AGGCTAGCTACACGA 24

RESULT 10
 AR201840 30 bp DNA linear PAT 20-APR-2002
 LOCUS AR201840
 DEFINITION Sequence 55 from patent US 6361941.
 ACCESSION AR201840

VERSION AR201840.1 GI:20256379
 KEYWORDS
 SOURCE Unknown.
 ORGANISM
 REFERENCE
 1 (bases 1 to 30)
 AUTHORS Todd,A.V., Fuery,C.J. and Cairns,M.J.
 TITLE Catalytic nucleic acid-based diagnostic methods
 JOURNAL Patent: US 6361941-A 55 26-MAR-2002;
 FEATURES
 source location/Qualifiers
 1..30
 /organism="unknown"

BASE COUNT 12 a 7 c 5 g 6 t

ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 30;
 Best Local Similarity 87.5%; Pred. No. 3.1e+02;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16
 :|||||:|||||
 Db 8 AGGCTAGCTACACGA 23

RESULT 11
 AX009377 30 bp DNA linear PAT 06-SEP-2000
 LOCUS AX009377
 DEFINITION Sequence 7 from Patent WO9963066.
 ACCESSION AX009377
 VERSION AX009377.1 GI:9996678
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM
 REFERENCE
 1
 AUTHORS Sloud,M.
 TITLE Amino-modified ribozymes
 JOURNAL Patent: WO 9963066-A 7 09-DEC-1999;
 DZIEGLEWSKA HANNA EVA (GB); SLOUD MOUNUDY (NO); NORWEGIAN RADTUM
 HOSPITAL RESE (NO)
 FEATURES
 source location/Qualifiers
 1..30
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="PKC alpha ribozyme"

BASE COUNT 7 a 11 c 8 g 4 t

ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 30;
 Best Local Similarity 87.5%; Pred. No. 3.1e+02;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCHACACGA 16
 :|||||:|||||
 Db 8 AGGCTAGCTACACGA 23

RESULT 12
 AX111628 30 bp DNA linear PAT 30-APR-2001
 LOCUS AX111628/c
 DEFINITION Sequence 3 from Patent WO0125419.
 ACCESSION AX111628
 VERSION AX111628.1 GI:13927904
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM
 REFERENCE
 1
 AUTHORS Conrad,C.A. and Chen,Y.
 TITLE Altering gene expression with ssdna produced in vivo
 JOURNAL Patent: WO 0125419-A 3 12-APR-2001;
 Cytogenix, Inc. (US)

FEATURES
SOURCE
1. 30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

BASE COUNT 5 a 8 c 8 g 9 t

ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 30;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCHACACGA 16
:|||||:|||||
24 AGGCTAGCTACACGA 9

Db

RESULT 13
LOCUS AX274718 30 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 2287 from Patent WO0162911.
ACCESSION AX274718
VERSION AX274718.1 GI:16547457
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Jarvis,T., von Carlwiltz,I., Mcswigen,J.A., Hamblin,P.A. and Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNML Patent: WO 0162911-A 2287 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
1. 30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"

misc_feature 1. 7
/note="2'-O-Methyl"

misc_feature 23. 29
/note="2'-O-Methyl"

misc_feature 30
/note="n strands for inverted deoxyabasic derivative"

BASE COUNT 7 a 9 c 6 g 7 t 1 others

ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 30;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCHACACGA 16
:|||||:|||||
7 GGGCTAGCTACACGA 22

Db

RESULT 14
LOCUS AX274719 30 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 2288 from Patent WO0162911.
ACCESSION AX274719
VERSION AX274719.1 GI:16547458
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Jarvis,T., von Carlwiltz,I., Mcswigen,J.A., Hamblin,P.A. and Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNML Patent: WO 0162911-A 2288 30-AUG-2001;

FEATURES
SOURCE
1. 30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"

BASE COUNT 10 a 7 c 7 g 5 t 1 others

ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 30;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCHACACGA 16
:|||||:|||||
7 AGGCTAGCTACACGA 22

Db

RESULT 15
LOCUS AX274720 30 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 2289 from Patent WO0162911.
ACCESSION AX274720
VERSION AX274720.1 GI:16547459
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Jarvis,T., von Carlwiltz,I., Mcswigen,J.A., Hamblin,P.A. and Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNML Patent: WO 0162911-A 2289 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
1. 30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"

misc_feature 1. 7
/note="2'-O-Methyl"

misc_feature 23. 29
/note="2'-O-Methyl"

misc_feature 30
/note="n strands for inverted deoxyabasic derivative"

BASE COUNT 10 a 4 c 9 g 6 t 1 others

ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 30;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCHACACGA 16
:|||||:|||||
7 AGGCTAGCTACACGA 22

Db

RESULT 16
LOCUS AX274721 30 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 2290 from Patent WO0162911.
ACCESSION AX274721
VERSION AX274721.1 GI:16547460
KEYWORDS
SOURCE synthetic construct

```

ORGANISM    synthetic construct
REFERENCE    artificial sequences.
AUTHORS      1 Jarvis, T., von Carlowitz, I., Mcswigen, J.A., Hamblin, P.A. and
              Ellis, J.H.
TITLE        Method and reagent for the inhibition of grid
JOURNAL      Patent: WO 0162911-A 2290 30-AUG-2001; GLAXO GROUP LIMITED (GB)
FEATURES     RIBOZYME PHARMACEUTICALS, INC. (US)
SOURCE       Location/Qualifiers
            1..30
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
            /note="Enzymatic Nucleic Acid"
            misc_feature 1..7
            /note="2'-O-Methyl"
            misc_feature 23..29
            /note="2'-O-Methyl"
            misc_feature 30
            /note="n stands for inverted deoxyabasic derivative"
            misc_feature 4 c 10 g 6 t 1 others
BASE COUNT  9 a 4 c 10 g 6 t 1 others
ORIGIN
Query Match 92.5%; Score 14.8; DB 6; Length 30;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACACGA 16
Db 7 AGCTAGCTACACGA 22

RESULT 17
LOCUS       AX274722 30 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 2291 from Patent WO0162911.
ACCESSION  AX274722
VERSION     AX274722.1 GI:16547461
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE    1 Jarvis, T., von Carlowitz, I., Mcswigen, J.A., Hamblin, P.A. and
              Ellis, J.H.
TITLE        Method and reagent for the inhibition of grid
JOURNAL      Patent: WO 0162911-A 2291 30-AUG-2001;
              RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES     Location/Qualifiers
            1..30
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
            /note="Enzymatic Nucleic Acid"
            misc_feature 1..7
            /note="2'-O-Methyl"
            misc_feature 23..29
            /note="2'-O-Methyl"
            misc_feature 30
            /note="n stands for inverted deoxyabasic derivative"
            misc_feature 7 c 10 g 4 t 1 others
BASE COUNT  8 a 7 c 10 g 4 t 1 others
ORIGIN
Query Match 92.5%; Score 14.8; DB 6; Length 30;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACACGA 16
Db 7 GGGCTAGCTACACGA 22

RESULT 18

```

```

AR116975    AR116975 31 bp DNA linear PAT 16-MAY-2001
LOCUS       AR116975
DEFINITION Sequence 5 from patent US 6140055.
ACCESSION  AR116975
VERSION     AR116975.1 GI:14097881
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 31)
              Todd, A.V., Fuery, C.J. and Cairns, M.J.
TITLE        Zymogenic nucleic acid detection methods and related kits
JOURNAL      Patent: US 6140055-A 5 31-OCT-2000;
              Location/Qualifiers
FEATURES     source 1..31
              /organism="unknown"
BASE COUNT  10 a 7 c 7 g 7 t
ORIGIN
Query Match 92.5%; Score 14.8; DB 6; Length 31;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACACGA 16
Db 8 AGCTAGCTACACGA 23

RESULT 19
LOCUS       AR201827 31 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 42 from patent US 6361941.
ACCESSION  AR201827
VERSION     AR201827.1 GI:20256366
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 31)
              Todd, A.V., Fuery, C.J. and Cairns, M.J.
TITLE        Catalytic nucleic acid-based diagnostic methods
JOURNAL      Patent: US 6361941-A 42 26-MAR-2002;
              Location/Qualifiers
FEATURES     source 1..31
              /organism="unknown"
BASE COUNT  10 a 10 c 5 g 6 t
ORIGIN
Query Match 92.5%; Score 14.8; DB 6; Length 31;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACACGA 16
Db 10 AGCTAGCTACACGA 25

RESULT 20
LOCUS       AR201830 31 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 45 from patent US 6361941.
ACCESSION  AR201830
VERSION     AR201830.1 GI:20256369
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 31)
              Todd, A.V., Fuery, C.J. and Cairns, M.J.
TITLE        Catalytic nucleic acid-based diagnostic methods
JOURNAL      Patent: US 6361941-A 45 26-MAR-2002;
              Location/Qualifiers
FEATURES     source 1..31

```

BASE COUNT 11 a 9 c 5 g 6 t
ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 31;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCHACAAGA 16
Db 10 AGGCTAGCTACAAGA 25

RESULT 21
LOCUS AR201833 31 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 48 from patent US 6361941.
ACCESSION AR201833
VERSION AR201833.1 GI:20256372
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 31)
AUTHORS Todd A.V., Puery,C.J. and Cairns,M.J.
TITLE Catalytic nucleic acid-based diagnostic methods
JOURNAL Patent: US 6361941-A 48 26-MAR-2002;
FEATURES Location/Qualifiers
source 1..31

BASE COUNT 10 a 6 c 12 g 3 t
ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 31;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCHACAAGA 16
Db 9 GGGCTAGCTACAAGA 24

RESULT 22
LOCUS AR201836 31 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 51 from patent US 6361941.
ACCESSION AR201836
VERSION AR201836.1 GI:20256375
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 31)
AUTHORS Todd A.V., Puery,C.J. and Cairns,M.J.
TITLE Catalytic nucleic acid-based diagnostic methods
JOURNAL Patent: US 6361941-A 51 26-MAR-2002;
FEATURES Location/Qualifiers
source 1..31

BASE COUNT 11 a 6 c 11 g 3 t
ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 31;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCHACAAGA 16
Db 9 AGGCTAGCTACAAGA 24

RESULT 23
AR204371

LOCUS AR204371 31 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 5 from patent US 6365724.
ACCESSION AR204371
VERSION AR204371.1 GI:21501005
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 31)
AUTHORS Todd A.V., Puery,C.J. and Cairns,M.J.
TITLE Zymogenic nucleic acid detection methods, and related molecules and kits
JOURNAL Patent: US 6365724-A 5 02-APR-2002;
FEATURES Location/Qualifiers
source 1..31

BASE COUNT 10 a 7 c 7 g 7 t
ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 31;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCHACAAGA 16
Db 8 AGGCTAGCTACAAGA 23

RESULT 24
LOCUS AX220546 31 bp DNA linear PAT 07-SEP-2001
DEFINITION Sequence 5988 from Patent W00159103.
ACCESSION AX220546
VERSION AX220546.1 GI:15548270
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Blatt,L., Meswigen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 5988 16-AUG-2001;
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; Meswigen, James (US) ; Chowrira, Bharat M. (US)
source 1..31

FEATURES
source 1..31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT 10 a 8 c 8 g 5 t
ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 31;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCHACAAGA 16
Db 8 GGGCTAGCTACAAGA 23

RESULT 25
LOCUS AX220547 31 bp DNA linear PAT 07-SEP-2001
DEFINITION Sequence 5989 from Patent W00159103.
ACCESSION AX220547
VERSION AX220547.1 GI:15548271
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Blatt,L., Meswigen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 5988 16-AUG-2001;
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; Meswigen, James (US) ; Chowrira, Bharat M. (US)
source 1..31

REFERENCE
AUTHORS
TITLE
JOURNAL

1 Blatt, L., McSwiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 5989 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES

source

1.31
Location/Qualifiers/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT
10 a 7 c 11 g 3 t

ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 31;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY
1 RGGCTAGCHACAACA 16
8 GGGCTAGCTACAACA 23

RESULT 26

AX220548

LOCUS

AX220548 31 bp DNA

DEFINITION

Sequence 5990 from Patent WO0159103.

ACCESSION

AX220548.1 GI:15548272

VERSION

AX220548.1 GI:15548272

KEYWORDS

synthetic construct
synthetic construct
artificial sequences.

SOURCE

synthetic construct
synthetic construct
artificial sequences.

ORGANISM

synthetic construct
synthetic construct
artificial sequences.

REFERENCE
AUTHORS
TITLE
JOURNAL

1 Blatt, L., McSwiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 5990 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES

source

1.31
Location/Qualifiers/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT
9 a 8 c 6 g 8 t

ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 31;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY
1 RGGCTAGCHACAACA 16
8 AGGCTAGCTACAACA 23

RESULT 27

AX220549

LOCUS

AX220549 31 bp DNA

DEFINITION

Sequence 5991 from Patent WO0159103.

ACCESSION

AX220549.1 GI:15548273

VERSION

AX220549.1 GI:15548273

KEYWORDS

synthetic construct
synthetic construct
artificial sequences.

SOURCE

synthetic construct
synthetic construct
artificial sequences.

ORGANISM

synthetic construct
synthetic construct
artificial sequences.

REFERENCE
AUTHORS
TITLE
JOURNAL

1 Blatt, L., McSwiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 5993 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;

JOURNAL
nogo gene expression
Patent: WO 0159103-A 5991 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES

source

1.31
Location/Qualifiers/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT
11 a 7 c 8 g 5 t

ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 31;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY
1 RGGCTAGCHACAACA 16
8 AGGCTAGCTACAACA 23

RESULT 28

AX220550

LOCUS

AX220550 31 bp DNA

DEFINITION

Sequence 5992 from Patent WO0159103.

ACCESSION

AX220550.1 GI:15548274

VERSION

AX220550.1 GI:15548274

KEYWORDS

synthetic construct
synthetic construct
artificial sequences.

SOURCE

synthetic construct
synthetic construct
artificial sequences.

ORGANISM

synthetic construct
synthetic construct
artificial sequences.

REFERENCE

1 Blatt, L., McSwiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 5992 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)

JOURNAL

FEATURES

source

1.31
Location/Qualifiers/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT
10 a 7 c 7 g 7 t

ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 31;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY
1 RGGCTAGCHACAACA 16
8 GGGCTAGCTACAACA 23

RESULT 29

AX220551

LOCUS

AX220551 31 bp DNA

DEFINITION

Sequence 5993 from Patent WO0159103.

ACCESSION

AX220551.1 GI:15548275

VERSION

AX220551.1 GI:15548275

KEYWORDS

synthetic construct
synthetic construct
artificial sequences.

SOURCE

synthetic construct
synthetic construct
artificial sequences.

ORGANISM

synthetic construct
synthetic construct
artificial sequences.

REFERENCE
AUTHORS
TITLE
JOURNAL

1 Blatt, L., McSwiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 5993 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;

FEATURES
source
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
1. .31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT
ORIGIN
9 a 5 c 10 g 7 t

Query Match
Best Local Similarity 92.5%; Score 14.8; DB 6; Length 31;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy
1 RGCTAGCHACACGA 16
:|||||:|||||
8 GGCTAGCTACACGA 23

RESULT 30
AX220552 31 bp DNA linear PAT 07-SEP-2001
LOCUS
DEFINITION
Sequence 5994 from Patent WO0159103.
ACCESSION
AX220552
VERSION
AX220552.1 GI:15548276
KEYWORDS
SOURCE
synthetic construct
ORGANISM
synthetic construct
artificial sequences.

REFERENCE
1
AUTHORS
Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL
Patent: WO 0159103-A 5994 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
location/Qualifiers

FEATURES
source
1. .31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT
ORIGIN
9 a 6 c 9 g 7 t

Query Match
Best Local Similarity 92.5%; Score 14.8; DB 6; Length 31;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy
1 RGCTAGCHACACGA 16
:|||||:|||||
8 GGCTAGCTACACGA 23

Db
1 RGCTAGCHACACGA 16
:|||||:|||||
8 GGCTAGCTACACGA 23

RESULT 31
AX220553 31 bp DNA linear PAT 07-SEP-2001
LOCUS
DEFINITION
Sequence 5995 from Patent WO0159103.
ACCESSION
AX220553
VERSION
AX220553.1 GI:15548277
KEYWORDS
SOURCE
synthetic construct
ORGANISM
synthetic construct
artificial sequences.

REFERENCE
1
AUTHORS
Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL
Patent: WO 0159103-A 5995 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
location/Qualifiers

FEATURES
source
1. .31

FEATURES
source
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
1. .31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT
ORIGIN
9 a 5 c 8 g 9 t

Query Match
Best Local Similarity 92.5%; Score 14.8; DB 6; Length 31;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy
1 RGCTAGCHACACGA 16
:|||||:|||||
8 GGCTAGCTACACGA 23

Db
1 RGCTAGCHACACGA 16
:|||||:|||||
8 GGCTAGCTACACGA 23

RESULT 32
AX220554 31 bp DNA linear PAT 07-SEP-2001
LOCUS
DEFINITION
Sequence 5996 from Patent WO0159103.
ACCESSION
AX220554
VERSION
AX220554.1 GI:15548278
KEYWORDS
SOURCE
synthetic construct
ORGANISM
synthetic construct
artificial sequences.

REFERENCE
1
AUTHORS
Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL
Patent: WO 0159103-A 5996 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
location/Qualifiers

FEATURES
source
1. .31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT
ORIGIN
9 a 6 c 6 g 10 t

Query Match
Best Local Similarity 92.5%; Score 14.8; DB 6; Length 31;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy
1 RGCTAGCHACACGA 16
:|||||:|||||
8 GGCTAGCTACACGA 23

Db
1 RGCTAGCHACACGA 16
:|||||:|||||
8 GGCTAGCTACACGA 23

RESULT 33
AX220555 31 bp DNA linear PAT 07-SEP-2001
LOCUS
DEFINITION
Sequence 5997 from Patent WO0159103.
ACCESSION
AX220555
VERSION
AX220555.1 GI:15548279
KEYWORDS
SOURCE
synthetic construct
ORGANISM
synthetic construct
artificial sequences.

REFERENCE
1
AUTHORS
Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL
Patent: WO 0159103-A 5997 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
location/Qualifiers

FEATURES
source
1. .31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

BASE COUNT 8 a 7 c 9 g 7 t
ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 31;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGGACACGA 16
8 GGGCTAGCTACACGA 23

RESULT 34
AX220556 31 bp DNA linear PAT 07-SEP-2001
LOCUS Sequence 5998 from Patent WO0159103.
DEFINITION AX220556
ACCESSION AX220556.1 GI:15548280
VERSION
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1 Blatt, L., McSwiggen, J. and Chowrira, B.M.
AUTHORS Method and reagent for the modulation and diagnosis of cd20 and
TITLE nogo gene expression
JOURNAL Patent: WO 0159103-A 5998 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)

FEATURES
source 1..31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT 11 a 6 c 9 g 5 t
ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 31;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGGACACGA 16
8 GGGCTAGCTACACGA 23

RESULT 35
AX220557 31 bp DNA linear PAT 07-SEP-2001
LOCUS Sequence 5999 from Patent WO0159103.
DEFINITION AX220557
ACCESSION AX220557.1 GI:15548281
VERSION
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1 Blatt, L., McSwiggen, J. and Chowrira, B.M.
AUTHORS Method and reagent for the modulation and diagnosis of cd20 and
TITLE nogo gene expression
JOURNAL Patent: WO 0159103-A 5999 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)

FEATURES
source 1..31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT 11 a 6 c 8 g 6 t
ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 31;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGGACACGA 16
8 GGGCTAGCTACACGA 23

RESULT 36
AX220558 31 bp DNA linear PAT 07-SEP-2001
LOCUS Sequence 6000 from Patent WO0159103.
DEFINITION AX220558
ACCESSION AX220558.1 GI:15548282
VERSION
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1 Blatt, L., McSwiggen, J. and Chowrira, B.M.
AUTHORS Method and reagent for the modulation and diagnosis of cd20 and
TITLE nogo gene expression
JOURNAL Patent: WO 0159103-A 6000 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)

FEATURES
source 1..31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT 8 a 10 c 7 g 6 t
ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 31;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGGACACGA 16
8 AGGCTAGCTACACGA 23

RESULT 37
AX220559 31 bp DNA linear PAT 07-SEP-2001
LOCUS Sequence 6001 from Patent WO0159103.
DEFINITION AX220559
ACCESSION AX220559.1 GI:15548283
VERSION
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1 Blatt, L., McSwiggen, J. and Chowrira, B.M.
AUTHORS Method and reagent for the modulation and diagnosis of cd20 and
TITLE nogo gene expression
JOURNAL Patent: WO 0159103-A 6001 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)

FEATURES
source 1..31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT 8 a 10 c 6 g 7 t
ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 31;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;

Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACACGA 16
:|||||:|||||
Db 8 AGGCTAGCTACACGA 23

RESULT 38
AX220560
LOCUS AX220560 31 bp DNA linear PAT 07-SEP-2001
DEFINITION Sequence 6002 from Patent WO0159103.
ACCESSION AX220560
VERSION AX220560.1 GI:15548284
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Blatt, L., McSwiggen, J. and Chowitra, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 6002 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowitra, Bharat M. (US)
FEATURES
source
1. .31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT 8 a 12 c 5 g 6 t

ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 31;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACACGA 16
:|||||:|||||
Db 8 AGGCTAGCTACACGA 23

RESULT 39
AX220561
LOCUS AX220561 31 bp DNA linear PAT 07-SEP-2001
DEFINITION Sequence 6003 from Patent WO0159103.
ACCESSION AX220561
VERSION AX220561.1 GI:15548285
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Blatt, L., McSwiggen, J. and Chowitra, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 6003 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowitra, Bharat M. (US)
FEATURES
source
1. .31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT 12 a 9 c 5 g 5 t

ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 31;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACACGA 16
:|||||:|||||
Db 8 AGGCTAGCTACACGA 23

Db 8 AGGCTAGCTACACGA 23
:|||||:|||||

RESULT 40
AX220562
LOCUS AX220562 31 bp DNA linear PAT 07-SEP-2001
DEFINITION Sequence 6004 from Patent WO0159103.
ACCESSION AX220562
VERSION AX220562.1 GI:15548286
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Blatt, L., McSwiggen, J. and Chowitra, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 6004 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowitra, Bharat M. (US)
FEATURES
source
1. .31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT 13 a 6 c 7 g 5 t

ORIGIN

Query Match 92.5%; Score 14.8; DB 6; Length 31;
Best Local Similarity 87.5%; Pred. No. 3.1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCHACACGA 16
:|||||:|||||
Db 8 GGGCTAGCTACACGA 23

Search completed: January 21, 2004, 07:26:45
Job time : 1007 secs

THIS PAGE BLANK (USPTO)

Lacourciere
09/423035 Page 1
Seq. IDs 121 & 122

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 05:19:13 ; Search time 1004.5 Seconds
(without alignments)
651.622 Million cell updates/sec

Title: US-09-423-035B-121
Perfect score: 16
Sequence: 1 rggctagctacaaga 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues
Total number of hits satisfying chosen parameters: 1520254

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_cm:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: gb_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vi:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htg_mus:*
- 34: em_htg_pln:*
- 35: em_htg_rdd:*
- 36: em_htg_mam:*
- 37: em_htg_vrt:*
- 38: em_sy:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.6	97.5	16	AX223826	AX223826 Sequence
2	15.6	97.5	16	AX229619	AX229619 Sequence
3	15.6	97.5	16	AX274735	AX274735 Sequence
4	15.6	97.5	16	AX282449	AX282449 Sequence
5	15.6	97.5	16	AX227010	AX227010 Sequence
6	15.6	97.5	16	AX583609	AX583609 Sequence
7	15.6	97.5	29	AR201808	AR201808 Sequence
8	15.6	97.5	29	AR201810	AR201810 Sequence
9	15.6	97.5	30	AR201840	AR201840 Sequence
10	15.6	97.5	30	AX009377	AX009377 Sequence
11	15.6	97.5	30	AX111628	AX111628 Sequence
12	15.6	97.5	30	AX274718	AX274718 Sequence
13	15.6	97.5	30	AX274719	AX274719 Sequence
14	15.6	97.5	30	AX274720	AX274720 Sequence
15	15.6	97.5	30	AX274721	AX274721 Sequence
16	15.6	97.5	30	AX274722	AX274722 Sequence
17	15.6	97.5	31	AR116975	AR116975 Sequence
18	15.6	97.5	31	AR201827	AR201827 Sequence
19	15.6	97.5	31	AR201830	AR201830 Sequence
20	15.6	97.5	31	AR201833	AR201833 Sequence
21	15.6	97.5	31	AR201836	AR201836 Sequence
22	15.6	97.5	31	AR204371	AR204371 Sequence
23	15.6	97.5	31	AX220546	AX220546 Sequence
24	15.6	97.5	31	AX220547	AX220547 Sequence
25	15.6	97.5	31	AX220548	AX220548 Sequence
26	15.6	97.5	31	AX220549	AX220549 Sequence
27	15.6	97.5	31	AX220550	AX220550 Sequence
28	15.6	97.5	31	AX220551	AX220551 Sequence
29	15.6	97.5	31	AX220552	AX220552 Sequence
30	15.6	97.5	31	AX220553	AX220553 Sequence
31	15.6	97.5	31	AX220554	AX220554 Sequence
32	15.6	97.5	31	AX220555	AX220555 Sequence
33	15.6	97.5	31	AX220556	AX220556 Sequence
34	15.6	97.5	31	AX220557	AX220557 Sequence
35	15.6	97.5	31	AX220558	AX220558 Sequence
36	15.6	97.5	31	AX220559	AX220559 Sequence
37	15.6	97.5	31	AX220560	AX220560 Sequence
38	15.6	97.5	31	AX220561	AX220561 Sequence
39	15.6	97.5	31	AX220562	AX220562 Sequence
40	15.6	97.5	31	AX220563	AX220563 Sequence
41	15.6	97.5	31	AX220564	AX220564 Sequence
42	15.6	97.5	31	AX220565	AX220565 Sequence
43	15.6	97.5	31	AX220566	AX220566 Sequence
44	15.6	97.5	31	AX220567	AX220567 Sequence
45	15.6	97.5	31	AX220568	AX220568 Sequence
46	15.6	97.5	31	AX220569	AX220569 Sequence
47	15.6	97.5	31	AX220570	AX220570 Sequence
48	15.6	97.5	31	AX220571	AX220571 Sequence
49	15.6	97.5	31	AX220572	AX220572 Sequence
50	15.6	97.5	31	AX220573	AX220573 Sequence
51	15.6	97.5	31	AX220574	AX220574 Sequence
52	15.6	97.5	31	AX220575	AX220575 Sequence
53	15.6	97.5	31	AX220576	AX220576 Sequence
54	15.6	97.5	31	AX220577	AX220577 Sequence
55	15.6	97.5	31	AX220578	AX220578 Sequence
56	15.6	97.5	31	AX220579	AX220579 Sequence
57	15.6	97.5	31	AX220580	AX220580 Sequence
58	15.6	97.5	31	AX220581	AX220581 Sequence
59	15.6	97.5	31	AX220582	AX220582 Sequence
60	15.6	97.5	31	AX220583	AX220583 Sequence
61	15.6	97.5	31	AX220584	AX220584 Sequence
62	15.6	97.5	31	AX220585	AX220585 Sequence
63	15.6	97.5	31	AX220586	AX220586 Sequence
64	15.6	97.5	31	AX220587	AX220587 Sequence
65	15.6	97.5	31	AX220588	AX220588 Sequence

212	15.6	97.5	31	6	AX220735	Sequence	285	15.6	97.5	31	6	AX220808	Sequence	AX220809	Sequence
213	15.6	97.5	31	6	AX220736	Sequence	286	15.6	97.5	31	6	AX220809	Sequence	AX220810	Sequence
214	15.6	97.5	31	6	AX220737	Sequence	287	15.6	97.5	31	6	AX220810	Sequence	AX220811	Sequence
215	15.6	97.5	31	6	AX220738	Sequence	288	15.6	97.5	31	6	AX220811	Sequence	AX220812	Sequence
216	15.6	97.5	31	6	AX220739	Sequence	289	15.6	97.5	31	6	AX220812	Sequence	AX220813	Sequence
217	15.6	97.5	31	6	AX220740	Sequence	290	15.6	97.5	31	6	AX220813	Sequence	AX220814	Sequence
218	15.6	97.5	31	6	AX220741	Sequence	291	15.6	97.5	31	6	AX220814	Sequence	AX220815	Sequence
219	15.6	97.5	31	6	AX220742	Sequence	292	15.6	97.5	31	6	AX220815	Sequence	AX220816	Sequence
220	15.6	97.5	31	6	AX220743	Sequence	293	15.6	97.5	31	6	AX220816	Sequence	AX220817	Sequence
221	15.6	97.5	31	6	AX220744	Sequence	294	15.6	97.5	31	6	AX220817	Sequence	AX220818	Sequence
222	15.6	97.5	31	6	AX220745	Sequence	295	15.6	97.5	31	6	AX220818	Sequence	AX220819	Sequence
223	15.6	97.5	31	6	AX220746	Sequence	296	15.6	97.5	31	6	AX220819	Sequence	AX220820	Sequence
224	15.6	97.5	31	6	AX220747	Sequence	297	15.6	97.5	31	6	AX220820	Sequence	AX220821	Sequence
225	15.6	97.5	31	6	AX220748	Sequence	298	15.6	97.5	31	6	AX220821	Sequence	AX220822	Sequence
226	15.6	97.5	31	6	AX220749	Sequence	299	15.6	97.5	31	6	AX220822	Sequence	AX220823	Sequence
227	15.6	97.5	31	6	AX220750	Sequence	300	15.6	97.5	31	6	AX220823	Sequence	AX220824	Sequence
228	15.6	97.5	31	6	AX220751	Sequence	301	15.6	97.5	31	6	AX220824	Sequence	AX220825	Sequence
229	15.6	97.5	31	6	AX220752	Sequence	302	15.6	97.5	31	6	AX220825	Sequence	AX220826	Sequence
230	15.6	97.5	31	6	AX220753	Sequence	303	15.6	97.5	31	6	AX220826	Sequence	AX220827	Sequence
231	15.6	97.5	31	6	AX220754	Sequence	304	15.6	97.5	31	6	AX220827	Sequence	AX220828	Sequence
232	15.6	97.5	31	6	AX220755	Sequence	305	15.6	97.5	31	6	AX220828	Sequence	AX220829	Sequence
233	15.6	97.5	31	6	AX220756	Sequence	306	15.6	97.5	31	6	AX220829	Sequence	AX220830	Sequence
234	15.6	97.5	31	6	AX220757	Sequence	307	15.6	97.5	31	6	AX220830	Sequence	AX220831	Sequence
235	15.6	97.5	31	6	AX220758	Sequence	308	15.6	97.5	31	6	AX220831	Sequence	AX220832	Sequence
236	15.6	97.5	31	6	AX220759	Sequence	309	15.6	97.5	31	6	AX220832	Sequence	AX220833	Sequence
237	15.6	97.5	31	6	AX220760	Sequence	310	15.6	97.5	31	6	AX220833	Sequence	AX220834	Sequence
238	15.6	97.5	31	6	AX220761	Sequence	311	15.6	97.5	31	6	AX220834	Sequence	AX220835	Sequence
239	15.6	97.5	31	6	AX220762	Sequence	312	15.6	97.5	31	6	AX220835	Sequence	AX220836	Sequence
240	15.6	97.5	31	6	AX220763	Sequence	313	15.6	97.5	31	6	AX220836	Sequence	AX220837	Sequence
241	15.6	97.5	31	6	AX220764	Sequence	314	15.6	97.5	31	6	AX220837	Sequence	AX220838	Sequence
242	15.6	97.5	31	6	AX220765	Sequence	315	15.6	97.5	31	6	AX220838	Sequence	AX220839	Sequence
243	15.6	97.5	31	6	AX220766	Sequence	316	15.6	97.5	31	6	AX220839	Sequence	AX220840	Sequence
244	15.6	97.5	31	6	AX220767	Sequence	317	15.6	97.5	31	6	AX220840	Sequence	AX220841	Sequence
245	15.6	97.5	31	6	AX220768	Sequence	318	15.6	97.5	31	6	AX220841	Sequence	AX220842	Sequence
246	15.6	97.5	31	6	AX220769	Sequence	319	15.6	97.5	31	6	AX220842	Sequence	AX220843	Sequence
247	15.6	97.5	31	6	AX220770	Sequence	320	15.6	97.5	31	6	AX220843	Sequence	AX220844	Sequence
248	15.6	97.5	31	6	AX220771	Sequence	321	15.6	97.5	31	6	AX220844	Sequence	AX220845	Sequence
249	15.6	97.5	31	6	AX220772	Sequence	322	15.6	97.5	31	6	AX220845	Sequence	AX220846	Sequence
250	15.6	97.5	31	6	AX220773	Sequence	323	15.6	97.5	31	6	AX220846	Sequence	AX220847	Sequence
251	15.6	97.5	31	6	AX220774	Sequence	324	15.6	97.5	31	6	AX220847	Sequence	AX220848	Sequence
252	15.6	97.5	31	6	AX220775	Sequence	325	15.6	97.5	31	6	AX220848	Sequence	AX220849	Sequence
253	15.6	97.5	31	6	AX220776	Sequence	326	15.6	97.5	31	6	AX220849	Sequence	AX220850	Sequence
254	15.6	97.5	31	6	AX220777	Sequence	327	15.6	97.5	31	6	AX220850	Sequence	AX220851	Sequence
255	15.6	97.5	31	6	AX220778	Sequence	328	15.6	97.5	31	6	AX220851	Sequence	AX220852	Sequence
256	15.6	97.5	31	6	AX220779	Sequence	329	15.6	97.5	31	6	AX220852	Sequence	AX220853	Sequence
257	15.6	97.5	31	6	AX220780	Sequence	330	15.6	97.5	31	6	AX220853	Sequence	AX220854	Sequence
258	15.6	97.5	31	6	AX220781	Sequence	331	15.6	97.5	31	6	AX220854	Sequence	AX220855	Sequence
259	15.6	97.5	31	6	AX220782	Sequence	332	15.6	97.5	31	6	AX220855	Sequence	AX220856	Sequence
260	15.6	97.5	31	6	AX220783	Sequence	333	15.6	97.5	31	6	AX220856	Sequence	AX220857	Sequence
261	15.6	97.5	31	6	AX220784	Sequence	334	15.6	97.5	31	6	AX220857	Sequence	AX220858	Sequence
262	15.6	97.5	31	6	AX220785	Sequence	335	15.6	97.5	31	6	AX220858	Sequence	AX220859	Sequence
263	15.6	97.5	31	6	AX220786	Sequence	336	15.6	97.5	31	6	AX220859	Sequence	AX220860	Sequence
264	15.6	97.5	31	6	AX220787	Sequence	337	15.6	97.5	31	6	AX220860	Sequence	AX220861	Sequence
265	15.6	97.5	31	6	AX220788	Sequence	338	15.6	97.5	31	6	AX220861	Sequence	AX220862	Sequence
266	15.6	97.5	31	6	AX220789	Sequence	339	15.6	97.5	31	6	AX220862	Sequence	AX220863	Sequence
267	15.6	97.5	31	6	AX220790	Sequence	340	15.6	97.5	31	6	AX220863	Sequence	AX220864	Sequence
268	15.6	97.5	31	6	AX220791	Sequence	341	15.6	97.5	31	6	AX220864	Sequence	AX220865	Sequence
269	15.6	97.5	31	6	AX220792	Sequence	342	15.6	97.5	31	6	AX220865	Sequence	AX220866	Sequence
270	15.6	97.5	31	6	AX220793	Sequence	343	15.6	97.5	31	6	AX220866	Sequence	AX220867	Sequence
271	15.6	97.5	31	6	AX220794	Sequence	344	15.6	97.5	31	6	AX220867	Sequence	AX220868	Sequence
272	15.6	97.5	31	6	AX220795	Sequence	345	15.6	97.5	31	6	AX220868	Sequence	AX220869	Sequence
273	15.6	97.5	31	6	AX220796	Sequence	346	15.6	97.5	31	6	AX220869	Sequence	AX220870	Sequence
274	15.6	97.5	31	6	AX220797	Sequence	347	15.6	97.5	31	6	AX220870	Sequence	AX220871	Sequence
275	15.6	97.5	31	6	AX220798	Sequence	348	15.6	97.5	31	6	AX220871	Sequence	AX220872	Sequence
276	15.6	97.5	31	6	AX220799	Sequence	349	15.6	97.5	31	6	AX220872	Sequence	AX220873	Sequence
277	15.6	97.5	31	6	AX220800	Sequence	350	15.6	97.5	31	6	AX220873	Sequence	AX220874	Sequence
278	15.6	97.5	31	6	AX220801	Sequence	351	15.6	97.5	31	6	AX220874	Sequence	AX220875	Sequence
279	15.6	97.5	31	6	AX220802	Sequence	352	15.6	97.5	31	6	AX220875	Sequence	AX220876	Sequence
280	15.6	97.5	31	6	AX220803	Sequence	353	15.6	97.5	31	6	AX220876	Sequence	AX220877	Sequence
281	15.6	97.5	31	6	AX220804	Sequence	354	15.6	97.5	31	6	AX220877	Sequence	AX220878	Sequence
282	15.6	97.5	31	6	AX220805	Sequence	355	15.6	97.5	31	6	AX220878	Sequence	AX220879	Sequence
283	15.6	97.5	31	6	AX220806	Sequence	356	15.6	97.5	31	6	AX220879	Sequence	AX220880	Sequence
284	15.6	97.5	31	6	AX220807	Sequence	357	15.6	97.5	31	6	AX220880	Sequence		

358	15.6	97.5	31	6	AX220881	Sequence	431	15.6	97.5	31	6	AX220954	Sequence	AX220954
359	15.6	97.5	31	6	AX220882	Sequence	432	15.6	97.5	31	6	AX220955	Sequence	AX220955
360	15.6	97.5	31	6	AX220883	Sequence	433	15.6	97.5	31	6	AX220956	Sequence	AX220956
361	15.6	97.5	31	6	AX220884	Sequence	434	15.6	97.5	31	6	AX220957	Sequence	AX220957
362	15.6	97.5	31	6	AX220885	Sequence	435	15.6	97.5	31	6	AX220958	Sequence	AX220958
363	15.6	97.5	31	6	AX220886	Sequence	436	15.6	97.5	31	6	AX220959	Sequence	AX220959
364	15.6	97.5	31	6	AX220887	Sequence	437	15.6	97.5	31	6	AX220960	Sequence	AX220960
365	15.6	97.5	31	6	AX220888	Sequence	438	15.6	97.5	31	6	AX220961	Sequence	AX220961
366	15.6	97.5	31	6	AX220889	Sequence	439	15.6	97.5	31	6	AX220962	Sequence	AX220962
367	15.6	97.5	31	6	AX220890	Sequence	440	15.6	97.5	31	6	AX220963	Sequence	AX220963
368	15.6	97.5	31	6	AX220891	Sequence	441	15.6	97.5	31	6	AX220964	Sequence	AX220964
369	15.6	97.5	31	6	AX220892	Sequence	442	15.6	97.5	31	6	AX220965	Sequence	AX220965
370	15.6	97.5	31	6	AX220893	Sequence	443	15.6	97.5	31	6	AX220966	Sequence	AX220966
371	15.6	97.5	31	6	AX220894	Sequence	444	15.6	97.5	31	6	AX220967	Sequence	AX220967
372	15.6	97.5	31	6	AX220895	Sequence	445	15.6	97.5	31	6	AX220968	Sequence	AX220968
373	15.6	97.5	31	6	AX220896	Sequence	446	15.6	97.5	31	6	AX220969	Sequence	AX220969
374	15.6	97.5	31	6	AX220897	Sequence	447	15.6	97.5	31	6	AX220970	Sequence	AX220970
375	15.6	97.5	31	6	AX220898	Sequence	448	15.6	97.5	31	6	AX220971	Sequence	AX220971
376	15.6	97.5	31	6	AX220899	Sequence	449	15.6	97.5	31	6	AX220972	Sequence	AX220972
377	15.6	97.5	31	6	AX220898	Sequence	450	15.6	97.5	31	6	AX220973	Sequence	AX220973
378	15.6	97.5	31	6	AX220900	Sequence	451	15.6	97.5	31	6	AX220974	Sequence	AX220974
379	15.6	97.5	31	6	AX220901	Sequence	452	15.6	97.5	31	6	AX220975	Sequence	AX220975
380	15.6	97.5	31	6	AX220902	Sequence	453	15.6	97.5	31	6	AX220976	Sequence	AX220976
381	15.6	97.5	31	6	AX220903	Sequence	454	15.6	97.5	31	6	AX220977	Sequence	AX220977
382	15.6	97.5	31	6	AX220904	Sequence	455	15.6	97.5	31	6	AX220978	Sequence	AX220978
383	15.6	97.5	31	6	AX220905	Sequence	456	15.6	97.5	31	6	AX220979	Sequence	AX220979
384	15.6	97.5	31	6	AX220906	Sequence	457	15.6	97.5	31	6	AX220980	Sequence	AX220980
385	15.6	97.5	31	6	AX220907	Sequence	458	15.6	97.5	31	6	AX220981	Sequence	AX220981
386	15.6	97.5	31	6	AX220908	Sequence	459	15.6	97.5	31	6	AX220982	Sequence	AX220982
387	15.6	97.5	31	6	AX220909	Sequence	460	15.6	97.5	31	6	AX220983	Sequence	AX220983
388	15.6	97.5	31	6	AX220910	Sequence	461	15.6	97.5	31	6	AX220984	Sequence	AX220984
389	15.6	97.5	31	6	AX220911	Sequence	462	15.6	97.5	31	6	AX220985	Sequence	AX220985
390	15.6	97.5	31	6	AX220912	Sequence	463	15.6	97.5	31	6	AX220986	Sequence	AX220986
391	15.6	97.5	31	6	AX220913	Sequence	464	15.6	97.5	31	6	AX220987	Sequence	AX220987
392	15.6	97.5	31	6	AX220914	Sequence	465	15.6	97.5	31	6	AX220988	Sequence	AX220988
393	15.6	97.5	31	6	AX220915	Sequence	466	15.6	97.5	31	6	AX220989	Sequence	AX220989
394	15.6	97.5	31	6	AX220916	Sequence	467	15.6	97.5	31	6	AX220990	Sequence	AX220990
395	15.6	97.5	31	6	AX220917	Sequence	468	15.6	97.5	31	6	AX220991	Sequence	AX220991
396	15.6	97.5	31	6	AX220918	Sequence	469	15.6	97.5	31	6	AX220992	Sequence	AX220992
397	15.6	97.5	31	6	AX220919	Sequence	470	15.6	97.5	31	6	AX220993	Sequence	AX220993
398	15.6	97.5	31	6	AX220920	Sequence	471	15.6	97.5	31	6	AX220994	Sequence	AX220994
399	15.6	97.5	31	6	AX220921	Sequence	472	15.6	97.5	31	6	AX220995	Sequence	AX220995
400	15.6	97.5	31	6	AX220922	Sequence	473	15.6	97.5	31	6	AX220996	Sequence	AX220996
401	15.6	97.5	31	6	AX220923	Sequence	474	15.6	97.5	31	6	AX220997	Sequence	AX220997
402	15.6	97.5	31	6	AX220924	Sequence	475	15.6	97.5	31	6	AX220998	Sequence	AX220998
403	15.6	97.5	31	6	AX220925	Sequence	476	15.6	97.5	31	6	AX220999	Sequence	AX220999
404	15.6	97.5	31	6	AX220926	Sequence	477	15.6	97.5	31	6	AX221000	Sequence	AX221000
405	15.6	97.5	31	6	AX220927	Sequence	478	15.6	97.5	31	6	AX221001	Sequence	AX221001
406	15.6	97.5	31	6	AX220928	Sequence	479	15.6	97.5	31	6	AX221002	Sequence	AX221002
407	15.6	97.5	31	6	AX220929	Sequence	480	15.6	97.5	31	6	AX221003	Sequence	AX221003
408	15.6	97.5	31	6	AX220930	Sequence	481	15.6	97.5	31	6	AX221004	Sequence	AX221004
409	15.6	97.5	31	6	AX220931	Sequence	482	15.6	97.5	31	6	AX221005	Sequence	AX221005
410	15.6	97.5	31	6	AX220932	Sequence	483	15.6	97.5	31	6	AX221006	Sequence	AX221006
411	15.6	97.5	31	6	AX220933	Sequence	484	15.6	97.5	31	6	AX221007	Sequence	AX221007
412	15.6	97.5	31	6	AX220934	Sequence	485	15.6	97.5	31	6	AX221008	Sequence	AX221008
413	15.6	97.5	31	6	AX220935	Sequence	486	15.6	97.5	31	6	AX221009	Sequence	AX221009
414	15.6	97.5	31	6	AX220936	Sequence	487	15.6	97.5	31	6	AX221010	Sequence	AX221010
415	15.6	97.5	31	6	AX220937	Sequence	488	15.6	97.5	31	6	AX221011	Sequence	AX221011
416	15.6	97.5	31	6	AX220938	Sequence	489	15.6	97.5	31	6	AX221012	Sequence	AX221012
417	15.6	97.5	31	6	AX220939	Sequence	490	15.6	97.5	31	6	AX221013	Sequence	AX221013
418	15.6	97.5	31	6	AX220940	Sequence	491	15.6	97.5	31	6	AX221014	Sequence	AX221014
419	15.6	97.5	31	6	AX220941	Sequence	492	15.6	97.5	31	6	AX221015	Sequence	AX221015
420	15.6	97.5	31	6	AX220942	Sequence	493	15.6	97.5	31	6	AX221016	Sequence	AX221016
421	15.6	97.5	31	6	AX220943	Sequence	494	15.6	97.5	31	6	AX221017	Sequence	AX221017
422	15.6	97.5	31	6	AX220944	Sequence	495	15.6	97.5	31	6	AX221018	Sequence	AX221018
423	15.6	97.5	31	6	AX220945	Sequence	496	15.6	97.5	31	6	AX221019	Sequence	AX221019
424	15.6	97.5	31	6	AX220946	Sequence	497	15.6	97.5	31	6	AX221020	Sequence	AX221020
425	15.6	97.5	31	6	AX220947	Sequence	498	15.6	97.5	31	6	AX221021	Sequence	AX221021
426	15.6	97.5	31	6	AX220948	Sequence	499	15.6	97.5	31	6	AX221022	Sequence	AX221022
427	15.6	97.5	31	6	AX220949	Sequence	500	15.6	97.5	31	6	AX221023	Sequence	AX221023
428	15.6	97.5	31	6	AX220950	Sequence	501	15.6	97.5	31	6	AX221024	Sequence	AX221024
429	15.6	97.5	31	6	AX220951	Sequence	502	15.6	97.5	31	6	AX221025	Sequence	AX221025
430	15.6	97.5	31	6	AX220952	Sequence	503	15.6	97.5	31	6	AX221026	Sequence	AX221026
					AX220953	Sequence								AX220954
														AX220955
														AX220956
														AX220957
														AX220958
														AX220959
														AX220960
														AX220961
														AX220962
														AX220963
														AX220964
														AX220965
														AX220966
														AX220967
														AX220968
														AX220969
														AX220970
														AX220971
														AX220972
														AX220973
														AX220974
														AX220975
														AX220976
														AX220977
														AX220978
														AX220979
														AX220980
														AX220981
														AX220982
														AX220983
														AX220984
														AX220985
														AX220986
														AX220987
														AX220988
														AX220989
														AX220990
														AX220991
														AX220992
														AX220993

504	15.6	97.5	31	6	AX221027	Sequence	AX221027	Sequence	577	15.6	97.5	31	6	AX221100	Sequence	AX221100	Sequence
505	15.6	97.5	31	6	AX221028	Sequence	AX221028	Sequence	578	15.6	97.5	31	6	AX221101	Sequence	AX221101	Sequence
506	15.6	97.5	31	6	AX221029	Sequence	AX221029	Sequence	579	15.6	97.5	31	6	AX221102	Sequence	AX221102	Sequence
507	15.6	97.5	31	6	AX221030	Sequence	AX221030	Sequence	580	15.6	97.5	31	6	AX221103	Sequence	AX221103	Sequence
508	15.6	97.5	31	6	AX221031	Sequence	AX221031	Sequence	581	15.6	97.5	31	6	AX221104	Sequence	AX221104	Sequence
509	15.6	97.5	31	6	AX221032	Sequence	AX221032	Sequence	582	15.6	97.5	31	6	AX221105	Sequence	AX221105	Sequence
510	15.6	97.5	31	6	AX221033	Sequence	AX221033	Sequence	583	15.6	97.5	31	6	AX221106	Sequence	AX221106	Sequence
511	15.6	97.5	31	6	AX221034	Sequence	AX221034	Sequence	584	15.6	97.5	31	6	AX221107	Sequence	AX221107	Sequence
512	15.6	97.5	31	6	AX221035	Sequence	AX221035	Sequence	585	15.6	97.5	31	6	AX221108	Sequence	AX221108	Sequence
513	15.6	97.5	31	6	AX221036	Sequence	AX221036	Sequence	586	15.6	97.5	31	6	AX221109	Sequence	AX221109	Sequence
514	15.6	97.5	31	6	AX221037	Sequence	AX221037	Sequence	587	15.6	97.5	31	6	AX221110	Sequence	AX221110	Sequence
515	15.6	97.5	31	6	AX221038	Sequence	AX221038	Sequence	588	15.6	97.5	31	6	AX221111	Sequence	AX221111	Sequence
516	15.6	97.5	31	6	AX221039	Sequence	AX221039	Sequence	589	15.6	97.5	31	6	AX221112	Sequence	AX221112	Sequence
517	15.6	97.5	31	6	AX221040	Sequence	AX221040	Sequence	590	15.6	97.5	31	6	AX221113	Sequence	AX221113	Sequence
518	15.6	97.5	31	6	AX221041	Sequence	AX221041	Sequence	591	15.6	97.5	31	6	AX221114	Sequence	AX221114	Sequence
519	15.6	97.5	31	6	AX221042	Sequence	AX221042	Sequence	592	15.6	97.5	31	6	AX221115	Sequence	AX221115	Sequence
520	15.6	97.5	31	6	AX221043	Sequence	AX221043	Sequence	593	15.6	97.5	31	6	AX221116	Sequence	AX221116	Sequence
521	15.6	97.5	31	6	AX221044	Sequence	AX221044	Sequence	594	15.6	97.5	31	6	AX221117	Sequence	AX221117	Sequence
522	15.6	97.5	31	6	AX221045	Sequence	AX221045	Sequence	595	15.6	97.5	31	6	AX221118	Sequence	AX221118	Sequence
523	15.6	97.5	31	6	AX221046	Sequence	AX221046	Sequence	596	15.6	97.5	31	6	AX221119	Sequence	AX221119	Sequence
524	15.6	97.5	31	6	AX221047	Sequence	AX221047	Sequence	597	15.6	97.5	31	6	AX221120	Sequence	AX221120	Sequence
525	15.6	97.5	31	6	AX221048	Sequence	AX221048	Sequence	598	15.6	97.5	31	6	AX221121	Sequence	AX221121	Sequence
526	15.6	97.5	31	6	AX221049	Sequence	AX221049	Sequence	599	15.6	97.5	31	6	AX221122	Sequence	AX221122	Sequence
527	15.6	97.5	31	6	AX221050	Sequence	AX221050	Sequence	600	15.6	97.5	31	6	AX221123	Sequence	AX221123	Sequence
528	15.6	97.5	31	6	AX221051	Sequence	AX221051	Sequence	601	15.6	97.5	31	6	AX221124	Sequence	AX221124	Sequence
529	15.6	97.5	31	6	AX221052	Sequence	AX221052	Sequence	602	15.6	97.5	31	6	AX221125	Sequence	AX221125	Sequence
530	15.6	97.5	31	6	AX221053	Sequence	AX221053	Sequence	603	15.6	97.5	31	6	AX221126	Sequence	AX221126	Sequence
531	15.6	97.5	31	6	AX221054	Sequence	AX221054	Sequence	604	15.6	97.5	31	6	AX221127	Sequence	AX221127	Sequence
532	15.6	97.5	31	6	AX221055	Sequence	AX221055	Sequence	605	15.6	97.5	31	6	AX221128	Sequence	AX221128	Sequence
533	15.6	97.5	31	6	AX221056	Sequence	AX221056	Sequence	606	15.6	97.5	31	6	AX221129	Sequence	AX221129	Sequence
534	15.6	97.5	31	6	AX221057	Sequence	AX221057	Sequence	607	15.6	97.5	31	6	AX221130	Sequence	AX221130	Sequence
535	15.6	97.5	31	6	AX221058	Sequence	AX221058	Sequence	608	15.6	97.5	31	6	AX221131	Sequence	AX221131	Sequence
536	15.6	97.5	31	6	AX221059	Sequence	AX221059	Sequence	609	15.6	97.5	31	6	AX221132	Sequence	AX221132	Sequence
537	15.6	97.5	31	6	AX221060	Sequence	AX221060	Sequence	610	15.6	97.5	31	6	AX221133	Sequence	AX221133	Sequence
538	15.6	97.5	31	6	AX221061	Sequence	AX221061	Sequence	611	15.6	97.5	31	6	AX221134	Sequence	AX221134	Sequence
539	15.6	97.5	31	6	AX221062	Sequence	AX221062	Sequence	612	15.6	97.5	31	6	AX221135	Sequence	AX221135	Sequence
540	15.6	97.5	31	6	AX221063	Sequence	AX221063	Sequence	613	15.6	97.5	31	6	AX221136	Sequence	AX221136	Sequence
541	15.6	97.5	31	6	AX221064	Sequence	AX221064	Sequence	614	15.6	97.5	31	6	AX221137	Sequence	AX221137	Sequence
542	15.6	97.5	31	6	AX221065	Sequence	AX221065	Sequence	615	15.6	97.5	31	6	AX221138	Sequence	AX221138	Sequence
543	15.6	97.5	31	6	AX221066	Sequence	AX221066	Sequence	616	15.6	97.5	31	6	AX221139	Sequence	AX221139	Sequence
544	15.6	97.5	31	6	AX221067	Sequence	AX221067	Sequence	617	15.6	97.5	31	6	AX221140	Sequence	AX221140	Sequence
545	15.6	97.5	31	6	AX221068	Sequence	AX221068	Sequence	618	15.6	97.5	31	6	AX221141	Sequence	AX221141	Sequence
546	15.6	97.5	31	6	AX221069	Sequence	AX221069	Sequence	619	15.6	97.5	31	6	AX221142	Sequence	AX221142	Sequence
547	15.6	97.5	31	6	AX221070	Sequence	AX221070	Sequence	620	15.6	97.5	31	6	AX221143	Sequence	AX221143	Sequence
548	15.6	97.5	31	6	AX221071	Sequence	AX221071	Sequence	621	15.6	97.5	31	6	AX221144	Sequence	AX221144	Sequence
549	15.6	97.5	31	6	AX221072	Sequence	AX221072	Sequence	622	15.6	97.5	31	6	AX221145	Sequence	AX221145	Sequence
550	15.6	97.5	31	6	AX221073	Sequence	AX221073	Sequence	623	15.6	97.5	31	6	AX221146	Sequence	AX221146	Sequence
551	15.6	97.5	31	6	AX221074	Sequence	AX221074	Sequence	624	15.6	97.5	31	6	AX221147	Sequence	AX221147	Sequence
552	15.6	97.5	31	6	AX221075	Sequence	AX221075	Sequence	625	15.6	97.5	31	6	AX221148	Sequence	AX221148	Sequence
553	15.6	97.5	31	6	AX221076	Sequence	AX221076	Sequence	626	15.6	97.5	31	6	AX221149	Sequence	AX221149	Sequence
554	15.6	97.5	31	6	AX221077	Sequence	AX221077	Sequence	627	15.6	97.5	31	6	AX221150	Sequence	AX221150	Sequence
555	15.6	97.5	31	6	AX221078	Sequence	AX221078	Sequence	628	15.6	97.5	31	6	AX221151	Sequence	AX221151	Sequence
556	15.6	97.5	31	6	AX221079	Sequence	AX221079	Sequence	629	15.6	97.5	31	6	AX221152	Sequence	AX221152	Sequence
557	15.6	97.5	31	6	AX221080	Sequence	AX221080	Sequence	630	15.6	97.5	31	6	AX221153	Sequence	AX221153	Sequence
558	15.6	97.5	31	6	AX221081	Sequence	AX221081	Sequence	631	15.6	97.5	31	6	AX221154	Sequence	AX221154	Sequence
559	15.6	97.5	31	6	AX221082	Sequence	AX221082	Sequence	632	15.6	97.5	31	6	AX221155	Sequence	AX221155	Sequence
560	15.6	97.5	31	6	AX221083	Sequence	AX221083	Sequence	633	15.6	97.5	31	6	AX221156	Sequence	AX221156	Sequence
561	15.6	97.5	31	6	AX221084	Sequence	AX221084	Sequence	634	15.6	97.5	31	6	AX221157	Sequence	AX221157	Sequence
562	15.6	97.5	31	6	AX221085	Sequence	AX221085	Sequence	635	15.6	97.5	31	6	AX221158	Sequence	AX221158	Sequence
563	15.6	97.5	31	6	AX221086	Sequence	AX221086	Sequence	636	15.6	97.5	31	6	AX221159	Sequence	AX221159	Sequence
564	15.6	97.5	31	6	AX221087	Sequence	AX221087	Sequence	637	15.6	97.5	31	6	AX221160	Sequence	AX221160	Sequence
565	15.6	97.5	31	6	AX221088	Sequence	AX221088	Sequence	638	15.6	97.5	31	6	AX221161	Sequence	AX221161	Sequence
566	15.6	97.5	31	6	AX221089	Sequence	AX221089	Sequence	639	15.6	97.5	31	6	AX221162	Sequence	AX221162	Sequence
567	15.6	97.5	31	6	AX221090	Sequence	AX221090	Sequence	640	15.6	97.5	31	6	AX221163	Sequence	AX221163	Sequence
568	15.6	97.5	31	6	AX221091	Sequence	AX221091	Sequence	641	15.6	97.5	31	6	AX221164	Sequence	AX221164	Sequence
569	15.6	97.5	31	6	AX221092	Sequence	AX221092	Sequence	642	15.6	97.5	31	6	AX221165	Sequence	AX221165	Sequence
570	15.6	97.5	31	6	AX221093	Sequence	AX221093	Sequence	643	15.6	97.5	31	6	AX221166	Sequence	AX221166	Sequence
571	15.6	97.5	31	6	AX221094	Sequence	AX221094	Sequence	644	15.6	97.5	31	6	AX221167	Sequence	AX221167	Sequence
572	15.6	97.5	31	6	AX221095	Sequence	AX221095	Sequence	645	15.6	97.5	31	6	AX221168	Sequence	AX221168	Sequence
573	15.6	97.5	31	6	AX221096	Sequence	AX221096	Sequence	646	15.6	97.5	31	6	AX221169	Sequence	AX221169	Sequence
574	15.6	97.5	31	6	AX221097	Sequence	AX221097	Sequence	647	15.6	97.5	31	6	AX221170	Sequence	AX221170	Sequence
575	15.6	97.5	31	6	AX221098	Sequence	AX221098	Sequence	648	15.6	97.5	31	6	AX221171	Sequence	AX221171	Sequence
576	15.6	97.5	31	6	AX221099	Sequence	AX221099	Sequence	649	15.6	97.5	31	6	AX221172	Sequence	AX221172	Sequence

942	15.6	97.5	31	6	AX223248	Sequence
943	15.6	97.5	31	6	AX223249	Sequence
944	15.6	97.5	31	6	AX223250	Sequence
945	15.6	97.5	31	6	AX223251	Sequence
946	15.6	97.5	31	6	AX223252	Sequence
947	15.6	97.5	31	6	AX223253	Sequence
948	15.6	97.5	31	6	AX223254	Sequence
949	15.6	97.5	31	6	AX223255	Sequence
950	15.6	97.5	31	6	AX223256	Sequence
951	15.6	97.5	31	6	AX223257	Sequence
952	15.6	97.5	31	6	AX223258	Sequence
953	15.6	97.5	31	6	AX223259	Sequence
954	15.6	97.5	31	6	AX223260	Sequence
955	15.6	97.5	31	6	AX223261	Sequence
956	15.6	97.5	31	6	AX223262	Sequence
957	15.6	97.5	31	6	AX223263	Sequence
958	15.6	97.5	31	6	AX223264	Sequence
959	15.6	97.5	31	6	AX223265	Sequence
960	15.6	97.5	31	6	AX223266	Sequence
961	15.6	97.5	31	6	AX223267	Sequence
962	15.6	97.5	31	6	AX223268	Sequence
963	15.6	97.5	31	6	AX223269	Sequence
964	15.6	97.5	31	6	AX223270	Sequence
965	15.6	97.5	31	6	AX223271	Sequence
966	15.6	97.5	31	6	AX223272	Sequence
967	15.6	97.5	31	6	AX223273	Sequence
968	15.6	97.5	31	6	AX223274	Sequence
969	15.6	97.5	31	6	AX223275	Sequence
970	15.6	97.5	31	6	AX223276	Sequence
971	15.6	97.5	31	6	AX223277	Sequence
972	15.6	97.5	31	6	AX223278	Sequence
973	15.6	97.5	31	6	AX223279	Sequence
974	15.6	97.5	31	6	AX223280	Sequence
975	15.6	97.5	31	6	AX223281	Sequence
976	15.6	97.5	31	6	AX223282	Sequence
977	15.6	97.5	31	6	AX223283	Sequence
978	15.6	97.5	31	6	AX223284	Sequence
979	15.6	97.5	31	6	AX223285	Sequence
980	15.6	97.5	31	6	AX223286	Sequence
981	15.6	97.5	31	6	AX223287	Sequence
982	15.6	97.5	31	6	AX223288	Sequence
983	15.6	97.5	31	6	AX223289	Sequence
984	15.6	97.5	31	6	AX223290	Sequence
985	15.6	97.5	31	6	AX223291	Sequence
986	15.6	97.5	31	6	AX223292	Sequence
987	15.6	97.5	31	6	AX223293	Sequence
988	15.6	97.5	31	6	AX223294	Sequence
989	15.6	97.5	31	6	AX223295	Sequence
990	15.6	97.5	31	6	AX223296	Sequence
991	15.6	97.5	31	6	AX223297	Sequence
992	15.6	97.5	31	6	AX223298	Sequence
993	15.6	97.5	31	6	AX223299	Sequence
994	15.6	97.5	31	6	AX223300	Sequence
995	15.6	97.5	31	6	AX223301	Sequence
996	15.6	97.5	31	6	AX223302	Sequence
997	15.6	97.5	31	6	AX223303	Sequence
998	15.6	97.5	31	6	AX223304	Sequence
999	15.6	97.5	31	6	AX223305	Sequence
1000	15.6	97.5	31	6	BD136890	Method of

ALIGNMENTS

RESULT 1
 LOCUS AX223826 16 bp DNA
 DEFINITION Sequence 9268 from Patent WO0159103.
 ACCESSION AX223826
 VERSION AX223826.1 GI:15551550
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct

linear PAT 07-SEP-2001

artificial sequences.
 REFERENCE 1
 AUTHORS Blatt, L., Mcswigen, J. and Chowrira, B.M.
 TITLE Method and reagent for the modulation and diagnosis of cd20 and
 JOURNAL nogo gene expression
 Patent: WO 0159103-A 9268 16-AUG-2001;
 RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
 Mcswigen, James (US) ; Chowrira, Bharat M. (US)
 Location/Qualifiers
 1..16
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="Nucleic Acid"
 BASE COUNT 5 a 4 c 4 g 2 t 1 others
 ORIGIN
 Query Match 97.5%; Score 15.6; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGCGTAGCTACACGA 16
 Db 1 RGCGTAGCTACACGA 16
 RESULT 3
 LOCUS AX274735 16 bp DNA
 DEFINITION Sequence 2304 from Patent WO0162911.
 ACCESSION AX274735
 VERSION AX274735.1 GI:16547474
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Jarvis, T., von Carlowitz, I., Mcswigen, J.A., Hamblin, P.A. and
 Ellis, J.H.
 TITLE Method and reagent for the inhibition of grid

JOURNAL Patent: WO 0162911-A 2304 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)

FEATURES
SOURCE
1. .16
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT 5 a 4 c 4 g 2 t 1 others

ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
1 RGGCTAGCTACACGA 16

Db 1 RGGCTAGCTACACGA 16

RESULT 4
AX282449 16 bp DNA linear PAT 02-NOV-2001
LOCUS Sequence 21 from Patent WO0166721.
DEFINITION AX282449
ACCESSION AX282449
VERSION AX282449.1 GI:16609580
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Ueman,N., Mcswigen,J.A., Zinnen,S., Seiwert,S., Haeblerl,P., Chowrita,B. and Blatt,J.
TITLE Nucleic acid sensor molecules
JOURNAL Patent: WO 0166721-A 21 13-SEP-2001;
RIBOZYME PHARMACEUTICALS, INC. (US)

FEATURES
SOURCE
1. .16
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid Motif"

BASE COUNT 5 a 4 c 4 g 2 t 1 others

ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
1 RGGCTAGCTACACGA 16

Db 1 RGGCTAGCTACACGA 16

RESULT 5
AX427010 16 bp DNA linear PAT 18-JUN-2002
LOCUS Sequence 5346 from Patent WO0188124.
DEFINITION AX427010
ACCESSION AX427010
VERSION AX427010.1 GI:21530396
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswigen,J.A., McLaughlin,F.G. and Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 5346 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)

FEATURES
SOURCE
1. .16
/organism="synthetic construct"

/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"

BASE COUNT 5 a 4 c 4 g 2 t 1 others

ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
1 RGGCTAGCTACACGA 16

Db 1 RGGCTAGCTACACGA 16

RESULT 6
AX583609 16 bp DNA linear PAT 10-JAN-2003
LOCUS Sequence 5447 from Patent WO0211674.
DEFINITION AX583609
ACCESSION AX583609
VERSION AX583609.1 GI:27655419
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Thompson,J., Mcswigen,J., McKenzie,T., Myers,D., Szymkowski,D.E. and Grupe,A.
TITLE Method and reagent for the inhibition of calcium activated chloride
JOURNAL Patent: WO 0211674-A 5447 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)

FEATURES
SOURCE
1. .16
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"

BASE COUNT 5 a 4 c 4 g 2 t 1 others

ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
1 RGGCTAGCTACACGA 16

Db 1 RGGCTAGCTACACGA 16

RESULT 7
AR201808 29 bp DNA linear PAT 20-APR-2002
LOCUS Sequence 23 from patent US 6361941.
DEFINITION AR201808
ACCESSION AR201808
VERSION AR201808.1 GI:20256347
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 29)
AUTHORS Todd,A.V., Fuery,C.J. and Cairns,M.J.
TITLE Catalytic nucleic acid-based diagnostic methods
JOURNAL Patent: US 6361941-A 23 26-MAR-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Glaxo Group Limited (GB)

FEATURES
SOURCE
1. .29
/organism="unknown"

BASE COUNT 10 a 5 c 10 g 3 t 1 others

ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 29;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACACGA 16
:|||||
8 AGGCTAGCTACACGA 23

RESULT 8
AR201810 29 bp DNA linear PAT 20-APR-2002

LOCUS AR201810
DEFINITION Sequence 25 from patent US 6361941.
ACCESSION AR201810
VERSION AR201810.1 GI:20256349

KEYWORDS
SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 29)
AUTHORS Todd,A.V., Fuery,C.J. and Cairns,M.J.
TITLE Catalytic nucleic acid-based diagnostic methods
JOURNAL Patent: US 6361941-A 25 26-MAR-2002;
FEATURES Location/Qualifiers
source 1..29
/organism="unknown"

BASE COUNT 7 a 10 c 5 g 7 t
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 29;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACACGA 16
:|||||
9 AGGCTAGCTACACGA 24

Db

RESULT 9
AR201840 30 bp DNA linear PAT 20-APR-2002

LOCUS AR201840
DEFINITION Sequence 55 from patent US 6361941.
ACCESSION AR201840
VERSION AR201840.1 GI:20256379

KEYWORDS
SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 30)
AUTHORS Todd,A.V., Fuery,C.J. and Cairns,M.J.
TITLE Catalytic nucleic acid-based diagnostic methods
JOURNAL Patent: US 6361941-A 55 26-MAR-2002;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"

BASE COUNT 12 a 7 c 5 g 6 t
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 30;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACACGA 16
:|||||
8 AGGCTAGCTACACGA 23

Db

RESULT 10
AX009377 30 bp DNA linear PAT 06-SEP-2000

LOCUS AX009377
DEFINITION Sequence 7 from Patent WO9963066.
ACCESSION AX009377
VERSION AX009377.1 GI:9996678
KEYWORDS
SOURCE synthetic construct

ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Sioud,M.
TITLE Amino-modified ribozymes
JOURNAL Patent: WO 9963066-A 7 09-DEC-1999;
DZIEGLESKA HANNA EVA (GB); SIOD MOUNDY (NO); NORWEGIAN RADIUM
HOSPITAL RESE (NO)

FEATURES Location/Qualifiers
source 1..30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="PKC alpha ribozyme"

BASE COUNT 7 a 11 c 8 g 4 t
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 30;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACACGA 16
:|||||
8 AGGCTAGCTACACGA 23

Db

RESULT 11
AX111628 30 bp DNA linear PAT 30-APR-2001

LOCUS AX111628
DEFINITION Sequence 3 from Patent WO0125419.
ACCESSION AX111628
VERSION AX111628.1 GI:13927904

KEYWORDS
SOURCE synthetic construct

ORGANISM synthetic construct

artificial sequences.

REFERENCE 1
AUTHORS Conrad,C.A. and Chen,Y.
TITLE Altering gene expression with adna produced in vivo
JOURNAL Patent: WO 0125419-A 3 12-APR-2001;
Cyrogenix, Inc. (US)
FEATURES Location/Qualifiers
source 1..30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

BASE COUNT 5 a 8 c 8 g 9 t
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 30;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACACGA 16
:|||||
24 AGGCTAGCTACACGA 9

Db

RESULT 12
AX274718 30 bp DNA linear PAT 29-OCT-2001

LOCUS AX274718
DEFINITION Sequence 2287 from Patent WO0162911.
ACCESSION AX274718
VERSION AX274718.1 GI:16547457

KEYWORDS
SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1
AUTHORS Garvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
Ellis,J.H.
TITLE Method and reagent for the inhibition of grid

JOURNAL Patent: WO 0162911-A 2287 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
SOURCE
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"
misc_feature
1. .7
/note="2'-O-Methyl"
misc_feature
23. .29
/note="2'-O-Methyl"
misc_feature
30
/note="n stands for inverted deoxyabasic derivative"
BASE COUNT 7 a 9 c 6 g 7 t 1 others
ORIGIN
Query Match 97.5%; Score 15.6; DB 6; Length 30;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RGCTAGCTACAACGA 16
Db 7 GGCTAGCTACAACGA 22
RESULT 13
AX274719 30 bp DNA linear PAT 29-OCT-2001
LOCUS
DEFINITION Sequence 2288 from Patent WO0162911.
ACCESSION AX274719
VERSION AX274719.1 GI:16547458
KEYWORDS
ORGANISM
SOURCE
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamlin, P.A. and Ellis, J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 2288 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
SOURCE
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"
misc_feature
1. .7
/note="2'-O-Methyl"
misc_feature
23. .29
/note="2'-O-Methyl"
misc_feature
30
/note="n stands for inverted deoxyabasic derivative"
BASE COUNT 10 a 7 c 7 g 5 t 1 others
ORIGIN
Query Match 97.5%; Score 15.6; DB 6; Length 30;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RGCTAGCTACAACGA 16
Db 7 AGGCTAGCTACAACGA 22
RESULT 14
AX274720 30 bp DNA linear PAT 29-OCT-2001
LOCUS
DEFINITION Sequence 2289 from Patent WO0162911.
ACCESSION AX274720
VERSION AX274720.1 GI:16547459
KEYWORDS

SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamlin, P.A. and Ellis, J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 2289 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
SOURCE
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"
misc_feature
1. .7
/note="2'-O-Methyl"
misc_feature
23. .29
/note="2'-O-Methyl"
misc_feature
30
/note="n stands for inverted deoxyabasic derivative"
BASE COUNT 9 a 4 c 10 g 6 t 1 others
ORIGIN
Query Match 97.5%; Score 15.6; DB 6; Length 30;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RGCTAGCTACAACGA 16
Db 7 AGGCTAGCTACAACGA 22
RESULT 15
AX274721 30 bp DNA linear PAT 29-OCT-2001
LOCUS
DEFINITION Sequence 2290 from Patent WO0162911.
ACCESSION AX274721
VERSION AX274721.1 GI:16547460
KEYWORDS
ORGANISM
SOURCE
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamlin, P.A. and Ellis, J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 2290 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
SOURCE
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"
misc_feature
1. .7
/note="2'-O-Methyl"
misc_feature
23. .29
/note="2'-O-Methyl"
misc_feature
30
/note="n stands for inverted deoxyabasic derivative"
BASE COUNT 9 a 4 c 10 g 6 t 1 others
ORIGIN
Query Match 97.5%; Score 15.6; DB 6; Length 30;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RGCTAGCTACAACGA 16
Db 7 AGGCTAGCTACAACGA 22

RESULT 16
 AX274722 30 bp DNA linear PAT 29-OCT-2001
 LOCUS Sequence 2291 from Patent WO0162911.
 DEFINITION AX274722
 VERSION AX274722.1 GI:16547461
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 source
 1. 30
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="Enzymatic Nucleic Acid"
 misc_feature
 1. 7
 /note="2'-O-Methyl"
 misc_feature
 23. 29
 /note="2'-O-Methyl"
 misc_feature
 30
 /note="n stands for inverted deoxybasic derivative"
 BASE COUNT 8 a 7 c 10 g 4 t 1 others
 ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 30;
 Best Local Similarity 93.8%; Pred. No. 2.8e+02;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCGTAGCTACACGA 16
 :|||||
 Db 7 GCGCTAGCTACACGA 22

RESULT 17
 AR116975 31 bp DNA linear PAT 16-MAY-2001
 LOCUS Sequence 5 from patent US 6140055.
 DEFINITION AR116975
 ACCESSION AR116975
 VERSION AR116975.1 GI:14097881
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 source
 1. 31
 /organism="unknown"
 BASE COUNT 10 a 7 c 7 g 7 t

Query Match 97.5%; Score 15.6; DB 6; Length 31;
 Best Local Similarity 93.8%; Pred. No. 2.8e+02;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCGTAGCTACACGA 16
 :|||||
 Db 8 AGGCTAGCTACACGA 23

RESULT 18
 AR201827 31 bp DNA linear PAT 20-APR-2002
 LOCUS Sequence 42 from patent US 6361941.
 DEFINITION

ACCESSION AR201827
 VERSION AR201827.1 GI:20256366
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 source
 1. 31
 /organism="unknown"
 BASE COUNT 10 a 10 c 5 g 6 t

Query Match 97.5%; Score 15.6; DB 6; Length 31;
 Best Local Similarity 93.8%; Pred. No. 2.8e+02;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCGTAGCTACACGA 16
 :|||||
 Db 10 AGGCTAGCTACACGA 25

RESULT 19
 AR201830 31 bp DNA linear PAT 20-APR-2002
 LOCUS Sequence 45 from patent US 6361941.
 DEFINITION AR201830
 ACCESSION AR201830
 VERSION AR201830.1 GI:20256369
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 source
 1. 31
 /organism="unknown"
 BASE COUNT 11 a 9 c 5 g 6 t

Query Match 97.5%; Score 15.6; DB 6; Length 31;
 Best Local Similarity 93.8%; Pred. No. 2.8e+02;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCGTAGCTACACGA 16
 :|||||
 Db 10 AGGCTAGCTACACGA 25

RESULT 20
 AR201833 31 bp DNA linear PAT 20-APR-2002
 LOCUS Sequence 48 from patent US 6361941.
 DEFINITION AR201833
 ACCESSION AR201833
 VERSION AR201833.1 GI:20256372
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 source
 1. 31
 /organism="unknown"
 BASE COUNT 10 a 6 c 12 g 3 t

Query Match 97.5%; Score 15.6; DB 6; Length 31;
 Best Local Similarity 93.8%; Pred. No. 2.8e+02;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCGTAGCTACACGA 16
 :|||||
 Db 10 AGGCTAGCTACACGA 25

Query Match 97.5%; Score 15.6; DB 6; Length 31;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCGTAGCTACACGA 16
: |||||
Db 9 GCGCTAGCTACACGA 24

RESULT 21
LOCUS AR201836 31 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 51 from patent US 6361941.
ACCESSION AR201836
VERSION AR201836.1 GI:20256375
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
FEATURES
REFERENCE 1 (bases 1 to 31)
AUTHORS Todd,A.V., Fuery,C.J. and Cairns,M.J.
TITLE Catalytic nucleic acid-based diagnostic methods
JOURNAL Patent: US 6361941-A 51 26-MAR-2002;
FEATURES
source 1. 31
/organism="unknown"
BASE COUNT 11 a 6 c 11 g 3 t
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 31;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCGTAGCTACACGA 16
: |||||
Db 9 AGGCTAGCTACACGA 24

RESULT 22
LOCUS AR204371 31 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 5 from patent US 6365724.
ACCESSION AR204371
VERSION AR204371.1 GI:21501005
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
FEATURES
REFERENCE 1 (bases 1 to 31)
AUTHORS Todd,A.V., Fuery,C.J. and Cairns,M.J.
TITLE Zymogenic nucleic acid detection methods, and related molecules and kits
JOURNAL Patent: US 6365724-A 5 02-APR-2002;
FEATURES
source 1. 31
/organism="unknown"
BASE COUNT 10 a 7 c 7 g 7 t
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 31;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCGTAGCTACACGA 16
: |||||
Db 8 AGGCTAGCTACACGA 23

RESULT 23
LOCUS AX220546 31 bp DNA linear PAT 07-SEP-2001
DEFINITION Sequence 5988 from Patent WO0159103.

ACCESSION AX220546
VERSION AX220546.1 GI:15548270
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowitra,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 5988 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowitra, Bharat M. (US)
FEATURES
source 1. 31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT 10 a 8 c 8 g 5 t
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 31;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCGTAGCTACACGA 16
: |||||
Db 8 GCGCTAGCTACACGA 23

RESULT 24
LOCUS AX220547 31 bp DNA linear PAT 07-SEP-2001
DEFINITION Sequence 5989 from Patent WO0159103.
ACCESSION AX220547
VERSION AX220547.1 GI:15548271
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowitra,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 5989 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowitra, Bharat M. (US)
FEATURES
source 1. 31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT 10 a 7 c 11 g 3 t
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 31;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCGTAGCTACACGA 16
: |||||
Db 8 GCGCTAGCTACACGA 23

RESULT 25
LOCUS AX220548 31 bp DNA linear PAT 07-SEP-2001
DEFINITION Sequence 5990 from Patent WO0159103.
ACCESSION AX220548
VERSION AX220548.1 GI:15548272
KEYWORDS

SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 5990 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
1..31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT 9 a 8 c 6 g 8 t

ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 31;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACAACGA 16
:|||||
8 AGGCTAGCTACAACGA 23

RESULT 26
AX220549 31 bp DNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 5991 from Patent WO0159103.
ACCESSION AX220549
VERSION AX220549.1 GI:15548273
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 5991 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
1..31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT 11 a 7 c 8 g 5 t

ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 31;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACAACGA 16
:|||||
8 AGGCTAGCTACAACGA 23

RESULT 27
AX220550 31 bp DNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 5992 from Patent WO0159103.
ACCESSION AX220550
VERSION AX220550.1 GI:15548274
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 5992 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
1..31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT 10 a 7 c 7 g 7 t

ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 31;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACAACGA 16
:|||||
8 GGGCTAGCTACAACGA 23

RESULT 28
AX220551 31 bp DNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 5993 from Patent WO0159103.
ACCESSION AX220551
VERSION AX220551.1 GI:15548275
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 5993 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
1..31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT 9 a 5 c 10 g 7 t

ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 31;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACAACGA 16
:|||||
8 AGGCTAGCTACAACGA 23

RESULT 29
AX220552 31 bp DNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 5994 from Patent WO0159103.
ACCESSION AX220552
VERSION AX220552.1 GI:15548276
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and

nogo gene expression
Patent: WO 0159103-A 5994 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
location/Qualifiers
1. .31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT
9 a 6 c 9 g 7 t
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 31;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16
:|||||
8 GGCTAGCTACACGA 23

Db

RESULT 30
AX220553 31 bp DNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 5995 from Patent W00159103.
ACCESSION AX220553
VERSION AX220553.1 GI:15548277
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.

REFERENCE
1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 5995 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
location/Qualifiers

FEATURES
source
1. .31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT
9 a 5 c 8 g 9 t
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 31;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16
:|||||
8 GGCTAGCTACACGA 23

Db

RESULT 31
AX220554 31 bp DNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 5996 from Patent W00159103.
ACCESSION AX220554
VERSION AX220554.1 GI:15548278
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.

REFERENCE
1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 5996 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;

McSwiggen, James (US) ; Chowrira, Bharat M. (US)
location/Qualifiers
1. .31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT
9 a 6 c 6 g 10 t
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 31;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16
:|||||
8 GGCTAGCTACACGA 23

Db

RESULT 32
AX220555 31 bp DNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 5997 from Patent W00159103.
ACCESSION AX220555
VERSION AX220555.1 GI:15548279
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.

REFERENCE
1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 5997 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
location/Qualifiers

FEATURES
source
1. .31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT
8 a 7 c 9 g 7 t
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 31;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16
:|||||
8 GGCTAGCTACACGA 23

Db

RESULT 33
AX220556 31 bp DNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 5998 from Patent W00159103.
ACCESSION AX220556
VERSION AX220556.1 GI:15548280
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.

REFERENCE
1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 5998 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
location/Qualifiers

FEATURES
source
1. .31

/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT 11 a 6 c 9 g 5 t

ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 31;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
:|||||
8 GGGCTAGCTACACGA 23

Db

RESULT 34
AX220557 31 bp DNA linear PAT 07-SEP-2001
LOCUS AX220557
DEFINITION Sequence 5999 from Patent WO0159103.
ACCESSION AX220557
VERSION AX220557.1 GI:15548281
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 5999 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source 1..31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT 11 a 6 c 8 g 6 t

ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 31;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
:|||||
8 GGGCTAGCTACACGA 23

Db

RESULT 35
AX220558 31 bp DNA linear PAT 07-SEP-2001
LOCUS AX220558
DEFINITION Sequence 6000 from Patent WO0159103.
ACCESSION AX220558
VERSION AX220558.1 GI:15548282
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 6000 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source 1..31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

/note="Nucleic Acid"

BASE COUNT 8 a 10 c 7 g 6 t

ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 31;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
:|||||
8 AGGCTAGCTACACGA 23

Db

RESULT 36
AX220559 31 bp DNA linear PAT 07-SEP-2001
LOCUS AX220559
DEFINITION Sequence 6001 from Patent WO0159103.
ACCESSION AX220559
VERSION AX220559.1 GI:15548283
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 6001 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source 1..31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT 8 a 10 c 6 g 7 t

ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 31;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
:|||||
8 AGGCTAGCTACACGA 23

Db

RESULT 37
AX220560 31 bp DNA linear PAT 07-SEP-2001
LOCUS AX220560
DEFINITION Sequence 6002 from Patent WO0159103.
ACCESSION AX220560
VERSION AX220560.1 GI:15548284
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 6002 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source 1..31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT 8 a 12 c 5 g 6 t

ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 31;

Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACAACA 16
:|||||
8 AGGCTAGCTACAACA 23

RESULT 38
AX220561 31 bp DNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 6003 from Patent WO0159103.
ACCESSION AX220561
VERSION AX220561.1 GI:15548285
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1

AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 6003 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
location/Qualifiers

FEATURES
source 1..31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT 12 a 9 c 5 t
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 31;

Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACAACA 16
:|||||
8 AGGCTAGCTACAACA 23

RESULT 39
AX220562 31 bp DNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 6004 from Patent WO0159103.
ACCESSION AX220562
VERSION AX220562.1 GI:15548286
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 6004 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
location/Qualifiers

FEATURES
source 1..31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT 13 a 6 c 7 g 5 t
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 31;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACAACA 16
:|||||
8 GGGCTAGCTACAACA 23

RESULT 40
AX220563 31 bp DNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 6005 from Patent WO0159103.
ACCESSION AX220563
VERSION AX220563.1 GI:15548287
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1

AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 6005 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
location/Qualifiers

FEATURES
source 1..31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT 7 a 7 c 11 g 6 t
ORIGIN

Query Match 97.5%; Score 15.6; DB 6; Length 31;

Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACAACA 16
:|||||
8 GGGCTAGCTACAACA 23

Search completed: January 21, 2004, 07:26:43
Job time : 1009 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 05:18:03 ; Search time 151.5 Seconds
(without alignments)
285.089 Million cell updates/sec

Title: US-09-423-035B-121

Perfect score: 16
Sequence: 1 rggctagctacaacga 16

Scoring table: IDENTITY_NUC
Gap 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 2722628

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database :

N_Geneseq_19Jun03.*
1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB ID	Description
1	15.6	97.5	16	20	AAV82953	Enzymatic DNA core
2	15.6	97.5	16	21	AA63474	DNAzyme catalytic
3	15.6	97.5	16	22	AA63475	DNAzyme catalytic
4	15.6	97.5	16	22	ABA02749	DNAzyme motif SEQ
5	15.6	97.5	16	22	AAH97756	DNAzyme ribozyme m
6	15.6	97.5	16	23	ABK09278	DNAzyme motif. SY
7	15.6	97.5	16	24	ABK61076	Human C1CA1 gene e
8	15.6	97.5	16	24	ABK22719	DNAzyme motif. SY

9	15.6	97.5	16	25	ACA10109	Necrosis factor ka
10	15.6	97.5	16	25	ABZ58432	DNAzyme motif. SY
11	15.6	97.5	27	25	ABZ65525	Human HER2 synthe
12	15.6	97.5	27	25	ABZ65527	Human HER2 synthe
13	15.6	97.5	29	20	AAZ24361	Nucleic acid-based
14	15.6	97.5	29	20	AAZ24363	Nucleic acid-based
15	15.6	97.5	29	21	AAZ62623	Hammerhead ribozym
16	15.6	97.5	29	25	ABZ65526	Human HER2 synthe
17	15.6	97.5	29	25	ABZ65528	Human HER2 synthe
18	15.6	97.5	29	25	ABZ65529	Human HER2 synthe
19	15.6	97.5	29	25	ABZ66549	Human HIV enzymati
20	15.6	97.5	29	25	ABZ66550	Human HIV enzymati
21	15.6	97.5	29	25	ABZ66551	Human HIV enzymati
22	15.6	97.5	29	25	ABZ66552	Human HIV enzymati
23	15.6	97.5	29	25	ABZ66553	Human HIV enzymati
24	15.6	97.5	29	25	ABZ66554	Deoxy-ribozyme, c1
25	15.6	97.5	29	25	ABZ66555	Deoxy-ribozyme, c1
26	15.6	97.5	29	25	ABZ66556	Deoxy-ribozyme, c1
27	15.6	97.5	29	25	ABZ66557	Deoxy-ribozyme, c1
28	15.6	97.5	29	25	ABZ66558	Deoxy-ribozyme, c1
29	15.6	97.5	29	25	ABZ66559	Deoxy-ribozyme, c1
30	15.6	97.5	29	25	ABZ66560	Deoxy-ribozyme, c1
31	15.6	97.5	29	25	ABZ66561	Deoxy-ribozyme, c1
32	15.6	97.5	29	25	ABZ66562	Deoxy-ribozyme, c1
33	15.6	97.5	29	25	ABZ66563	Deoxy-ribozyme, c1
34	15.6	97.5	29	25	ABZ66564	Deoxy-ribozyme, c1
35	15.6	97.5	29	25	ABZ66565	Deoxy-ribozyme, c1
36	15.6	97.5	29	25	ABZ66566	Deoxy-ribozyme, c1
37	15.6	97.5	29	25	ABZ66567	Deoxy-ribozyme, c1
38	15.6	97.5	29	25	ABZ66568	Deoxy-ribozyme, c1
39	15.6	97.5	29	25	ABZ66569	Deoxy-ribozyme, c1
40	15.6	97.5	29	25	ABZ66570	Deoxy-ribozyme, c1
41	15.6	97.5	29	25	ABZ66571	Deoxy-ribozyme, c1
42	15.6	97.5	29	25	ABZ66572	Deoxy-ribozyme, c1
43	15.6	97.5	29	25	ABZ66573	Deoxy-ribozyme, c1
44	15.6	97.5	29	25	ABZ66574	Deoxy-ribozyme, c1
45	15.6	97.5	29	25	ABZ66575	Deoxy-ribozyme, c1
46	15.6	97.5	29	25	ABZ66576	Deoxy-ribozyme, c1
47	15.6	97.5	29	25	ABZ66577	Deoxy-ribozyme, c1
48	15.6	97.5	29	25	ABZ66578	Deoxy-ribozyme, c1
49	15.6	97.5	29	25	ABZ66579	Deoxy-ribozyme, c1
50	15.6	97.5	29	25	ABZ66580	Deoxy-ribozyme, c1
51	15.6	97.5	29	25	ABZ66581	Deoxy-ribozyme, c1
52	15.6	97.5	29	25	ABZ66582	Deoxy-ribozyme, c1
53	15.6	97.5	29	25	ABZ66583	Deoxy-ribozyme, c1
54	15.6	97.5	29	25	ABZ66584	Deoxy-ribozyme, c1
55	15.6	97.5	29	25	ABZ66585	Deoxy-ribozyme, c1
56	15.6	97.5	29	25	ABZ66586	Deoxy-ribozyme, c1
57	15.6	97.5	29	25	ABZ66587	Deoxy-ribozyme, c1
58	15.6	97.5	29	25	ABZ66588	Deoxy-ribozyme, c1
59	15.6	97.5	29	25	ABZ66589	Deoxy-ribozyme, c1
60	15.6	97.5	29	25	ABZ66590	Deoxy-ribozyme, c1
61	15.6	97.5	29	25	ABZ66591	Deoxy-ribozyme, c1
62	15.6	97.5	29	25	ABZ66592	Deoxy-ribozyme, c1
63	15.6	97.5	29	25	ABZ66593	Deoxy-ribozyme, c1
64	15.6	97.5	29	25	ABZ66594	Deoxy-ribozyme, c1
65	15.6	97.5	29	25	ABZ66595	Deoxy-ribozyme, c1
66	15.6	97.5	29	25	ABZ66596	Deoxy-ribozyme, c1
67	15.6	97.5	29	25	ABZ66597	Deoxy-ribozyme, c1
68	15.6	97.5	29	25	ABZ66598	Deoxy-ribozyme, c1
69	15.6	97.5	29	25	ABZ66599	Deoxy-ribozyme, c1
70	15.6	97.5	29	25	ABZ66600	Deoxy-ribozyme, c1
71	15.6	97.5	29	25	ABZ66601	Deoxy-ribozyme, c1
72	15.6	97.5	29	25	ABZ66602	Deoxy-ribozyme, c1
73	15.6	97.5	29	25	ABZ66603	Deoxy-ribozyme, c1
74	15.6	97.5	29	25	ABZ66604	Deoxy-ribozyme, c1
75	15.6	97.5	29	25	ABZ66605	Deoxy-ribozyme, c1
76	15.6	97.5	29	25	ABZ66606	Deoxy-ribozyme, c1
77	15.6	97.5	29	25	ABZ66607	Deoxy-ribozyme, c1
78	15.6	97.5	29	25	ABZ66608	Deoxy-ribozyme, c1
79	15.6	97.5	29	25	ABZ66609	Deoxy-ribozyme, c1
80	15.6	97.5	29	25	ABZ66610	Deoxy-ribozyme, c1
81	15.6	97.5	29	25	ABZ66611	Deoxy-ribozyme, c1

958	15.6	97.5	31	23	ABK06477	Human NOGO DNzyme
959	15.6	97.5	31	23	ABK06478	Human NOGO DNzyme
960	15.6	97.5	31	23	ABK06479	Human NOGO DNzyme
961	15.6	97.5	31	23	ABK06480	Human NOGO DNzyme
962	15.6	97.5	31	23	ABK06481	Human NOGO DNzyme
963	15.6	97.5	31	23	ABK06482	Human NOGO DNzyme
964	15.6	97.5	31	23	ABK06483	Human NOGO DNzyme
965	15.6	97.5	31	23	ABK06484	Human NOGO DNzyme
966	15.6	97.5	31	23	ABK06485	Human NOGO DNzyme
967	15.6	97.5	31	23	ABK06486	Human NOGO DNzyme
968	15.6	97.5	31	23	ABK06487	Human NOGO DNzyme
969	15.6	97.5	31	23	ABK06488	Human NOGO DNzyme
970	15.6	97.5	31	23	ABK06489	Human NOGO DNzyme
971	15.6	97.5	31	23	ABK06490	Human NOGO DNzyme
972	15.6	97.5	31	23	ABK06491	Human NOGO DNzyme
973	15.6	97.5	31	23	ABK06492	Human NOGO DNzyme
974	15.6	97.5	31	23	ABK06493	Human NOGO DNzyme
975	15.6	97.5	31	23	ABK06494	Human NOGO DNzyme
976	15.6	97.5	31	23	ABK06495	Human NOGO DNzyme
977	15.6	97.5	31	23	ABK06496	Human NOGO DNzyme
978	15.6	97.5	31	23	ABK06497	Human NOGO DNzyme
979	15.6	97.5	31	23	ABK06498	Human NOGO DNzyme
980	15.6	97.5	31	23	ABK06499	Human NOGO DNzyme
981	15.6	97.5	31	23	ABK06500	Human NOGO DNzyme
982	15.6	97.5	31	23	ABK06501	Human NOGO DNzyme
983	15.6	97.5	31	23	ABK06502	Human NOGO DNzyme
984	15.6	97.5	31	23	ABK06503	Human NOGO DNzyme
985	15.6	97.5	31	23	ABK06504	Human NOGO DNzyme
986	15.6	97.5	31	23	ABK06505	Human NOGO DNzyme
987	15.6	97.5	31	23	ABK06506	Human NOGO DNzyme
988	15.6	97.5	31	23	ABK06507	Human NOGO DNzyme
989	15.6	97.5	31	23	ABK06508	Human NOGO DNzyme
990	15.6	97.5	31	23	ABK06509	Human NOGO DNzyme
991	15.6	97.5	31	23	ABK06510	Human NOGO DNzyme
992	15.6	97.5	31	23	ABK06511	Human NOGO DNzyme
993	15.6	97.5	31	23	ABK06512	Human NOGO DNzyme
994	15.6	97.5	31	23	ABK06513	Human NOGO DNzyme
995	15.6	97.5	31	23	ABK06514	Human NOGO DNzyme
996	15.6	97.5	31	23	ABK06515	Human NOGO DNzyme
997	15.6	97.5	31	23	ABK06516	Human NOGO DNzyme
998	15.6	97.5	31	23	ABK06517	Human NOGO DNzyme
999	15.6	97.5	31	23	ABK06518	Human NOGO DNzyme
1000	15.6	97.5	31	25	ABL53699	Prostate cancer ma

ALIGNMENTS

```

RESULT 1
AAV82953
ID AAV82953 standard; DNA; 16 BP.
XX
AC AAV82953;
XX
DT 05-MAR-1999 (first entry)
XX
DE Enzymatic DNA core motif region.
XX
KW Enzyme; catalysis; cleavage; target; pharmaceutical; medical; substrate;
XX regulator; detergent; dental hygiene; meat tenderiser; ss.
XX
OS Synthetic.
XX
PN WO9849346-A1.
XX
PD 05-NOV-1998.
XX
PF 29-APR-1998; 98WO-US08677.
XX
PR 29-APR-1997; 97US-0045228.
XX
PA (SCRI ) SCRIPPS RES INST.
XX

```

```

PI Breaker RR, Joyce GF;
XX
DR WPI; 1999-034670/03.
XX
PT New catalytic DNA molecules - having site-specific endonuclease
XX activity in a substrate nucleic acid, used for cleaving target
XX nucleic acid sequences
XX
PS Claim 1; Page 96; 161pp; English.
XX
CC This sequence is used in a method which involves the production of
XX catalytic DNA molecules which can be used for cleaving target nucleic
XX acid molecules. Such DNA molecules can be used in pharmaceutical and
XX medical products (e.g. for wound debridement, clot dissolution), as well
XX as in household items (e.g. detergents, dental hygiene products, meat
XX tenderisers). Other suitable substrates include those comprising or
XX produced by picornaviruses, hepadnaviridae, (e.g. HBV, HCV),
XX papillomaviruses (e.g. HPV), gammaherpesvirinae (e.g. EBV),
XX lymphocryptoviruses, leukemia viruses (e.g. HTLV-1 and -11),
XX flaviviruses, togaviruses, herpesviruses (including alphaherpesvirus
XX and betaherpesviruses), cytomegaloviruses (CMV), influenza viruses,
XX viruses and retroviruses contributing to immunodeficiency diseases and
XX syndromes (e.g. HIV-1 and -2), simian and feline immunodeficiency
XX viruses and bovine leukemia viruses. They can also be used as regulators
XX of gene expression.
XX
SQ Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;
XX
Query Match 97.5%; Score 15.6; DB 20; Length 16;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RGCGTACTACACGA 16
Db 1 RGGCTAGCTACACGA 16

```

```

RESULT 2
AAC63474
ID AAC63474 standard; DNA; 16 BP.
XX
AC AAC63474;
XX
DT 07-FEB-2001 (first entry)
XX
DE DNzyme catalytic core #2.
XX
KW Antisense; ribozyme; DNzyme; ss.
XX
OS Unidentified.
XX
PN WO200060115-A2.
XX
PD 12-OCT-2000.
XX
PF 27-MAR-2000; 2000WO-US07920.
XX
PR 02-APR-1999; 99US-0127529.
XX
PA (CITY ) CITY OF HOPE.
XX
PI Rossi J, Riggs A, Scherr M;
XX
DR WPI; 2000-665016/64.
XX
XX
PT Identifying sites on a target or in vitro-synthesized RNA accessible to
XX antisense, ribozyme, or DNzyme binding comprises incubating
XX hybridizing the target RNA with an antisense oligodeoxynucleotide,
XX ribozymes or DNzymes
XX
PS Disclosure; Page 7; 38pp; English.
XX
CC The present invention relates to a method for identifying sites on a

```


DE DNazyme ribozyme motif SEQ ID NO: 3186.
 XX Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;
 KW RNA cleavage; cancer; ss.
 XX Unidentified.
 OS WO200157206-A2.
 PN
 XX
 PD 09-AUG-2001.
 XX
 PF 02-FEB-2001; 2001WO-US03504.
 XX
 PR 03-FEB-2000; 2000US-0179983.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (FATT/) FATTAEY A R.
 PI Fatteay AR, Jarvis T, McSwiggen J, Booher RN, Holman PS;
 DR WPI; 2001-496922/54.
 XX
 PT Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid
 PT molecules, which downregulate expression of a checkpoint kinase-1
 PT gene, useful for treating colorectal, lung, breast or prostate cancers
 PT -
 PS Claim 8; Fig 5; 115pp; English.
 XX
 CC The present invention provides nucleic acid molecules capable of
 CC downregulating the expression of the human checkpoint kinase-1 (Chk1)
 CC gene. These may be antisense or ribozyme sequences, and are useful in the
 CC treatment of diseases associated with conditions affected by Chk1 levels,
 CC including cancer. The present sequence is an oligonucleotide described in
 CC the exemplification of the invention.
 CC
 SQ Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;
 XX
 QY Query Match 97.5%; Score 15.6; DB 22; Length 16;
 XX Best Local Similarity 100.0%; Pred. No. 34;
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 RGCTAGCTACACGA 16
 1 RGCTAGCTACACGA 16
 XX
 RESULT 6
 ABR09278
 ID ABR09278 standard; DNA; 16 BP.
 XX
 AC ABR09278;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE DNazyme motif.
 XX
 KW Human; ss; antisense therapy; cytosstatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hampered ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberszyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Synthetic.
 XX
 PN WO200159103-A2.

XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US04273.
 XX
 PR 11-FEB-2000; 2000US-181797P.
 PR 28-FEB-2000; 2000US-185516P.
 PR 06-MAR-2000; 2000US-187128P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 PI Blatt L, McSwiggen J, Chowrira BM;
 DR WPI; 2001-607195/69.
 XX
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
 PT and central nervous system injury -
 PT -
 PS Disclosure; Fig 5; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO).
 CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN
 CC motif) or an amberszyme (cleaving RNA with an NGN triplex), a zinzyme
 CC (cleaving RNA with a VXY motif). The CD20-targeting nucleic acid is used
 CC to cleave RNA of CD20 in the presence of a divalent cation that is
 CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce
 CC CD20 activity of the cell and treat a patient having a condition
 CC associated with the level of CD20. The treatment may further comprise the
 CC use of one or more therapies. In particular, the CD20 targeting
 CC nucleic acid may be used to treat lymphoma, leukaemia, B-cell
 CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
 CC low-grade or follicular NHL, lymphocytic leukaemia, HIV (human
 CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
 CC immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune
 CC thrombocytopaenia, and inflammatory arthropathy. The NOGO-targeting
 CC nucleic acid is used to cleave RNA of the NOGO gene in the presence of a
 CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid
 CC may be contacted with a cell to reduce NOGO activity of the cell and
 CC treat a patient having a condition associated with the level of NOGO. The
 CC treatment may further comprise the use of one or more therapies.
 CC In particular, the NOGO-targeting nucleic acid may be used to treat
 CC central nervous system (CNS) injury and cerebrovascular accident (CVA,
 CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The
 CC present sequence is a DNazyme molecule of the invention.
 CC
 SQ Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;
 XX
 QY Query Match 97.5%; Score 15.6; DB 22; Length 16;
 XX Best Local Similarity 100.0%; Pred. No. 34;
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 RGCTAGCTACACGA 16
 1 RGCTAGCTACACGA 16
 XX
 RESULT 7
 ABR61076
 ID ABR61076 standard; DNA; 16 BP.
 XX
 XX

RESULT 9
 ID ACA10109 standard; DNA; 16 BP.
 AC ACA10109;
 XX
 XX 03-JUN-2003 (first entry)
 DE Necrosis factor kappa B (NFkB) modulating DNazyme motif.
 KM Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;
 KM G-cleaver; amberyze; cancer; REL-A activity; breast cancer;
 KM lung cancer; prostate cancer; colorectal cancer; brain cancer;
 KM oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
 KM cervical cancer; head and neck cancer; ovarian cancer; melanoma;
 KM lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
 KM chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
 KM cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;
 KM gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
 KM rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
 KM gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
 KM transplant/graft rejection; reperfusion injury; glomerulonephritis;
 KM allergic airway inflammation; inflammatory bowel disease; infection;
 KM ss.
 OS Synthetic.
 XX
 XX US200217568-A1.
 XX
 XX 28-NOV-2002.
 XX
 XX 23-MAY-2001; 2001US-0864785.
 XX
 XX 15-AUG-1994; 94US-0291932.
 XX 07-DEC-1992; 92US-0987132.
 XX 18-MAY-1994; 94US-0245466.
 XX 23-DEC-1996; 96US-0777916.
 XX
 XX (STIN/) STINCHOMB D T.
 XX (MCSW/) MCSWIGEN J.
 XX (DRAP/) DRAPER K G.
 XX
 XX Stinchcomb DT, Mcswigen J, Draper KG;
 PI
 DR WPI; 2003-340953/32.
 XX
 XX Novel enzymatic nucleic acid molecules which down regulates expression
 PT of a sequence encoding a subunit of nuclear factor kappa B useful for
 PT treating cancer, inflammatory disorders and autoimmune diseases -
 XX
 XX Fig 4; SEQ ID NO 3928; 72pp; English.
 XX
 XX The invention describes an enzymatic nucleic acid molecule (I) which down
 CC regulates expression of a sequence encoding a subunit of nuclear factor
 CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberyze
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat
 CC cancer and is useful for down-regulating REL-A activity in a cell, for
 CC treating a patient having a condition associated with the level of REL-A.
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
 CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
 CC antisense nucleic acid molecules are useful for treating breast, lung,
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
 CC multidrug resistant cancer. The method involves use of other drug
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
 CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
 CC acid molecules are also useful for treating inflammatory disease such as
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
 CC rejection, gene therapy applications, ischaemia/reperfusion injury

CC (central nervous system (CNS) and myocardial), glomerulonephritis,
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or
 CC infection. This sequence represents a motif of an enzymatic nucleic acid
 CC used to modulate the function of a necrosis factor kappa B sub-unit.
 XX
 XX SQ Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;
 Query Match 97.5%; Score 15.6; DB 25; Length 16;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RGCGTACGTACACGA 16
 DB 1 RGCGTACGTACACGA 16
 ID AB258432 standard; DNA; 16 BP.
 XX
 XX AB258432
 AC AB258432;
 XX
 XX 08-MAY-2003 (first entry)
 DE
 XX DNazyme motif.
 XX
 XX DNazyme; enzymatic nucleic acid; enzyme; transporter; drug
 KM delivery; cytostatic; virucide; gene therapy; ss.
 KM
 OS Synthetic.
 XX
 XX WO2003008628-A2.
 XX
 XX 30-JAN-2003.
 XX
 XX 22-JUL-2002; 2002WO-US23324.
 XX
 XX 20-JUL-2001; 2001US-306995F.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Beigelman L, Azhayer A, Azhayera E;
 PI
 DR WPI; 2003-247828/25.
 XX
 XX New transporter compounds useful for delivering molecules into
 PT biological system such as cells, and for treating cancer and viral
 PT infections -
 XX
 XX Disclosure; Fig 4; 88pp; English.
 XX
 XX The present sequence is an example of a DNazyme, an enzymatic
 CC nucleic acid (ENA) that does not require the presence of a 2'-OH
 CC group for its activity. DNazymes can be used as the ENA moiety in
 CC novel ENA peptide conjugates (II) of the invention that facilitate
 CC delivery of molecules into biological systems, such as cells. The
 CC peptide part of the conjugate is typically a fusogenic peptide such
 CC as a peptide given in ABP72298-ABP7305. The conjugates can be
 CC used to treat a cancer patient, where the cancer is breast, lung,
 CC colorectal, brain, oesophageal, stomach, bladder, pancreas, cervix,
 CC head and neck or ovary cancer, melanoma, lymphoma, glioma or
 CC multidrug resistant cancer, or to treat a virus infection, where
 CC the virus is HIV, hepatitis B virus, hepatitis C virus,
 CC cytomegalovirus, Rous sarcoma virus, herpes simplex virus,
 CC poliovirus, influenza virus, rhinovirus, west nile virus, Ebola
 CC virus, foot and mouth disease virus or papilloma virus (all
 CC claimed). (I) are useful for introducing nucleosides,
 CC nucleosides, nucleic acid molecules, lipids, peptides, proteins
 CC and/or non-nucleosidic small molecules into a cell and to detect
 CC the presence of a target molecule in a biological system such as
 CC tissue, cell or cell lysate. They are useful as diagnostic tools
 CC to examine genetic drift and mutations within diseased cells or to

CC detect the presence of a disease-related RNA in a cell.

XX Sequence 16 BP; 5 A; 4 C; 4 G; 2 T; 1 other;

Query Match 97.5%; Score 15.6; DB 25; Length 16;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
DB 1 RGGCTAGCTACACGA 16

RESULT 11

AB266525
ID AB266525 standard; RNA; 27 BP.

XX AB266525;

DT 21-MAR-2003 (first entry)

XX Human HER2 synthetic DNzyme #1.

XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;
KM anti-rheumatic; cancer; AIDS; ss.

XX Homo sapiens.

XX WO200297114-A2.

XX 05-DEC-2002.

XX 29-MAY-2002; 2002WO-US16840.

XX 29-MAY-2001; 2001US-294140P.

XX 06-JUN-2001; 2001US-296249P.

XX 10-SEP-2001; 2001US-318471P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Mcwigen J;

XX WPI; 2003-140484/13.

XX Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX Claim 3; Page 153; 185pp; English.

XX The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytosolic, anti-HIV, and
CC anti-rheumatic activity. The nucleic acid molecules are useful for
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
CC acids are also useful for treating breast, ovarian, colorectal, lung,
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
CC The sequences shown in AB262217 - AB264543, AB265532 - AB265519,
CC AB266525 - AB266529, AB266586 - AB266588 represent human ribozymes of the
CC invention.

XX Sequence 27 BP; 6 A; 6 C; 10 G; 2 T; 3 U; 0 other;

Query Match 97.5%; Score 15.6; DB 25; Length 27;

Best Local Similarity 93.8%; Pred. No. 35;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
DB 6 AGGCTAGCTACACGA 21

RESULT 12

AB266527
ID AB266527 standard; RNA; 27 BP.

XX AB266527;

DT 21-MAR-2003 (first entry)

XX Human HER2 synthetic DNzyme #3.

XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;
KM anti-rheumatic; cancer; AIDS; ss.

XX Homo sapiens.

XX WO200297114-A2.

XX 05-DEC-2002.

XX 29-MAY-2002; 2002WO-US16840.

XX 29-MAY-2001; 2001US-294140P.

XX 06-JUN-2001; 2001US-296249P.

XX 10-SEP-2001; 2001US-318471P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Mcwigen J;

XX WPI; 2003-140484/13.

XX Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX Claim 3; Page 153; 185pp; English.

XX The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytosolic, anti-HIV, and
CC anti-rheumatic activity. The nucleic acid molecules are useful for
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
CC acids are also useful for treating breast, ovarian, colorectal, lung,
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
CC The sequences shown in AB262217 - AB264543, AB265532 - AB265519,
CC AB266525 - AB266529, AB266586 - AB266588 represent human ribozymes of the
CC invention.

XX Sequence 27 BP; 11 A; 8 C; 6 G; 2 T; 0 other;

Query Match 97.5%; Score 15.6; DB 25; Length 27;

Best Local Similarity 93.8%; Pred. No. 35;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
DB 6 AGGCTAGCTACACGA 21

RESULT 13

AA234361
ID AA234361 standard; DNA; 29 BP.

XX AA234361;

DT 14-DEC-1999 (first entry)

XX Nucleic acid-based diagnostic exemplification oligonucleotide #23.

XX Catalytic nucleic acid-based diagnostic method; determination; AIDS;
 KM mutation; ribozyme; target; cleavage; amplification; PCR primer;
 KM probe; cancer; human immune deficiency virus; cystic fibrosis; HIV; ss.
 XX Synthetic.
 XX WO9950452-A1.
 XX PN 07-OCT-1999.
 XX PD 16-MAR-1999; 99WO-IB00848.
 XX PF 27-MAR-1999; 98US-0079651.
 XX PR (JOHN) JOHNSON & JOHNSON RES PTY LTD.
 XX PA Todd AV, Fuery CJ, Cairns MJ;
 XX PI WPI; 1999-591332/50.
 XX DR Detecting diseases associated with a known mutation by amplification
 XX PT and cleavage with catalytic nucleic acids, particularly for cancer,
 XX PT human immune deficiency virus and cystic fibrosis
 XX PS Disclosure; Page 20; 57pp; English.
 XX The present invention describes a method for determining whether a
 CC subject is afflicted with a disorder characterised by the presence of
 CC a known nucleic acid. The method comprises: (i) amplifying, in an
 CC isolated sample from the subject, the nucleic acid segment that, in an
 CC affected individual contains (A), (ii) treating the amplicons with a
 CC catalytic nucleic acid (I) that specifically recognizes and cleaves a
 CC target sequence present in either the mutated or wild-type segments,
 CC but not in both; and (iii) detecting any cleavage caused by (I). Step
 CC (iii) may be performed concurrently with (i). The method is specifically
 CC used to diagnose cancer (especially), acquired immune deficiency
 CC syndrome and cystic fibrosis. (i) recognises as few as two bp to create
 CC a cleavage site (contrast at least 4 bp required by enzymes used in
 CC restriction fragment length polymorphism (RFLP) analysis); such sites
 CC occur more frequently than restriction enzyme sites, and mismatched
 CC primers can be used to induce cleavage sites for (I). The method is
 CC potentially more flexible than RFLP and does not require any enzymes or
 CC toxic compounds. AA23439 to AA234450 represent oligonucleotide
 CC sequences used in the exemplification of the present invention.
 CC
 CC Sequence 29 BP; 10 A; 5 C; 10 G; 3 T; 1 other;
 CC SQ
 CC Query Match 97.5%; Score 15.6; DB 20; Length 29;
 CC Best Local Similarity 93.8%; Pred. No. 35;
 CC Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 RGGCTAGCTACACGA 16
 CC :|||||
 CC DB 8 AGGCTAGCTACACGA 23
 CC
 CC RESULT 14
 CC AA234363
 CC ID AA234363 standard; DNA; 29 BP.
 CC XX
 CC AC AA234363;
 CC XX
 CC DT 14-DEC-1999 (first entry)
 CC XX
 CC DE Nucleic acid-based diagnostic exemplification oligonucleotide #25.
 CC XX
 CC XX Catalytic nucleic acid-based diagnostic method; determination; AIDS;
 CC KM mutation; ribozyme; target; cleavage; amplification; PCR primer;
 CC KM probe; cancer; human immune deficiency virus; cystic fibrosis; HIV; ss.
 CC XX
 CC OS Synthetic.
 CC XX

PN WO9950452-A1.
 XX PD 07-OCT-1999.
 XX PF 16-MAR-1999; 99WO-IB00848.
 XX PR 27-MAR-1999; 98US-0079651.
 XX PA (JOHN) JOHNSON & JOHNSON RES PTY LTD.
 XX PI Todd AV, Fuery CJ, Cairns MJ;
 XX PI WPI; 1999-591332/50.
 XX DR Detecting diseases associated with a known mutation by amplification
 XX PT and cleavage with catalytic nucleic acids, particularly for cancer,
 XX PT human immune deficiency virus and cystic fibrosis
 XX PS Disclosure; Page 20; 57pp; English.
 XX The present invention describes a method for determining whether a
 CC subject is afflicted with a disorder characterised by the presence of
 CC a known nucleic acid. The method comprises: (i) amplifying, in an
 CC isolated sample from the subject, the nucleic acid segment that, in an
 CC affected individual contains (A), (ii) treating the amplicons with a
 CC catalytic nucleic acid (I) that specifically recognizes and cleaves a
 CC target sequence present in either the mutated or wild-type segments,
 CC but not in both; and (iii) detecting any cleavage caused by (I). Step
 CC (iii) may be performed concurrently with (i). The method is specifically
 CC used to diagnose cancer (especially), acquired immune deficiency
 CC syndrome and cystic fibrosis. (i) recognises as few as two bp to create
 CC a cleavage site (contrast at least 4 bp required by enzymes used in
 CC restriction fragment length polymorphism (RFLP) analysis); such sites
 CC occur more frequently than restriction enzyme sites, and mismatched
 CC primers can be used to induce cleavage sites for (I). The method is
 CC potentially more flexible than RFLP and does not require any enzymes or
 CC toxic compounds. AA23439 to AA234450 represent oligonucleotide
 CC sequences used in the exemplification of the present invention.
 CC
 CC Sequence 29 BP; 7 A; 10 C; 5 G; 7 T; 0 other;
 CC SQ
 CC Query Match 97.5%; Score 15.6; DB 20; Length 29;
 CC Best Local Similarity 93.8%; Pred. No. 35;
 CC Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 RGGCTAGCTACACGA 16
 CC :|||||
 CC DB 9 AGGCTAGCTACACGA 24
 CC
 CC RESULT 15
 CC AAC82623
 CC ID AAC82623 standard; DNA; 29 BP.
 CC XX
 CC AC AAC82623;
 CC XX
 CC DT 13-MAR-2001 (first entry)
 CC XX
 CC DE Hammerhead ribozyme DNA motif #23.
 CC XX
 CC KM Detection; amplification; pathogenic bacteria; hammerhead ribozyme;
 CC KM fluorescent signal; cleavage; ss.
 CC XX
 CC OS Synthetic.
 CC XX
 CC PN DE19915141-A1.
 CC XX
 CC PD 28-SEP-2000.
 CC XX
 CC PF 26-MAR-1999; 99DE-1015141.
 CC XX
 CC PR 26-MAR-1999; 99DE-1015141.
 CC XX

PA (ARTU-) ARTUS GES MOLEKULARBIOLOGISCHE DIAGNOSTI.
 XX Krupp G;
 XX WPI; 2000-603196/58.
 DR Real-time quantitative amplification of nucleic acid, useful for
 XX detecting bacterial pathogens, uses primer and labeled probe that
 PT combine to form a ribozyme -
 PS Disclosure; Fig 13; 39pp; German.
 XX This invention describes a novel method for the amplification and
 CC quantitative real-time determination of nucleic acid (I) using a primer
 CC attached to a 1-40 nucleotide sequence (II) in the transcription product.
 CC Amplification is done in the presence of an excess, preferably 50-500 nM,
 CC of a nucleic acid probe (III) and labeled by a reporter molecule and a
 CC quencher molecule. (I) encodes the motif 5'-GAA-3' (A), and (II)
 CC contains the motif 5'-CUGAACA-3' (B). (III) has 25-60, especially 50,
 CC nucleotides. The method is used to detect and quantify (I) from
 CC pathogenic bacteria. The method allows real-time detection and
 CC quantification of (I), particularly RNA by NASBA (RTM) (nucleic acid
 CC sequence-based amplification), without the difficulties associated with
 CC use of DNA probes (see Nucleic Acid Res., 26 (1998) 2150) and is suitable
 CC for routine use. Specifically the combination of (A) and (B) generates a
 CC hammerhead ribozyme that cleaves the probe and generates a fluorescent
 CC signal. Since many probes are cleaved, a high signal is produced,
 CC resulting in high sensitivity and shorter reaction times. The method is
 CC very specific since exact hybridization of probe to target is necessary
 CC for cleavage to occur. Complicated probes are not required because
 CC cleavage results in dissociation of the probe from the target (which
 CC allows multiplexing). Stable and inexpensive probes can be used,
 CC consisting mainly of 2'-deoxyribonucleotides.
 XX Sequence 29 BP; 5 A; 4 C; 4 G; 2 T; 14 other;
 SQ
 QY Query Match 97.5%; Score 15.6; DB 21; Length 29;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 RGCGTAGCTACACGA 16
 7 RGCGTAGCTACACGA 22
 RESULT 16
 ABZ66526
 ID ABZ66526 standard; RNA; 29 BP.
 XX
 AC ABZ66526;
 XX
 DT 21-MAR-2003 (first entry)
 XX
 DE Human HER2 synthetic DNAzyme #2.
 XX
 XX Human, ribozyme; short interfering RNA, siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;
 KW anti-rheumatic; cancer; AIDS; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200297114-A2.
 XX
 PD 05-DEC-2002.
 XX
 PF 29-MAY-2002; 2002WO-US16840.
 XX
 PR 29-MAY-2001; 2001US-294140P.
 PR 06-JUN-2001; 2001US-296249P.
 PR 10-SEP-2001; 2001US-318471P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX

PI Mcswiggen J;
 XX
 DR WPI; 2003-140484/13.
 XX
 PT Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
 XX
 PS Claim 3; Page 153; 185pp; English.
 XX
 CC The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytostatic, anti-HIV, and
 CC anti-rheumatic activity. The nucleic acid molecules are useful for
 CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
 CC acids are also useful for treating breast, ovarian, colorectal, lung,
 CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
 CC The sequences shown in ABZ62217 - ABZ64543, ABZ6532 - ABZ65519,
 CC ABZ66525 - ABZ66529, ABZ66586 - ABZ66658 represent human ribozymes of the
 CC invention.
 XX
 SQ Sequence 29 BP; 11 A; 7 C; 7 G; 2 T; 2 U; 0 other;
 QY Query Match 97.5%; Score 15.6; DB 25; Length 29;
 Best Local Similarity 93.8%; Pred. No. 35;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 1 RGCGTAGCTACACGA 16
 7 RGCGTAGCTACACGA 22
 RESULT 17
 ABZ66528
 ID ABZ66528 standard; RNA; 29 BP.
 XX
 AC ABZ66528;
 XX
 DT 21-MAR-2003 (first entry)
 XX
 DE Human HER2 synthetic DNAzyme #4.
 XX
 XX Human, ribozyme; short interfering RNA, siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;
 KW anti-rheumatic; cancer; AIDS; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200297114-A2.
 XX
 PD 05-DEC-2002.
 XX
 PF 29-MAY-2002; 2002WO-US16840.
 XX
 PR 29-MAY-2001; 2001US-294140P.
 PR 06-JUN-2001; 2001US-296249P.
 PR 10-SEP-2001; 2001US-318471P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Mcswiggen J;
 XX
 DR WPI; 2003-140484/13.
 XX
 PT Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
 XX
 PS Claim 3; Page 153; 185pp; English.
 XX
 CC The invention relates to a novel short interfering RNA (siRNA) nucleic

CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytoskeletal, anti-HIV, and
 CC anti-rheumatic activity. The nucleic acid molecules are useful for
 CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
 CC acids are also useful for treating breast, ovarian, colorectal, lung,
 CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
 CC The sequences shown in AB262217 - AB264543, AB26532 - AB265519,
 CC AB26525 - AB26529, AB26586 - AB26658 represent human ribozymes of the
 CC invention.

CC Sequence 29 BP; 9 A; 5 C; 11 G; 2 T; 2 U; 0 other;

XX
 SQ Query Match 97.5%; Score 15.6; DB 25; Length 29;
 Best Local Similarity 93.8%; Pred. No. 35;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCTACACGA 16
 : |||||
 Db 7 AGGCTAGCTACACGA 22

RESULT 18

AB26529
 ID AB266529 standard; RNA; 29 BP.

XX AC AB266529;

XX XX 21-MAR-2003 (first entry)

DE Human HER2 synthetic DNzyme #5.

XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;

KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytoskeletal; anti-HIV;

KM anti-rheumatic; cancer; AIDS; ss.

XX Homo sapiens.

XX WO200297114-A2.

XX PD 05-DEC-2002.

XX PF 29-MAY-2002; 2002WO-US16840.

XX PR 29-MAY-2001; 2001US-294140P.

XX PR 06-JUN-2001; 2001US-296249P.

XX PR 10-SEP-2001; 2001US-318471P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI Mcswiggen J;

XX WPI; 2003-140484/13.

XX Novel short interfering RNA and enzymatic nucleic acid useful for

PT treating cancer, modulates the expression of a nucleic acid encoding

PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -

XX Claim 3; Page 153; 185pp; English.

XX The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytoskeletal, anti-HIV, and
 CC anti-rheumatic activity. The nucleic acid molecules are useful for
 CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
 CC acids are also useful for treating breast, ovarian, colorectal, lung,
 CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
 CC The sequences shown in AB262217 - AB264543, AB26532 - AB265519,
 CC AB26525 - AB26529, AB26586 - AB26658 represent human ribozymes of the
 CC invention.

XX
 SQ Sequence 29 BP; 7 A; 4 C; 11 G; 2 T; 5 U; 0 other;

XX Query Match 97.5%; Score 15.6; DB 25; Length 29;
 Best Local Similarity 93.8%; Pred. No. 35;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCTACACGA 16
 : |||||
 Db 7 AGGCTAGCTACACGA 22

RESULT 19

AB26649
 ID AB266649 standard; RNA; 29 BP.

XX AC AB266649;

XX XX 21-MAR-2003 (first entry)

DE Human HIV enzymatic nucleic acid #1.

XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;

KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytoskeletal; anti-HIV;

KM anti-rheumatic; cancer; AIDS; ss.

XX Homo sapiens.

XX WO200297114-A2.

XX PD 05-DEC-2002.

XX PF 29-MAY-2002; 2002WO-US16840.

XX PR 29-MAY-2001; 2001US-294140P.

XX PR 06-JUN-2001; 2001US-296249P.

XX PR 10-SEP-2001; 2001US-318471P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI Mcswiggen J;

XX WPI; 2003-140484/13.

XX Novel short interfering RNA and enzymatic nucleic acid useful for

PT treating cancer, modulates the expression of a nucleic acid encoding

PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -

XX Claim 122; Page 159; 185pp; English.

XX The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytoskeletal, anti-HIV, and
 CC anti-rheumatic activity. The nucleic acid molecules are useful for
 CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
 CC acids are also useful for treating breast, ovarian, colorectal, lung,
 CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
 CC The sequences shown in AB262217 - AB264543, AB26532 - AB265519,
 CC AB26525 - AB26529, AB26586 - AB26658 represent human ribozymes of the
 CC invention.

XX Sequence 29 BP; 7 A; 11 C; 5 G; 2 T; 4 U; 0 other;

XX Query Match 97.5%; Score 15.6; DB 25; Length 29;
 Best Local Similarity 93.8%; Pred. No. 35;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCTACACGA 16
 : |||||
 Db 7 AGGCTAGCTACACGA 22

```
RESULT 20
ABZ66650
ID ABZ66650 standard; RNA; 29 BP.
XX
AC ABZ66650;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human HIV enzymatic nucleic acid #2.
XX
KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PE 29-MAY-2002; 2002WO-US16840.
XX
PR 29-MAY-2001; 2001US-294140P.
PR 06-JUN-2001; 2001US-296249P.
PR 10-SEP-2001; 2001US-318471P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswigen J;
XX
DR WPI; 2003-140484/13.
XX
PT Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX
PS Claim 122; Page 159; 185pp; English.
XX
CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytosolic, anti-HIV, and
CC anti-rheumatic activity. The nucleic acid molecules are useful for
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
CC acids are also useful for treating breast, ovarian, colorectal, lung,
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
CC The sequences shown in ABZ62217 - ABZ64543, ABZ65532 - ABZ65519,
CC ABZ66525 - ABZ66529, ABZ66586 - ABZ66658 represent human ribozymes of the
CC invention.
XX
SQ Sequence 29 BP; 7 A; 9 C; 5 G; 2 T; 6 U; 0 other;
XX
Query Match 97.5%; Score 15.6; DB 25; Length 29;
Best Local Similarity 93.8%; Pred. No. 35;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RGGCTAGCTACACGA 16
Db 7 GGGCTAGCTACACGA 22
XX
RESULT 21
ABZ66651
ID ABZ66651 standard; RNA; 29 BP.
XX
AC ABZ66651;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human HIV enzymatic nucleic acid #3.
XX
```

```
KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PE 29-MAY-2002; 2002WO-US16840.
XX
PR 29-MAY-2001; 2001US-294140P.
PR 06-JUN-2001; 2001US-296249P.
PR 10-SEP-2001; 2001US-318471P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswigen J;
XX
DR WPI; 2003-140484/13.
XX
PT Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX
PS Claim 122; Page 159; 185pp; English.
XX
CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytosolic, anti-HIV, and
CC anti-rheumatic activity. The nucleic acid molecules are useful for
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
CC acids are also useful for treating breast, ovarian, colorectal, lung,
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
CC The sequences shown in ABZ62217 - ABZ64543, ABZ65532 - ABZ65519,
CC ABZ66525 - ABZ66529, ABZ66586 - ABZ66658 represent human ribozymes of the
CC invention.
XX
SQ Sequence 29 BP; 6 A; 9 C; 6 G; 2 T; 6 U; 0 other;
XX
Query Match 97.5%; Score 15.6; DB 25; Length 29;
Best Local Similarity 93.8%; Pred. No. 35;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RGGCTAGCTACACGA 16
Db 7 AGGCTAGCTACACGA 22
XX
RESULT 22
ABZ66652
ID ABZ66652 standard; RNA; 29 BP.
XX
AC ABZ66652;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human HIV enzymatic nucleic acid #4.
XX
KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PE 29-MAY-2002; 2002WO-US16840.
```

```

XX 29-MAY-2001; 2001US-294140P.
PR 06-JUN-2001; 2001US-296249P.
PR 10-SEP-2001; 2001US-318471P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J;
XX
XX WPI; 2003-140484/13.
XX
XX Novel short interfering RNA and enzymatic nucleic acid useful for
XX treating cancer, modulates the expression of a nucleic acid encoding
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX
XX Claim 122; Page 159; 185pp; English.
XX
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
XX acid molecule or an enzymatic nucleic acid molecule, that modulates
XX expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX acid molecule of the invention has cytosstatic, anti-HIV, and
XX anti-rheumatic activity. The nucleic acid molecules are useful for
XX reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
XX acids are also useful for treating breast, ovarian, colorectal, lung,
XX prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
XX The sequences shown in ABZ62217 - ABZ64543, ABZ65532 - ABZ65519,
XX ABZ66525 - ABZ66529, ABZ66586 - ABZ66588 represent human ribozymes of the
XX invention.
XX
XX Sequence 29 BP; 8 A; 6 C; 8 G; 2 T; 5 U; 0 other;
XX
XX Query Match 97.5%; Score 15.6; DB 25; Length 29;
XX Best Local Similarity 93.8%; Pred. No. 35;
XX Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 RGGCTAGCTACACGA 16
XX : |||||
XX 7 AGGCTAGCTACACGA 22
XX
XX RESULT 23
XX ABZ6653
XX ID ABZ6653 standard; RNA; 29 BP.
XX
XX AC ABZ6653;
XX
XX 21-MAR-2003 (first entry)
XX
XX Human HIV enzymatic nucleic acid #5.
XX
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
XX anti-rheumatic; cancer; AIDS; ss.
XX
XX Homo sapiens.
XX
XX WO200297114-A2.
XX
XX 05-DEC-2002.
XX
XX 29-MAY-2002; 2002WO-US16840.
XX
XX 29-MAY-2001; 2001US-294140P.
XX 06-JUN-2001; 2001US-296249P.
XX 10-SEP-2001; 2001US-318471P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J;
XX
XX WPI; 2003-140484/13.
XX

```

```

PT Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
PT
PT Claim 122; Page 159; 185pp; English.
PT
PT The invention relates to a novel short interfering RNA (siRNA) nucleic
PT acid molecule or an enzymatic nucleic acid molecule, that modulates
PT expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
PT human immunodeficiency virus (HIV) or a component of HIV. The nucleic
PT acid molecule of the invention has cytosstatic, anti-HIV, and
PT anti-rheumatic activity. The nucleic acid molecules are useful for
PT reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
PT acids are also useful for treating breast, ovarian, colorectal, lung,
PT prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
PT The sequences shown in ABZ62217 - ABZ64543, ABZ65532 - ABZ65519,
PT ABZ66525 - ABZ66529, ABZ66586 - ABZ66588 represent human ribozymes of the
PT invention.
PT
PT Sequence 29 BP; 7 A; 12 C; 5 G; 2 T; 3 U; 0 other;
PT
PT Query Match 97.5%; Score 15.6; DB 25; Length 29;
PT Best Local Similarity 93.8%; Pred. No. 35;
PT Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
PT
PT 1 RGGCTAGCTACACGA 16
PT : |||||
PT 7 AGGCTAGCTACACGA 22
PT
PT RESULT 24
PT ABX13988
PT ID ABX13988 standard; DNA; 29 BP.
PT
PT AC ABX13988;
PT
PT 25-FEB-2003 (first entry)
PT
PT Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1594.
PT
PT Catalytic DNA; catalytic RNA; hairless protein; ss;
PT hair loss; atichia; hair growth; hirsutism; catalytic nucleic acid;
PT ribozyme; DNzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;
PT catalytic core; cleavage site; pharmaceutical; hair production;
PT hair follicle; anagen phase; catagen phase; hair removal product;
PT depilatory.
PT
PT Homo sapiens.
PT
PT Synthetic.
PT
PT Key Location/Qualifiers
PT misc_feature 8..22
PT /*tag= a
PT /note= "Catalytic domain"
PT
PT WO200283891-A2.
PT
PT 24-OCT-2002.
PT
PT 12-APR-2002; 2002WO-US11683.
PT
PT 13-APR-2001; 2001US-283618P.
PT
PT (UYCO ) UNIV COLUMBIA NEW YORK.
PT
PT Christiano AM;
PT
PT WPI; 2003-093020/08.
PT
PT New catalytic nucleic acid molecule that specifically cleaves Hairless
PT Protein mRNA, useful for inhibiting hair production by a hair-producing
PT cell, or for inhibiting transition of a hair follicle from anagen phase
PT to catagen phase -
PT

```


XX Claim 3; Page 34; 65pp; English.

PS The invention discloses a new catalytic DNA or RNA molecule that

XX specifically cleaves, or inhibits expression of, Hairless protein mRNA

CC which comprises a catalytic domain that cleaves mRNA at a defined

CC consensus sequence and binding domains contiguous with the 5' and 3' ends

CC of the catalytic domain. Lack of expression of the hairless gene due to

CC inherited mutations leads to the complete loss of hair, known as

CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting

CC the genes promoting hair growth, and one way to get targeted, transient

CC gene suppression is through the use of catalytic nucleic acid technology,

CC including ribozymes and DNAzymes. Ribozymes are RNA structures which have

CC a self-catalytic enzymatic function and sequence specific RNA binding

CC ability. Small DNA oligonucleotides that have a similar structure to the

CC hammerhead ribozyme, called deoxy-ribozymes or DNAzymes, having a

CC catalytic core and two sequence specific arms. The deoxy-ribozymes have

CC more lenient consensus cleavage site requirements and are less likely to

CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids

CC are useful in pharmaceutical compositions for inhibiting hair production

CC by a hair-producing cell, for inhibiting hair growth and for inhibiting

CC the transition of a hair follicle from the anagen phase to the catagen

CC phase. A non-human transgenic mammal is useful as a model for testing

CC hair removal products which function by inhibiting hairless protein

CC expression. The sequence presented is the deoxy-ribozyme that cleaves the

CC human hairless protein mRNA immediately after nucleotide 1594.

XX

SQ Sequence 29 BP; 7 A; 10 C; 8 G; 4 T; 0 other;

Query Match 97.5%; Score 15.6; DB 25; Length 29;

Best Local Similarity 93.8%; Pred. No. 35;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16

Db 7 GGCTAGCTACACGA 22

RESULT 25

ABX13989

ID ABX13989 standard; DNA; 29 BP.

XX

AC ABX13989;

XX

DT 25-FEB-2003 (first entry)

XX

DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1597.

XX

KW Catalytic DNA; catalytic RNA; hairless protein; ss;

KW hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;

KW ribozyme; DNAzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;

KW catalytic core; cleavage site; pharmaceutical; hair production;

KW hair follicle; anagen phase; catagen phase; hair removal product;

KW depilatory.

XX

OS Homo sapiens.

OS Synthetic.

XX

XX Key Location/Qualifiers

FT misc_feature 8..22

FT /*tag= a

FT /note= "Catalytic domain"

XX

XX WO200283891-A2.

XX

XX 24-OCT-2002.

XX

XX 12-APR-2002; 2002WO-US11683.

XX

XX 13-APR-2001; 2001US-283618P.

XX

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX

PI Cristiano AM;

XX

DR WPI; 2003-093020/08.

XX

PT New catalytic nucleic acid molecule that specifically cleaves Hairless

PT protein mRNA, useful for inhibiting hair production by a hair-producing

PT cell, or for inhibiting transition of a hair follicle from anagen phase

PT to catagen phase

XX

PS Claim 3; Page 34; 65pp; English.

XX

XX The invention discloses a new catalytic DNA or RNA molecule that

CC specifically cleaves, or inhibits expression of, Hairless protein mRNA

CC which comprises a catalytic domain that cleaves mRNA at a defined

CC consensus sequence and binding domains contiguous with the 5' and 3' ends

CC of the catalytic domain. Lack of expression of the hairless gene due to

CC inherited mutations leads to the complete loss of hair, known as

CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting

CC the genes promoting hair growth, and one way to get targeted, transient

CC gene suppression is through the use of catalytic nucleic acid technology,

CC including ribozymes and DNAzymes. Ribozymes are RNA structures which have

CC a self-catalytic enzymatic function and sequence specific RNA binding

CC ability. Small DNA oligonucleotides that have a similar structure to the

CC hammerhead ribozyme, called deoxy-ribozymes or DNAzymes, having a

CC catalytic core and two sequence specific arms. The deoxy-ribozymes have

CC more lenient consensus cleavage site requirements and are less likely to

CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids

CC are useful in pharmaceutical compositions for inhibiting hair production

CC by a hair-producing cell, for inhibiting hair growth and for inhibiting

CC the transition of a hair follicle from the anagen phase to the catagen

CC phase. A non-human transgenic mammal is useful as a model for testing

CC hair removal products which function by inhibiting hairless protein

CC expression. The sequence presented is the deoxy-ribozyme that cleaves the

CC human hairless protein mRNA immediately after nucleotide 1597.

XX

SQ Sequence 29 BP; 7 A; 9 C; 10 G; 3 T; 0 other;

Query Match 97.5%; Score 15.6; DB 25; Length 29;

Best Local Similarity 93.8%; Pred. No. 35;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16

Db 7 AGCTAGCTACACGA 22

RESULT 26

ABX13990

ID ABX13990 standard; DNA; 29 BP.

XX

AC ABX13990;

XX

DT 25-FEB-2003 (first entry)

XX

DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1641.

XX

KW Catalytic DNA; catalytic RNA; hairless protein; ss;

KW hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;

KW ribozyme; DNAzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;

KW catalytic core; cleavage site; pharmaceutical; hair production;

KW hair follicle; anagen phase; catagen phase; hair removal product;

KW depilatory.

XX

OS Homo sapiens.

OS Synthetic.

XX

XX Key Location/Qualifiers

FT misc_feature 8..22

FT /*tag= a

FT /note= "Catalytic domain"

XX

XX WO200283891-A2.

XX

PD 24-OCT-2002.
 XX
 XX 12-APR-2002; 2002WO-US11683.
 PF
 XX 13-APR-2001; 2001US-283618P.
 PR
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 PA
 XX
 PI Cristiano AM;
 DR WPI; 2003-093020/08.
 XX
 XX New catalytic nucleic acid molecule that specifically cleaves Hairless
 PT Protein mRNA, useful for inhibiting hair production by a hair-producing
 PT cell, or for inhibiting transition of a hair follicle from anagen phase
 PT to catagen phase
 PS
 XX Claim 3; Page 34; 65pp; English.
 XX
 CC The invention discloses a new catalytic DNA or RNA molecule that
 CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA
 CC which comprises a catalytic domain that cleaves mRNA at a defined
 CC consensus sequence and binding domains contiguous with the 5' and 3' ends
 CC of the catalytic domain. Lack of expression of the hairless gene due to
 CC inherited mutations leads to the complete loss of hair, known as
 CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting
 CC the genes promoting hair growth, and one way to get targeted, transient
 CC gene suppression is through the use of catalytic nucleic acid technology,
 CC including ribozymes and DNazymes. Ribozymes are RNA structures which have
 CC a self-catalytic enzymatic function and sequence specific RNA binding
 CC ability. Small DNA oligonucleotides that have a similar structure to the
 CC hammerhead ribozyme, called deoxy-ribozymes or DNazymes, having a
 CC catalytic core and two sequence specific arms. The deoxy-ribozymes have
 CC more lenient consensus cleavage site requirements and are less likely to
 CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids
 CC are useful in pharmaceutical compositions for inhibiting hair production
 CC by a hair-producing cell, for inhibiting hair growth and for inhibiting
 CC the transition of a hair follicle from the anagen phase to the catagen
 CC phase. A non-human transgenic mammal is useful as a model for testing
 CC hair removal products which function by inhibiting hairless protein
 CC expression. The sequence presented is the deoxy-ribozyme that cleaves the
 CC human hairless protein mRNA immediately after nucleotide 1641.
 XX
 SQ Sequence 29 BP; 7 A; 11 C; 7 G; 4 T; 0 other;
 QY
 Query Match 97.5%; Score 15.6; DB 25; Length 29;
 Best Local Similarity 93.8%; Pred. No. 35;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 DB 1 RGGCTAGCTACACGA 16
 7 AGGCTAGCTACACGA 22
 RESULT 27
 ABX13991 standard; DNA; 29 BP.
 XX
 XX ABX13991;
 AC
 XX 25-FEB-2003 (first entry)
 DT
 XX
 DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1698.
 XX
 XX Catalytic DNA; catalytic RNA; hairless protein; ss;
 KW hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;
 KW ribozyme; DNazyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;
 KW catalytic core; cleavage site; pharmaceutical; hair production;
 KW hair follicle; anagen phase; catagen phase; hair removal product;
 KW depilatory.
 XX
 XX Homo sapiens.
 OS Synthetic.

XX
 FH Key Location/Qualifiers
 FT misc_feature 8..22
 FT /tag= a
 FT /note= "Catalytic domain"
 XX
 XX WO200283991-A2.
 XX
 XX 24-OCT-2002.
 XX
 XX 12-APR-2002; 2002WO-US11683.
 PF
 XX 13-APR-2001; 2001US-283618P.
 PR
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 PA
 XX
 PI Cristiano AM;
 DR WPI; 2003-093020/08.
 XX
 XX New catalytic nucleic acid molecule that specifically cleaves Hairless
 PT Protein mRNA, useful for inhibiting hair production by a hair-producing
 PT cell, or for inhibiting transition of a hair follicle from anagen phase
 PT to catagen phase
 PS
 XX Claim 3; Page 34; 65pp; English.
 XX
 CC The invention discloses a new catalytic DNA or RNA molecule that
 CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA
 CC which comprises a catalytic domain that cleaves mRNA at a defined
 CC consensus sequence and binding domains contiguous with the 5' and 3' ends
 CC of the catalytic domain. Lack of expression of the hairless gene due to
 CC inherited mutations leads to the complete loss of hair, known as
 CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting
 CC the genes promoting hair growth, and one way to get targeted, transient
 CC gene suppression is through the use of catalytic nucleic acid technology,
 CC including ribozymes and DNazymes. Ribozymes are RNA structures which have
 CC a self-catalytic enzymatic function and sequence specific RNA binding
 CC ability. Small DNA oligonucleotides that have a similar structure to the
 CC hammerhead ribozyme, called deoxy-ribozymes or DNazymes, having a
 CC catalytic core and two sequence specific arms. The deoxy-ribozymes have
 CC more lenient consensus cleavage site requirements and are less likely to
 CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids
 CC are useful in pharmaceutical compositions for inhibiting hair production
 CC by a hair-producing cell, for inhibiting hair growth and for inhibiting
 CC the transition of a hair follicle from the anagen phase to the catagen
 CC phase. A non-human transgenic mammal is useful as a model for testing
 CC hair removal products which function by inhibiting hairless protein
 CC expression. The sequence presented is the deoxy-ribozyme that cleaves the
 CC human hairless protein mRNA immediately after nucleotide 1698.
 XX
 SQ Sequence 29 BP; 7 A; 7 C; 10 G; 5 T; 0 other;
 QY
 Query Match 97.5%; Score 15.6; DB 25; Length 29;
 Best Local Similarity 93.8%; Pred. No. 35;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 DB 1 RGGCTAGCTACACGA 16
 7 AGGCTAGCTACACGA 22
 RESULT 28
 ABX13992 standard; DNA; 29 BP.
 XX
 XX ABX13992;
 AC
 XX 25-FEB-2003 (first entry)
 DT
 XX
 DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1732.
 XX
 XX Catalytic DNA; catalytic RNA; hairless protein; ss;
 KW

KW hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;
KW ribozyme; DNAzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;
KW catalytic core; cleavage site; pharmaceutical; hair production;
KW hair follicle; anagen phase; catagen phase; hair removal product;
KW depilatory.
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 8..22
FT /*tag= a
FT /note= "Catalytic domain"
XX
XX WO200283891-A2.
XX
XX 24-OCT-2002.
XX
XX 12-APR-2002; 2002WO-US11683.
XX
XX 13-APR-2001; 2001US-283618P.
XX
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX Christiano AM;
XX
XX WPI; 2003-093020/08.
XX
XX New catalytic nucleic acid molecule that specifically cleaves Hairless
PT Protein mRNA, useful for inhibiting hair production by a hair-producing
PT cell, or for inhibiting transition of a hair follicle from anagen phase
PT to catagen phase -
XX
XX Claim 3; Page 34; 65pp; English.
XX
XX The invention discloses a new catalytic DNA or RNA molecule that
CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA
CC which comprises a catalytic domain that cleaves mRNA at a defined
CC consensus sequence and binding domains contiguous with the 5' and 3' ends
CC of the catalytic domain. Lack of expression of the hairless gene due to
CC inherited mutations leads to the complete loss of hair, known as
CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting
CC the genes promoting hair growth, and one way to get targeted, transient
CC gene suppression is through the use of catalytic nucleic acid technology,
CC including ribozymes and DNAzymes. Ribozymes are RNA structures which have
CC a self-catalytic enzymatic function and sequence specific RNA binding
CC ability. Small DNA oligonucleotides that have a similar structure to the
CC hammerhead ribozyme, called deoxy-ribozymes or DNAzymes, having a
CC catalytic core and two sequence specific arms. The deoxy-ribozymes have
CC more lenient consensus cleavage site requirements and are less likely to
CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids
CC are useful in pharmaceutical compositions for inhibiting hair production
CC by a hair-producing cell, for inhibiting hair growth and for inhibiting
CC the transition of a hair follicle from the anagen phase to the catagen
CC phase. A non-human transgenic mammal is useful as a model for testing
CC hair removal products which function by inhibiting hairless protein
CC expression. The sequence presented is the deoxy-ribozyme that cleaves the
CC human hairless protein mRNA immediately after nucleotide 1732.
CC
XX
SQ Sequence 29 BP; 6 A; 10 C; 8 G; 5 T; 0 other;

Query Match 97.5%; Score 15.6; DB 25; Length 29;
Best Local Similarity 93.8%; Pred. No. 35;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RGGCTAGCTACACGA 16
: |||||
Db 7 AGGCTAGCTACACGA 22

RESULT 29
ABX13993
ID ABX13993 standard; DNA; 29 BP.

XX
AC ABX13993;
XX
DT 25-FEB-2003 (first entry)
XX
DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1750.
XX
KW Catalytic DNA; catalytic RNA; hairless protein; 88;
KW hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;
KW ribozyme; DNAzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;
KW catalytic core; cleavage site; pharmaceutical; hair production;
KW hair follicle; anagen phase; catagen phase; hair removal product;
KW depilatory.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 8..22
FT /*tag= a
FT /note= "Catalytic domain"
XX
XX WO200283891-A2.
XX
XX 24-OCT-2002.
XX
XX 12-APR-2002; 2002WO-US11683.
XX
XX 13-APR-2001; 2001US-283618P.
XX
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX Christiano AM;
XX
XX WPI; 2003-093020/08.
XX
XX New catalytic nucleic acid molecule that specifically cleaves Hairless
PT Protein mRNA, useful for inhibiting hair production by a hair-producing
PT cell, or for inhibiting transition of a hair follicle from anagen phase
PT to catagen phase -
XX
XX Claim 3; Page 34; 65pp; English.
XX
XX The invention discloses a new catalytic DNA or RNA molecule that
CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA
CC which comprises a catalytic domain that cleaves mRNA at a defined
CC consensus sequence and binding domains contiguous with the 5' and 3' ends
CC of the catalytic domain. Lack of expression of the hairless gene due to
CC inherited mutations leads to the complete loss of hair, known as
CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting
CC the genes promoting hair growth, and one way to get targeted, transient
CC gene suppression is through the use of catalytic nucleic acid technology,
CC including ribozymes and DNAzymes. Ribozymes are RNA structures which have
CC a self-catalytic enzymatic function and sequence specific RNA binding
CC ability. Small DNA oligonucleotides that have a similar structure to the
CC hammerhead ribozyme, called deoxy-ribozymes or DNAzymes, having a
CC catalytic core and two sequence specific arms. The deoxy-ribozymes have
CC more lenient consensus cleavage site requirements and are less likely to
CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids
CC are useful in pharmaceutical compositions for inhibiting hair production
CC by a hair-producing cell, for inhibiting hair growth and for inhibiting
CC the transition of a hair follicle from the anagen phase to the catagen
CC phase. A non-human transgenic mammal is useful as a model for testing
CC hair removal products which function by inhibiting hairless protein
CC expression. The sequence presented is the deoxy-ribozyme that cleaves the
CC human hairless protein mRNA immediately after nucleotide 1750.
CC
XX
SQ Sequence 29 BP; 8 A; 9 C; 7 G; 5 T; 0 other;

Query Match 97.5%; Score 15.6; DB 25; Length 29;
Best Local Similarity 93.8%; Pred. No. 35;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
 :|||||
 Db 7 GGGCTAGCTACACGA 22

RESULT 30
 ABX13994
 ID ABX13994 standard; DNA, 29 BP.
 AC ABX13994;
 XX
 DT 25-FEB-2003 (first entry)
 XX

Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1801.

XX
 KM Catalytic DNA; catalytic RNA; hairless protein; ss;
 KM hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;
 KM ribozyme; DNzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;
 KM catalytic core; cleavage site; pharmaceutical; hair production;
 KM hair follicle; anagen phase; catagen phase; hair removal product;
 KM depilatory.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 8..22
 FT /*tag= a
 FT /note= "Catalytic domain"
 XX
 PM WO200283891-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 12-APR-2002; 2002WO-US11683.
 XX
 PR 13-APR-2001; 2001US-283618P.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Cristiano AM;
 XX
 DR WPI; 2003-093020/08.
 XX

New catalytic nucleic acid molecule that specifically cleaves Hairless protein mRNA, useful for inhibiting hair production by a hair-producing cell, or for inhibiting transition of a hair follicle from anagen phase to catagen phase -

XX
 PS Claim 3; Page 34; 65pp; English.
 XX

The invention discloses a new catalytic DNA or RNA molecule that specifically cleaves, or inhibits expression of, Hairless Protein mRNA which comprises a catalytic domain that cleaves mRNA at a defined consensus sequence and binding domains contiguous with the 5' and 3' ends of the catalytic domain. Lack of expression of the hairless gene due to inherited mutations leads to the complete loss of hair, known as atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting the genes promoting hair growth, and one way to get targeted, transient gene suppression is through the use of catalytic nucleic acid technology, including ribozymes and DNzymes. Ribozymes are RNA structures which have a self-catalytic enzymatic function and sequence specific RNA binding ability. Small DNA oligonucleotides that have a similar structure to the hammerhead ribozyme, called deoxy-ribozymes or DNzymes, having a catalytic core and two sequence specific arms. The deoxy-ribozymes have more lenient consensus cleavage site requirements and are less likely to degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids are useful in pharmaceutical compositions for inhibiting hair production by a hair-producing cell, for inhibiting hair growth and for inhibiting the transition of a hair follicle from the anagen phase to the catagen phase. A non-human transgenic mammal is useful as a model for testing hair removal products which function by inhibiting hairless protein expression. The sequence presented is the deoxy-ribozyme that cleaves the

CC human hairless protein mRNA immediately after nucleotide 1801.
 XX
 SQ Sequence 29 BP; 9 A; 6 C; 11 G; 3 T; 0 other;
 XX

Query Match 97.5%; Score 15.6; DB 25; Length 29;
 Best Local Similarity 93.8%; Pred. No. 35;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
 :|||||
 Db 7 AGGCTAGCTACACGA 22

RESULT 31
 ABX13995
 ID ABX13995 standard; DNA, 29 BP.
 AC ABX13995;
 XX
 DT 25-FEB-2003 (first entry)
 XX

Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 1811.

XX
 KM Catalytic DNA; catalytic RNA; hairless protein; ss;
 KM hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;
 KM ribozyme; DNzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;
 KM catalytic core; cleavage site; pharmaceutical; hair production;
 KM hair follicle; anagen phase; catagen phase; hair removal product;
 KM depilatory.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 8..22
 FT /*tag= a
 FT /note= "Catalytic domain"
 XX
 PM WO200283891-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 12-APR-2002; 2002WO-US11683.
 XX
 PR 13-APR-2001; 2001US-283618P.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Cristiano AM;
 XX
 DR WPI; 2003-093020/08.
 XX

New catalytic nucleic acid molecule that specifically cleaves Hairless protein mRNA, useful for inhibiting hair production by a hair-producing cell, or for inhibiting transition of a hair follicle from anagen phase to catagen phase -

XX
 PS Claim 3; Page 35; 65pp; English.
 XX

The invention discloses a new catalytic DNA or RNA molecule that specifically cleaves, or inhibits expression of, Hairless Protein mRNA which comprises a catalytic domain that cleaves mRNA at a defined consensus sequence and binding domains contiguous with the 5' and 3' ends of the catalytic domain. Lack of expression of the hairless gene due to inherited mutations leads to the complete loss of hair, known as atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting the genes promoting hair growth, and one way to get targeted, transient gene suppression is through the use of catalytic nucleic acid technology, including ribozymes and DNzymes. Ribozymes are RNA structures which have a self-catalytic enzymatic function and sequence specific RNA binding ability. Small DNA oligonucleotides that have a similar structure to the hammerhead ribozyme, called deoxy-ribozymes or DNzymes, having a catalytic core and two sequence specific arms. The deoxy-ribozymes have

CC more lenient consensus cleavage site requirements and are less likely to
CC degrade, in vivo, that hammerhead ribozymes. The catalytic nucleic acids
CC are useful in pharmaceutical compositions for inhibiting hair production
CC by a hair-producing cell, for inhibiting hair growth and for inhibiting
CC the transition of a hair follicle from the anagen phase to the catagen
CC phase. A non-human transgenic mammal is useful as a model for testing
CC hair removal products which function by inhibiting hairless protein
CC expression. The sequence presented is the deoxy-ribozyme that cleaves the
CC human hairless protein mRNA immediately after nucleotide 1811.
SQ Sequence 29 BP; 9 A; 9 C; 9 G; 2 T; 0 other;
XX
Qy Query Match 97.5%; Score 15.6; DB 25; Length 29;
Best Local Similarity 93.8%; Pred. No. 35;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
1 RGGCTAGCTACACGA 16
7 AGGCTAGCTACACGA 22
Db
RESULT 32
ABX13996
XX ABX13996 standard; DNA; 29 BP.
XX
AC ABX13996;
XX
DT 25-FEB-2003 (first entry)
XX
DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 2028.
XX
KM Catalytic DNA; catalytic RNA; hairless protein; ss;
KM hair loss; atichia; hair growth; hirsutism; catalytic nucleic acid;
KM ribozyme; DNAzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;
KM catalytic core; cleavage site; pharmaceutical; hair production;
KM hair follicle; anagen phase; catagen phase; hair removal product;
KM depilatory.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 8..22
FT /*tag= a
FT /note= "Catalytic domain"
FT
FT
PN WO200283891-A2.
XX
PD 24-OCT-2002.
XX
PF 12-APR-2002; 2002WO-US11683.
XX
PR 13-APR-2001; 2001US-283618P.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Christiano AM;
XX
DR WPI; 2003-093020/08.
XX
PT New catalytic nucleic acid molecule that specifically cleaves Hairless
PT protein mRNA, useful for inhibiting hair production by a hair-producing
PT cell, or for inhibiting transition of a hair follicle from anagen phase
PT to catagen phase -
XX
PS Claim 3; Page 35; 65pp; English.
XX
CC The invention discloses a new catalytic DNA or RNA molecule that
CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA
CC which comprises a catalytic domain that cleaves mRNA at a defined
CC consensus sequence and binding domains contiguous with the 5' and 3' ends
CC of the catalytic domain. Lack of expression of the hairless gene due to
CC inherited mutations leads to the complete loss of hair, known as

CC atichia. Abundant hair growth, hirsutism, can be improved by inhibiting
CC the genes promoting hair growth, and one way to get targeted, transient
CC gene suppression is through the use of catalytic nucleic acid technology,
CC including ribozymes and DNAzymes. Ribozymes are RNA structures which have
CC a self-catalytic enzymatic function and sequence specific RNA binding
CC ability. Small DNA oligonucleotides that have a similar structure to the
CC hammerhead ribozyme, called deoxy-ribozymes or DNAzymes, having a
CC catalytic core and two sequence specific arms. The deoxy-ribozymes have
CC more lenient consensus cleavage site requirements and are less likely to
CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids
CC are useful in pharmaceutical compositions for inhibiting hair production
CC by a hair-producing cell, for inhibiting hair growth and for inhibiting
CC the transition of a hair follicle from the anagen phase to the catagen
CC phase. A non-human transgenic mammal is useful as a model for testing
CC hair removal products which function by inhibiting hairless protein
CC expression. The sequence presented is the deoxy-ribozyme that cleaves the
CC human hairless protein mRNA immediately after nucleotide 2028.
SQ Sequence 29 BP; 6 A; 7 C; 13 G; 3 T; 0 other;
XX
Qy Query Match 97.5%; Score 15.6; DB 25; Length 29;
Best Local Similarity 93.8%; Pred. No. 35;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
1 RGGCTAGCTACACGA 16
7 GGCTAGCTACACGA 22
Db
RESULT 33
ABX13997
XX ABX13997 standard; DNA; 29 BP.
XX
AC ABX13997;
XX
DT 25-FEB-2003 (first entry)
XX
DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 2033.
XX
KM Catalytic DNA; catalytic RNA; hairless protein; ss;
KM hair loss; atichia; hair growth; hirsutism; catalytic nucleic acid;
KM ribozyme; DNAzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;
KM catalytic core; cleavage site; pharmaceutical; hair production;
KM hair follicle; anagen phase; catagen phase; hair removal product;
KM depilatory.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 8..22
FT /*tag= a
FT /note= "Catalytic domain"
FT
FT
PN WO200283891-A2.
XX
PD 24-OCT-2002.
XX
PF 12-APR-2002; 2002WO-US11683.
XX
PR 13-APR-2001; 2001US-283618P.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Christiano AM;
XX
DR WPI; 2003-093020/08.
XX
PT New catalytic nucleic acid molecule that specifically cleaves Hairless
PT protein mRNA, useful for inhibiting hair production by a hair-producing
PT cell, or for inhibiting transition of a hair follicle from anagen phase
PT to catagen phase -
XX

XX 12-APR-2002; 2002WO-US11663.
 PR 13-APR-2001; 2001US-283618P.
 PR (UYCO) UNIV COLUMBIA NEW YORK.
 PA
 XX Christiano AM;
 PI
 XX WPI; 2003-093020/08.
 DR
 XX New catalytic nucleic acid molecule that specifically cleaves Hairless
 PT Protein mRNA, useful for inhibiting hair production by a hair-producing
 PT cell, or for inhibiting transition of a hair follicle from anagen phase
 PT to catagen phase -
 XX
 XX Claim 3; Page 35; 65pp; English.
 PS
 XX The invention discloses a new catalytic DNA or RNA molecule that
 CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA
 CC which comprises a catalytic domain that cleaves mRNA at a defined
 CC consensus sequence and binding domains contiguous with the 5' and 3' ends
 CC of the catalytic domain. Lack of expression of the hairless gene due to
 CC inherited mutations leads to the complete loss of hair, known as
 CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting
 CC the genes promoting hair growth, and one way to get targeted, transient
 CC gene suppression is through the use of catalytic nucleic acid technology,
 CC including ribozymes and DNAzymes. Ribozymes are RNA structures which have
 CC a self-catalytic enzymatic function and sequence specific RNA binding
 CC ability. Small DNA oligonucleotides that have a similar structure to the
 CC hammerhead ribozyme, called deoxy-ribozymes or DNAzymes, having a
 CC catalytic core and two sequence specific arms. The deoxy-ribozymes have
 CC more lenient consensus cleavage site requirements and are less likely to
 CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids
 CC are useful in pharmaceutical compositions for inhibiting hair production
 CC by a hair-producing cell, for inhibiting hair growth and for inhibiting
 CC the transition of a hair follicle from the anagen phase to the catagen
 CC phase. A non-human transgenic mammal is useful as a model for testing
 CC hair removal products which function by inhibiting hairless protein
 CC expression. The sequence presented is the deoxy-ribozyme that cleaves the
 CC human hairless protein mRNA immediately after nucleotide 2083.
 XX
 SQ Sequence 29 BP; 9 A; 7 C; 9 G; 4 T; 0 other;
 Query Match 97.5%; Score 15.6; DB 25; Length 29;
 Best Local Similarity 93.8%; Pred. No. 35;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGCTAGCTACACGA 16
 :|||||
 Db 7 GGCTAGCTACACGA 22
 :|||||
 RESULT 36
 ABX14001
 ID ABX14001 standard; DNA; 29 BP.
 XX
 AC ABX14001;
 XX
 DT 25-FEB-2003 (first entry)
 XX
 DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 2380.
 XX
 XX Catalytic DNA; catalytic RNA; hairless protein; ss;
 KM hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;
 KM ribozyme; DNAzyme; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;
 KM catalytic core; cleavage site; pharmaceutical; hair production;
 KM hair follicle; anagen phase; catagen phase; hair removal product;
 KM depilatory.
 XX
 XX Homo sapiens.
 OS Synthetic.
 XX

PH Key Location/Qualifiers
 FT misc_feature 8..22
 FT /*tag = a
 FT /note = "Catalytic domain"
 PN WO200283691-A2.
 XX
 XX 24-OCT-2002.
 PD
 XX 12-APR-2002; 2002WO-US11663.
 PR 13-APR-2001; 2001US-283618P.
 PR (UYCO) UNIV COLUMBIA NEW YORK.
 PA
 XX Christiano AM;
 PI
 XX WPI; 2003-093020/08.
 DR
 XX New catalytic nucleic acid molecule that specifically cleaves Hairless
 PT Protein mRNA, useful for inhibiting hair production by a hair-producing
 PT cell, or for inhibiting transition of a hair follicle from anagen phase
 PT to catagen phase -
 XX
 XX Claim 3; Page 35; 65pp; English.
 PS
 XX The invention discloses a new catalytic DNA or RNA molecule that
 CC specifically cleaves, or inhibits expression of, Hairless Protein mRNA
 CC which comprises a catalytic domain that cleaves mRNA at a defined
 CC consensus sequence and binding domains contiguous with the 5' and 3' ends
 CC of the catalytic domain. Lack of expression of the hairless gene due to
 CC inherited mutations leads to the complete loss of hair, known as
 CC atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting
 CC the genes promoting hair growth, and one way to get targeted, transient
 CC gene suppression is through the use of catalytic nucleic acid technology,
 CC including ribozymes and DNAzymes. Ribozymes are RNA structures which have
 CC a self-catalytic enzymatic function and sequence specific RNA binding
 CC ability. Small DNA oligonucleotides that have a similar structure to the
 CC hammerhead ribozyme, called deoxy-ribozymes or DNAzymes, having a
 CC catalytic core and two sequence specific arms. The deoxy-ribozymes have
 CC more lenient consensus cleavage site requirements and are less likely to
 CC degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids
 CC are useful in pharmaceutical compositions for inhibiting hair production
 CC by a hair-producing cell, for inhibiting hair growth and for inhibiting
 CC the transition of a hair follicle from the anagen phase to the catagen
 CC phase. A non-human transgenic mammal is useful as a model for testing
 CC hair removal products which function by inhibiting hairless protein
 CC expression. The sequence presented is the deoxy-ribozyme that cleaves the
 CC human hairless protein mRNA immediately after nucleotide 2380.
 XX
 SQ Sequence 29 BP; 6 A; 10 C; 8 G; 5 T; 0 other;
 Query Match 97.5%; Score 15.6; DB 25; Length 29;
 Best Local Similarity 93.8%; Pred. No. 35;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGCTAGCTACACGA 16
 :|||||
 Db 7 AGCTAGCTACACGA 22
 :|||||
 RESULT 37
 ABX14002
 ID ABX14002 standard; DNA; 29 BP.
 XX
 AC ABX14002;
 XX
 DT 25-FEB-2003 (first entry)
 XX
 DE Deoxy-ribozyme, cleaving hairless protein mRNA after nucleotide 2395.
 XX
 XX Catalytic DNA; catalytic RNA; hairless protein; ss;
 KM hair loss; atrichia; hair growth; hirsutism; catalytic nucleic acid;
 KM

KW ribozyme; DNase; self-catalytic; hammerhead ribozyme; deoxy-ribozyme;
KW catalytic core; cleavage site; pharmaceutical; hair production;
KW hair follicle; anagen phase; catagen phase; hair removal product;
KW deplatory.
OS Homo sapiens.
OS Synthetic.
XX
XX
XX Key Location/Qualifiers
FT misc_feature 8..22 /*tag= a
FT /note= "Catalytic domain"
XX
XX WO200283891-A2.
XX
XX PD 24-OCT-2002.
XX
XX PF 12-APR-2002; 2002WO-US11683.
XX
XX PR 13-APR-2001; 2001US-283618P.
XX
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX Cristiano AM;
XX
XX MPI; 2003-093020/08.
XX
XX New catalytic nucleic acid molecule that specifically cleaves Hairless
XX Protein mRNA, useful for inhibiting hair production by a hair-producing
XX cell, or for inhibiting transition of a hair follicle from anagen phase
XX to catagen phase -
XX
XX
XX Claim 3; Page 35; 65pp; English.
XX
XX The invention discloses a new catalytic DNA or RNA molecule that
XX specifically cleaves, or inhibits expression of, Hairless Protein mRNA
XX which comprises a catalytic domain that cleaves mRNA at a defined
XX consensus sequence and binding domain contiguous with the 5' and 3' ends
XX of the catalytic domain. Lack of expression of the hairless gene due to
XX inherited mutations leads to the complete loss of hair, known as
XX atrichia. Abundant hair growth, hirsutism, can be improved by inhibiting
XX the genes promoting hair growth, and one way to get targeted, transient
XX gene suppression is through the use of catalytic nucleic acid technology,
XX including ribozymes and DNase. Ribozymes are RNA structures which have
XX a self-catalytic enzymatic function and sequence specific RNA binding
XX ability. Small DNA oligonucleotides that have a similar structure to the
XX hammerhead ribozyme, called deoxy-ribozymes or DNase, having a
XX catalytic core and two sequence specific arms. The deoxy-ribozymes have
XX more lenient consensus cleavage site requirements and are less likely to
XX degrade, in vivo, than hammerhead ribozymes. The catalytic nucleic acids
XX are useful in pharmaceutical compositions for inhibiting hair production
XX by a hair-producing cell, for inhibiting hair growth and for inhibiting
XX the transition of a hair follicle from the anagen phase to the catagen
XX phase. A non-human transgenic mammal is useful as a model for testing
XX hair removal products which function by inhibiting hairless protein
XX expression. The sequence presented is the deoxy-ribozyme that cleaves the
XX human hairless protein mRNA immediately after nucleotide 2395.
XX
SQ Sequence 29 BP; 9 A; 9 C; 8 G; 3 T; 0 other;
XX
XX Query Match 97.5%; Score 15.6; DB 25; Length 29;
XX Best Local Similarity 93.8%; Pred. No. 35;
XX Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 RGGCTAGCTACACGA 16
XX :|||||||
XX 7 GGGCTAGCTACACGA 22

AC AA14525;
XX
XX 08-AUG-2000 (first entry)
XX
XX Oligonucleotide 5'-polynm-gaglink-(Pleio)-DNase-1023-B/P.
XX
XX Reverse transcriptase; RNase H; stem-loop structure; genetic element;
XX inverted tandem repeat; vector; inhibitory nucleic acid;
XX antisense sequence; aptamer; gene expression; ss.
XX
XX Synthetic.
XX
XX WO200022114-A1.
XX
XX PD 20-APR-2000.
XX
XX PF 12-OCT-1999; 99WO-US23936.
XX
XX PR 09-OCT-1998; 98US-0169793.
XX
XX PR 16-SEP-1999; 99US-0397782.
XX
XX PR 04-OCT-1999; 99US-0169793.
XX
XX (INGE-) INGENE INC.
XX
XX Conrad CA;
XX
XX MPI; 2000-317974/27.
XX
XX Genetic element for producing and delivering single-stranded cDNA,
XX comprises a gene encoding reverse transcriptase and a sequence of
XX interest flanked by an inverted tandem repeat and primer binding site
XX
XX
XX Disclosure; Page 45; 77pp; English.
XX
XX The specification describes methods for producing single-stranded cDNA
XX (ssCDNA) in eukaryotic cells. They use a DNA cassette that produces
XX ssCDNA in vivo. The cassette contains the Moloney murine leukemia virus
XX reverse transcriptase/RNase H, a bacterial restriction endonuclease
XX gene, and a sequence of interest which produces a RNA template from
XX which the reverse transcriptase synthesizes cDNA of a specified sequence.
XX The ssCDNA is then modified to remove all flanking vector sequences by
XX taking advantage of the stem-loop structure of the cDNA, which forms as
XX a result of the inclusion of an inverted tandem repeat that allows the
XX ssCDNA to fold back on itself, forming a double stranded DNA stem, in
XX the sequence of interest. The double-stranded stem contains one or more
XX functional genetic elements (GB), adapted for incorporation into a vector
XX for delivery to a cell. The vectors are is useful for producing a ssDNA
XX sequence of interest, particularly a cDNA transcript, an inhibitory
XX nucleic acid molecule which is an antisense sequence or aptamer, an mRNA
XX transcript and a heteroduplex molecule. Inhibitory nucleic acid molecules
XX to a target cell are useful for alleviating pathological conditions by
XX regulating gene expression. The present oligonucleotide was used to
XX produce a vector for use in the course of the invention.
XX
SQ Sequence 30 BP; 5 A; 8 C; 8 G; 9 T; 0 other;
XX
XX Query Match 97.5%; Score 15.6; DB 21; Length 30;
XX Best Local Similarity 93.8%; Pred. No. 35;
XX Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 RGGCTAGCTACACGA 16
XX :|||||||
XX 24 AGGCTAGCTACACGA 9

RESULT 38
AA14525/C
ID AA14525 standard; DNA; 30 BP.
XX

RESULT 39
AA287648
ID AA287648 standard; DNA; 30 BP.
XX
XX AA287648;
XX 09-MAY-2000 (first entry)
XX

XX Human short protein kinase C (PKC)alpha DNA ribozyme.
 DE Ribozyme; hammerhead; RNase degradation; catalytic; PKCalpha; VEGF;
 XX protein kinase C alpha; tumor necrosis factor alpha; TNFalpha; cancer;
 KW vascular epithelial growth factor; gene expression; malignant glioma;
 KM cell proliferation; cytostatic; human; ss.
 OS Homo sapiens.
 XX MO963066-A2.
 XX 09-DEC-1999.
 PD 28-MAY-1999; 99WO-GB01706.
 XX 01-JUN-1998; 98GB-0011750.
 PR (NORA-) NORMEGIAN RADIIUM HOSPITAL RES FOUND.
 PA (DZIE/) DZIEGLAWSKA H E.
 XX Sloud M;
 PI WPI; 2000-147046/13.
 DR Novel ribozymes, used for inhibiting the proliferation of cells, e.g.
 PT for treating or preventing cancers -
 XX Disclosure; Page 9; 93pp; English.
 PS The invention provides novel modified ribozymes that have 3 or more
 CC pyrimidine nucleotides (PMN) in the ribozyme modified at the 2'-position,
 CC where the PMNs are modified to 2'-amino PMNs and the ribozymes exhibit
 CC improved stability to RNase degradation and exhibits 85% or more
 CC catalytic activity to the unmodified ribozymes. The ribozymes of the
 CC invention are selected from rat and human protein kinase C (PKC)alpha
 CC ribozymes, tumor necrosis factor (TNF)alpha ribozyme, rat and human
 CC vascular epithelial growth factor (VEGF) ribozymes. These ribozymes can
 CC be used for treating or preventing a disease or condition responsive to
 CC an alteration in the expression of a gene, where the ribozyme is capable
 CC of cleaving the RNA transcribed from the gene. They can be used for
 CC treating or preventing a disease or condition associated with the
 CC proliferation of rapidly dividing cells, e.g. cancer such as malignant
 CC glioma. They can also be used for inhibiting the proliferation of cells.
 CC The use of 2'-amino modified pyrimidine can provide ribozymes of improved
 CC stability which retain the activity of the unmodified ribozyme. The
 CC present sequence represents a human short PKCalpha DNA ribozyme.
 CC
 XX Sequence 30 BP; 7 A; 11 C; 8 G; 4 T; 0 other;
 SQ
 Query Match 97.5%; Score 15.6; DB 21; Length 30;
 Best Local Similarity 93.8%; Pred. No. 35;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGGCTAGCTACACGA 16
 : |||||
 DB 8 AGGCTAGCTACACGA 23
 RESULT 40
 AAS02302/C
 ID AAS02302 standard; cDNA; 30 BP.
 XX AAS02302;
 AC
 XX 18-JUN-2001 (first entry)
 DT
 XX Synthetic oligodeoxynucleotide 5'-polyNM-gaglink-(Pleio)-DNase-1023-B/P.
 DE ODN, oligodeoxynucleotide; inverted tandem repeat; primer binding site;
 KW stem-loop; c-myc; viral gene; gene therapy; reverse transcription; ss;
 KM endogenous target nucleic acid; gene inactivation; RNA splicing;
 KW site-directed mutagenesis; cellular function interruption;

KW nucleic acid duplex binding; nucleic acid triplex binding.
 XX Synthetic.
 OS
 XX MO200125419-A1.
 XX 12-APR-2001.
 PD 04-OCT-2000; 2000WO-US27381.
 XX 04-OCT-1999; 99US-0411568.
 PR 28-FEB-2000; 2000US-0514707.
 XX (CYTO-) CYTOGENIX INC.
 PA Conrad CA, Chen Y;
 PI WPI; 2001-266304/27.
 DR Alteration of expression of an endogenous nucleic acid for use in gene
 XX therapy comprises the expression of a specific antisense sequence -
 PT Disclosure; Page 43; 61pp; English.
 PS The sequence represents a synthetic single stranded cDNA. This DNA exists
 CC in a target cell and is transfected with a cassette comprising a sequence
 CC of interest flanked by inverted tandem repeats (ITR) and a primer binding
 CC site (PBS) 3' to the tandem repeat. Transcription of the cassette by the
 CC target cell produces an RNA template which is reverse transcribed to
 CC produce ss-cDNA of a specified sequence. The ss-cDNA folds back on itself
 CC as a result of the inverted tandem repeat, to form a stem-loop structure.
 CC The loop is comprised of the sequence of interest. The cDNA transcript is
 CC bound to an endogenous nucleic acid target to alter expression of the
 CC target sequence. This method is useful for altering the expression of
 CC gene products e.g. c-myc or a viral gene product. It may be applied to
 CC gene therapy, with target genes mutated or introduced for therapeutic
 CC purposes, such as gene inactivation using duplex or triplex binding of
 CC nucleic acids, site-directed mutagenesis, interruption of cellular
 CC function by binding to specific cellular proteins and interfering with
 CC RNA splicing functions.
 CC
 XX Sequence 30 BP; 5 A; 8 C; 8 G; 9 T; 0 other;
 SQ
 Query Match 97.5%; Score 15.6; DB 22; Length 30;
 Best Local Similarity 93.8%; Pred. No. 35;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGGCTAGCTACACGA 16
 : |||||
 DB 24 AGGCTAGCTACACGA 9
 Search completed: January 21, 2004, 06:52:48
 Job time : 156.5 secs

4-29-98

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 06:45:02 ; Search time 38 Seconds
(without alignments)
185.846 Million cell updates/sec

Title: US-09-423-035B-121

Perfect score: 16
Sequence: 1 rrgctagctacacga 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 830498

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PTCUS_COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.6	97.5	16	4	US-09-536-393-19
2	15.6	97.5	16	4	US-09-536-393-20
3	15.6	97.5	29	4	US-09-270-140A-23
4	15.6	97.5	29	4	US-09-270-140A-25
5	15.6	97.5	30	4	US-09-270-140A-55
6	15.6	97.5	31	3	US-09-253-955-5
7	15.6	97.5	31	3	US-09-637-405-5
8	15.6	97.5	31	4	US-09-270-140A-42
9	15.6	97.5	31	4	US-09-270-140A-45
10	15.6	97.5	31	4	US-09-270-140A-48
11	15.6	97.5	31	4	US-09-270-140A-51
12	15.6	97.5	32	4	US-09-746-985B-5
13	15.6	97.5	32	4	US-09-270-140A-12
14	15.6	97.5	32	4	US-09-270-140A-15
15	15.6	97.5	32	4	US-09-270-140A-19
16	15.6	97.5	32	4	US-09-270-140A-28
17	15.6	97.5	32	4	US-09-270-140A-58
18	15.6	97.5	34	4	US-09-270-140A-9
19	15.6	97.5	34	4	US-09-270-140A-53
20	15.6	97.5	35	4	US-09-270-140A-3
21	15.6	97.5	35	4	US-09-270-140A-6
22	15.6	97.5	35	4	US-09-270-140A-31
23	15.6	97.5	35	4	US-09-270-140A-39
24	15.6	97.5	38	4	US-09-270-140A-34
25	15.6	97.5	38	4	US-09-270-140A-36
26	15.6	97.5	39	4	US-09-270-140A-91
27	15.6	97.5	39	4	US-09-270-140A-94

28	15.6	97.5	47	4	US-08-849-567A-85	Sequence 85, Appl
29	15.6	97.5	48	4	US-08-849-567A-87	Sequence 87, Appl
30	15.6	97.5	49	4	US-08-849-567A-81	Sequence 81, Appl
31	15.6	97.5	50	3	US-09-253-955-8	Sequence 8, Appl
32	15.6	97.5	50	3	US-09-637-405-8	Sequence 8, Appl
33	15.6	97.5	50	3	US-09-746-985B-8	Sequence 8, Appl
34	15.6	97.5	51	4	US-08-849-567A-86	Sequence 86, Appl
35	15.6	97.5	59	3	US-09-253-955-2	Sequence 2, Appl
36	15.6	97.5	59	3	US-09-637-405-2	Sequence 2, Appl
37	15.6	97.5	60	3	US-09-746-985B-2	Sequence 2, Appl
38	15.6	97.5	60	3	US-09-253-955-10	Sequence 10, Appl
39	15.6	97.5	60	3	US-09-637-405-10	Sequence 10, Appl
40	15.6	97.5	60	4	US-09-270-140A-95	Sequence 95, Appl
41	15.6	97.5	60	4	US-09-746-985B-10	Sequence 10, Appl
42	15.6	97.5	98	3	US-09-253-955-11	Sequence 11, Appl
43	15.6	97.5	98	3	US-09-637-405-11	Sequence 11, Appl
44	15.6	97.5	98	4	US-09-270-140A-96	Sequence 96, Appl
45	15.6	97.5	98	4	US-09-746-985B-11	Sequence 11, Appl
46	13	81.2	31	1	US-08-303-270-4	Sequence 4, Appl
47	12	75.0	20	4	US-09-198-452A-4924	Sequence 4924, Ap
48	12	75.0	20	4	US-09-198-452A-6403	Sequence 6403, Ap
49	12	75.0	40	1	US-08-741-881-83	Sequence 83, Appl
50	12	75.0	40	1	US-08-739-158-83	Sequence 83, Appl
51	12	75.0	40	2	US-08-739-167-83	Sequence 83, Appl
52	12	75.0	40	3	US-08-404-796-83	Sequence 83, Appl
53	12	75.0	40	3	US-08-931-869-83	Sequence 83, Appl
54	12	75.0	40	4	US-09-350-399-83	Sequence 83, Appl
55	12	75.0	40	4	US-09-236-140A-83	Sequence 83, Appl
56	11.8	73.8	75	4	US-09-702-705-242	Sequence 242, App
57	11.8	73.8	78	4	US-09-736-457-242	Sequence 242, App
58	11.8	73.8	78	4	US-09-702-705-1277	Sequence 1277, Ap
59	11.8	73.8	24	3	US-08-940-368-14	Sequence 14, Appl
60	11.4	71.2	27	4	US-09-109-329-26	Sequence 26, Appl
61	11.4	71.2	27	4	US-08-729-601A-18	Sequence 18, Appl
62	11.4	71.2	20	1	US-08-303-270-9	Sequence 9, Appl
63	11	68.8	17	1	US-08-180-209B-15	Sequence 15, Appl
64	10.8	67.5	17	3	US-08-385-388-15	Sequence 15, Appl
65	10.8	67.5	17	3	US-08-485-388-15	Sequence 15, Appl
66	10.8	67.5	17	3	US-08-474-853-15	Sequence 15, Appl
67	10.8	67.5	17	4	US-09-166-205B-15	Sequence 15, Appl
68	10.8	67.5	17	5	PCT-US94-02629-15	Sequence 15, Appl
69	10.8	67.5	26	1	US-08-412-614-17	Sequence 17, Appl
70	10.8	67.5	26	1	US-08-412-614-18	Sequence 18, Appl
71	10.8	67.5	26	1	US-08-412-614-19	Sequence 19, Appl
72	10.8	67.5	26	1	US-08-412-614-20	Sequence 20, Appl
73	10.8	67.5	26	2	US-08-435-637A-2	Sequence 2, Appl
74	10.8	67.5	26	2	US-08-635-761-17	Sequence 17, Appl
75	10.8	67.5	26	2	US-08-635-761-18	Sequence 18, Appl
76	10.8	67.5	26	2	US-08-635-761-19	Sequence 19, Appl
77	10.8	67.5	26	2	US-08-635-761-20	Sequence 20, Appl
78	10.8	67.5	26	3	US-09-312-520-17	Sequence 17, Appl
79	10.8	67.5	26	3	US-09-312-520-18	Sequence 18, Appl
80	10.8	67.5	26	3	US-09-312-520-19	Sequence 19, Appl
81	10.8	67.5	26	3	US-09-312-520-20	Sequence 20, Appl
82	10.8	67.5	27	3	US-08-981-189B-18	Sequence 18, Appl
83	10.8	67.5	30	3	US-09-242-797-5	Sequence 5, Appl
84	10.8	67.5	30	3	US-07-977-696C-8	Sequence 8, Appl
85	10.8	67.5	32	1	US-07-977-696C-8	Sequence 8, Appl
86	10.8	67.5	32	1	US-08-129-930B-8	Sequence 8, Appl
87	10.8	67.5	32	1	US-08-976-288A-8	Sequence 8, Appl
88	10.8	67.5	35	1	US-08-551-459-8	Sequence 8, Appl
89	10.8	67.5	35	1	US-09-085-720-15	Sequence 15, Appl
90	10.8	67.5	41	3	US-08-997-918-16	Sequence 16, Appl
91	10.8	67.5	41	3	US-09-079-984A-5	Sequence 5, Appl
92	10.8	67.5	42	4	US-09-390-729-5	Sequence 5, Appl
93	10.8	67.5	44	3	US-09-254-023B-7	Sequence 7, Appl
94	10.8	67.5	44	3	US-09-350-237-25	Sequence 25, Appl
95	10.8	67.5	45	3	US-09-315-794-4	Sequence 4, Appl
96	10.8	67.5	45	3	US-09-389-341-4	Sequence 4, Appl
97	10.8	67.5	48	3	US-08-997-918-13	Sequence 4, Appl
98	10.8	67.5	50	1	US-08-519-197-5	Sequence 5, Appl
99	10.8	67.5	50	1	US-08-997-918-11	Sequence 11, Appl
100	10.8	67.5	50	3	US-08-997-918-11	Sequence 41, Appl

101	10.8	67.5	50	3	US-09-292-071-3	Sequence 3, Appl1	174	10.4	65.0	55	1	US-08-477-329-11	Sequence 11, Appl1
102	10.8	67.5	50	3	US-09-292-071-4	Sequence 4, Appl1	175	10.4	65.0	55	2	US-08-811-492-135	Sequence 125, App
103	10.8	67.5	50	3	US-09-292-069A-3	Sequence 3, Appl1	176	10.4	65.0	55	2	US-08-475-458-10	Sequence 10, Appl1
104	10.8	67.5	50	3	US-09-292-069A-4	Sequence 4, Appl1	177	10.4	65.0	55	2	US-08-475-458-11	Sequence 11, Appl1
105	10.8	67.5	50	3	US-09-418-721-3	Sequence 3, Appl1	178	10.4	65.0	55	3	US-08-980-400-10	Sequence 10, Appl1
106	10.8	67.5	50	3	US-09-418-721-4	Sequence 4, Appl1	179	10.4	65.0	55	3	US-08-980-400-11	Sequence 11, Appl1
107	10.8	67.5	50	4	US-09-767-013-3	Sequence 3, Appl1	180	10.4	65.0	55	3	US-09-583-459A-10	Sequence 10, Appl1
108	10.8	67.5	50	4	US-09-767-013-4	Sequence 4, Appl1	181	10.4	65.0	55	3	US-09-583-459A-11	Sequence 11, Appl1
109	10.8	67.5	50	4	US-09-292-072-3	Sequence 3, Appl1	182	10.4	65.0	55	3	US-09-583-210-10	Sequence 10, Appl1
110	10.8	67.5	50	4	US-09-292-072-4	Sequence 4, Appl1	183	10.4	65.0	55	3	US-09-583-210-11	Sequence 11, Appl1
111	10.8	67.5	50	4	US-09-170-496D-237	Sequence 238, App	184	10.4	65.0	55	4	US-09-583-449A-10	Sequence 10, Appl1
112	10.8	67.5	50	4	US-09-170-496D-238	Sequence 48, Appl1	185	10.4	65.0	55	4	US-09-583-449A-11	Sequence 11, Appl1
113	10.8	67.5	55	3	US-08-997-918-48	Sequence 37, Appl1	186	10.4	65.0	55	4	US-09-435-052-11	Sequence 11, Appl1
114	10.8	67.5	55	3	US-08-290-736C-37	Sequence 67, Appl1	187	10.4	65.0	55	4	US-09-435-052-12	Sequence 12, Appl1
115	10.8	67.5	71	2	US-08-465-591A-67	Sequence 254, App	188	10.4	65.0	55	4	US-08-219-012-87	Sequence 87, Appl1
116	10.8	67.5	71	2	US-08-465-591A-67	Sequence 37, Appl1	189	10.4	65.0	55	4	US-08-219-012-87	Sequence 275, App
117	10.8	67.5	71	2	US-08-973-124-252	Sequence 46, Appl1	190	10.4	65.0	55	4	US-08-973-124-252	Sequence 16, Appl1
118	10.8	67.5	71	3	US-08-290-736C-46	Sequence 46, Appl1	191	10.2	63.7	33	1	US-07-979-966A-16	Sequence 44, Appl1
119	10.8	67.5	71	3	US-08-290-736C-47	Sequence 252, App	192	10.2	63.7	37	1	US-07-979-966A-16	Sequence 56, Appl1
120	10.8	67.5	71	3	PCT-US96-08014-252	Sequence 252, App	193	10.2	63.7	37	1	US-07-979-966A-16	Sequence 62, Appl1
121	10.8	67.5	74	3	US-09-315-794-2	Sequence 2, Appl1	194	10.2	63.7	37	1	US-07-979-966A-16	Sequence 62, Appl1
122	10.8	67.5	74	3	US-09-315-794-2	Sequence 2, Appl1	195	10.2	63.7	37	1	US-07-979-966A-16	Sequence 62, Appl1
123	10.8	67.5	76	3	US-09-390-867A-6	Sequence 6, Appl1	196	10.2	63.7	37	1	US-08-149-106-44	Sequence 56, Appl1
124	10.6	66.2	76	4	US-09-548-260-6	Sequence 6, Appl1	197	10.2	63.7	37	1	US-08-149-106-44	Sequence 62, Appl1
125	10.6	66.2	87	3	US-09-390-867A-1	Sequence 1, Appl1	198	10.2	63.7	37	1	US-08-149-106-44	Sequence 44, Appl1
126	10.6	66.2	87	3	US-09-548-260-1	Sequence 1, Appl1	199	10.2	63.7	37	1	US-08-149-106-44	Sequence 56, Appl1
127	10.4	65.0	19	2	US-08-598-607-4	Sequence 68, Appl1	200	10.2	63.7	37	1	US-08-298-021-62	Sequence 62, Appl1
128	10.4	65.0	20	3	US-09-289-267-68	Sequence 88, Appl1	201	10.2	63.7	37	1	US-08-298-021-62	Sequence 11, Appl1
129	10.4	65.0	20	3	US-09-101-886B-88	Sequence 15, Appl1	202	10.2	63.7	37	1	US-09-775-850-11	Sequence 5, Appl1
130	10.4	65.0	21	3	US-08-109-037-15	Sequence 88, Appl1	203	10.2	63.7	37	1	US-08-190-199A-5	Sequence 399, App
131	10.4	65.0	21	3	US-08-109-037-18	Sequence 88, Appl1	204	10.2	63.7	37	1	US-08-687-421-399	Sequence 59, Appl1
132	10.4	65.0	21	3	US-08-109-037-89	Sequence 90, Appl1	205	10.2	63.7	37	1	US-07-964-624D-59	Sequence 59, Appl1
133	10.4	65.0	21	3	US-08-109-037-90	Sequence 90, Appl1	206	10.2	63.7	37	1	US-08-442-062-59	Sequence 59, Appl1
134	10.4	65.0	23	1	US-08-244-269-3	Sequence 3, Appl1	207	10.2	63.7	37	1	US-08-442-062-59	Sequence 59, Appl1
135	10.4	65.0	23	1	US-08-348-683-16	Sequence 16, Appl1	208	10.2	63.7	37	1	US-09-165-616-59	Sequence 59, Appl1
136	10.4	65.0	25	1	US-08-244-269-4	Sequence 4, Appl1	209	10.2	63.7	37	1	US-09-027-998A-41	Sequence 41, Appl1
137	10.4	65.0	25	1	US-08-348-683-6	Sequence 18, Appl1	210	10.2	63.7	37	1	US-09-058-489-57	Sequence 57, Appl1
138	10.4	65.0	25	1	US-08-348-683-18	Sequence 18, Appl1	211	10.2	63.7	37	1	US-09-444-053-52	Sequence 52, Appl1
139	10.4	65.0	25	1	US-08-348-683-19	Sequence 19, Appl1	212	10.2	63.7	37	1	US-09-732-199A-51	Sequence 51, Appl1
140	10.4	65.0	30	1	US-08-049-473-15	Sequence 15, Appl1	213	10.2	63.7	37	1	US-09-732-199A-51	Sequence 32, Appl1
141	10.4	65.0	30	1	US-08-049-473-16	Sequence 16, Appl1	214	10.2	63.7	37	1	US-09-027-998A-42	Sequence 42, Appl1
142	10.4	65.0	30	1	US-08-312-648-15	Sequence 15, Appl1	215	10.2	63.7	37	1	US-08-936-107A-26	Sequence 26, Appl1
143	10.4	65.0	30	1	US-08-312-648-16	Sequence 16, Appl1	216	10.2	63.7	37	1	US-08-880-829-11	Sequence 11, Appl1
144	10.4	65.0	30	3	US-09-176-862-7	Sequence 43, Appl1	217	10.2	63.7	37	1	US-08-880-829-11	Sequence 19, Appl1
145	10.4	65.0	30	3	US-09-202-316-43	Sequence 43, Appl1	218	10.2	63.7	37	1	US-08-880-829-11	Sequence 26, Appl1
146	10.4	65.0	30	5	PCT-US94-04190-15	Sequence 15, Appl1	219	10.2	63.7	37	1	US-08-880-829-11	Sequence 16, Appl1
147	10.4	65.0	33	4	US-09-813-781-22	Sequence 22, Appl1	220	10.2	63.7	37	1	US-09-732-199A-6	Sequence 6, Appl1
148	10.4	65.0	33	4	US-09-813-781-22	Sequence 13, Appl1	221	10.2	63.7	37	1	US-08-678-304-7	Sequence 7, Appl1
149	10.4	65.0	34	1	US-08-334-503-13	Sequence 13, Appl1	222	10.2	63.7	37	1	US-08-678-304-7	Sequence 8, Appl1
150	10.4	65.0	36	1	US-08-399-696-15	Sequence 15, Appl1	223	10.2	63.7	37	1	US-09-523-686-6	Sequence 6, Appl1
151	10.4	65.0	40	2	US-08-882-083-4	Sequence 4, Appl1	224	10.2	63.7	37	1	US-09-027-998A-12	Sequence 12, Appl1
152	10.4	65.0	40	2	US-08-882-083-4	Sequence 4, Appl1	225	10.2	63.7	37	1	US-09-027-998A-13	Sequence 9, Appl1
153	10.4	65.0	40	2	US-08-558-107-4	Sequence 26, Appl1	226	10.2	63.7	37	1	US-09-027-998A-9	Sequence 10, Appl1
154	10.4	65.0	45	3	US-09-363-970-26	Sequence 56, Appl1	227	10.2	63.7	37	1	US-09-027-998A-10	Sequence 15, Appl1
155	10.4	65.0	46	1	US-07-994-469A-56	Sequence 959, App	228	10.2	63.7	37	1	US-09-027-998A-15	Sequence 15, Appl1
156	10.4	65.0	47	4	US-09-422-978-959	Sequence 1217, App	229	10.2	63.7	37	1	US-09-027-998A-16	Sequence 55, Appl1
157	10.4	65.0	47	4	US-09-422-978-1217	Sequence 124, App	230	10.2	63.7	37	1	US-08-530-492-55	Sequence 55, Appl1
158	10.4	65.0	48	2	US-08-811-492-124	Sequence 3, Appl1	231	10.2	63.7	37	1	US-08-906-517-85	Sequence 18, Appl1
159	10.4	65.0	48	2	US-08-882-083-3	Sequence 3, Appl1	232	10.2	63.7	37	1	US-09-027-998A-18	Sequence 19, Appl1
160	10.4	65.0	48	2	US-08-558-107-3	Sequence 26, Appl1	233	10.2	63.7	37	1	US-09-027-998A-19	Sequence 19, Appl1
161	10.4	65.0	49	1	US-08-644-271-26	Sequence 27, Appl1	234	10.2	63.7	37	1	US-08-986-727-16	Sequence 14, Appl1
162	10.4	65.0	49	1	US-08-644-271-26	Sequence 27, Appl1	235	10.2	63.7	37	1	US-08-880-829-13	Sequence 13, Appl1
163	10.4	65.0	49	3	US-09-363-970-27	Sequence 23, Appl1	236	10.2	63.7	37	1	US-08-880-829-14	Sequence 12, Appl1
164	10.4	65.0	49	3	US-09-363-970-27	Sequence 25, Appl1	237	10.2	63.7	37	1	US-08-880-829-12	Sequence 20, Appl1
165	10.4	65.0	50	1	US-07-994-469A-25	Sequence 20, Appl1	238	10.2	63.7	37	1	US-08-782-611A-20	Sequence 10, Appl1
166	10.4	65.0	50	1	US-08-445-640-20	Sequence 20, Appl1	239	10.2	63.7	37	1	US-07-982-712-10	Sequence 61, Appl1
167	10.4	65.0	50	3	US-08-170-558-20	Sequence 20, Appl1	240	10.2	63.7	37	1	US-09-039-555B-4	Sequence 2622, App
168	10.4	65.0	50	3	US-08-447-314-20	Sequence 20, Appl1	241	10.2	63.7	37	1	US-08-311-446C-61	Sequence 2622, App
169	10.4	65.0	52	1	US-08-445-461-10	Sequence 35, Appl1	242	10.2	63.7	37	1	US-08-584-040-2622	Sequence 1146, App
170	10.4	65.0	52	1	US-07-994-469A-35	Sequence 10, Appl1	243	10.2	63.7	37	1	US-08-584-040-2622	Sequence 1147, App
171	10.4	65.0	55	1	US-08-180-195-10	Sequence 11, Appl1	244	10.2	63.7	37	1	US-09-371-772B-1147	Sequence 49, Appl1
172	10.4	65.0	55	1	US-08-180-195-11	Sequence 10, Appl1	245	10.2	63.7	37	1	US-09-371-772B-1147	Sequence 49, Appl1
173	10.4	65.0	55	1	US-08-477-329-10	Sequence 10, Appl1	246	10.2	63.7	37	1	US-09-394-455-49	Sequence 49, Appl1

C 247	9.8	61.3	20	1	US-07-977-284A-39	Sequence 39, Appl	320	9.8	61.3	51	4	US-09-393-385B-7	Sequence 7, Appl
C 248	9.8	61.3	20	2	US-08-468-551-1	Sequence 1, Appl	321	9.8	61.3	51	4	US-09-394-455-55	Sequence 55, Appl
C 249	9.8	61.3	20	2	US-08-256-426B-39	Sequence 39, Appl	C 322	9.8	61.3	54	1	US-08-353-400-11	Sequence 11, Appl
C 250	9.8	61.3	20	3	US-09-280-799-83	Sequence 83, Appl	C 323	9.8	61.3	54	1	US-08-353-400-12	Sequence 12, Appl
C 251	9.8	61.3	20	3	US-09-560-594-49	Sequence 49, Appl	C 324	9.8	61.3	54	4	US-09-479-645A-169	Sequence 169, App
C 252	9.8	61.3	20	3	US-09-657-346A-33	Sequence 33, Appl	C 325	9.8	61.3	54	4	US-09-479-645A-175	Sequence 175, App
C 253	9.8	61.3	20	4	US-09-422-978-3992	Sequence 3992, Ap	C 326	9.8	61.3	59	1	US-08-160-670A-35	Sequence 35, Appl
C 254	9.8	61.3	20	4	US-09-920-759-87	Sequence 87, Appl	C 327	9.8	61.3	71	4	US-09-301-593A-87	Sequence 87, Appl
C 255	9.8	61.3	20	4	US-09-060-299-378	Sequence 378, App	C 328	9.8	61.3	72	1	US-08-105-483-211	Sequence 211, App
C 256	9.8	61.3	20	4	US-09-402-923A-378	Sequence 378, App	C 329	9.8	61.3	72	1	US-08-105-483-212	Sequence 212, App
C 257	9.8	61.3	21	1	US-08-435-480-6	Sequence 6, Appl	C 330	9.8	61.3	72	1	US-08-303-124-10	Sequence 10, Appl
C 258	9.8	61.3	21	2	US-08-946-241B-6	Sequence 6, Appl	C 331	9.8	61.3	72	1	US-08-303-124-11	Sequence 11, Appl
C 259	9.8	61.3	21	3	US-09-309-053-6	Sequence 6, Appl	C 332	9.8	61.3	72	1	US-08-204-729-10	Sequence 10, Appl
C 260	9.8	61.3	21	3	US-08-557-614-8	Sequence 8, Appl	C 333	9.8	61.3	72	1	US-08-204-729-11	Sequence 11, Appl
C 261	9.8	61.3	21	3	US-09-394-455-41	Sequence 41, Appl	C 334	9.8	61.3	72	1	US-08-475-063-28	Sequence 28, Appl
C 262	9.8	61.3	22	3	US-09-103-875-101	Sequence 101, App	C 335	9.8	61.3	72	1	US-08-207-792-28	Sequence 28, Appl
C 263	9.8	61.3	23	2	US-08-839-306-5	Sequence 5, Appl	C 336	9.8	61.3	72	1	US-08-709-209-211	Sequence 211, App
C 264	9.8	61.3	23	3	US-08-978-454-5	Sequence 5, Appl	C 337	9.8	61.3	72	1	US-08-709-209-212	Sequence 212, App
C 265	9.8	61.3	23	3	US-09-385-288-5	Sequence 5, Appl	C 338	9.8	61.3	72	1	US-08-458-101-211	Sequence 211, App
C 266	9.8	61.3	24	4	US-09-670-075A-11	Sequence 11, Appl	C 339	9.8	61.3	72	1	US-08-458-101-212	Sequence 212, App
C 267	9.8	61.3	25	1	US-08-336-132-8	Sequence 8, Appl	C 340	9.8	61.3	72	2	US-08-480-697B-10	Sequence 10, Appl
C 268	9.8	61.3	25	3	US-09-012-097A-15	Sequence 15, Appl	C 341	9.8	61.3	72	2	US-08-480-697B-11	Sequence 11, Appl
C 269	9.8	61.3	25	4	US-08-672-213-36	Sequence 36, Appl	C 342	9.8	61.3	73	1	US-08-475-063-29	Sequence 29, Appl
C 270	9.8	61.3	25	4	US-09-538-709-301	Sequence 301, App	C 343	9.8	61.3	73	1	US-08-207-792-29	Sequence 29, Appl
C 271	9.8	61.3	25	4	US-09-481-620A-31	Sequence 31, Appl	C 344	9.8	61.3	75	1	US-08-219-012-85	Sequence 85, Appl
C 272	9.8	61.3	27	2	US-08-232-081B-32	Sequence 32, Appl	C 345	9.8	61.3	75	1	US-08-219-012-85	Sequence 85, Appl
C 273	9.8	61.3	28	1	US-08-221-078A-1	Sequence 1, Appl	C 346	9.8	61.3	75	3	US-08-687-421-273	Sequence 273, App
C 274	9.8	61.3	28	1	US-08-221-171A-1	Sequence 1, Appl	C 347	9.8	61.3	75	3	US-08-687-421-276	Sequence 276, App
C 275	9.8	61.3	29	1	US-08-217-210B-26	Sequence 26, Appl	C 348	9.8	61.3	76	1	US-08-657-012-6	Sequence 6, Appl
C 276	9.8	61.3	29	4	US-08-054-970-4	Sequence 4, Appl	C 349	9.8	61.3	76	3	US-09-013-872-6	Sequence 6, Appl
C 277	9.8	61.3	29	4	US-09-304-232-853	Sequence 853, App	C 350	9.8	61.3	76	3	US-09-184-198-6	Sequence 6, Appl
C 278	9.8	61.3	30	1	US-08-160-670A-39	Sequence 39, Appl	C 351	9.8	61.3	76	4	US-09-633-653-6	Sequence 6, Appl
C 279	9.8	61.3	30	1	US-08-384-708A-9	Sequence 9, Appl	C 352	9.8	61.3	77	1	US-08-384-708A-190	Sequence 190, App
C 280	9.8	61.3	30	1	US-08-322-677A-13	Sequence 13, Appl	C 353	9.8	61.3	77	3	US-08-687-421-282	Sequence 282, App
C 281	9.8	61.3	30	1	US-08-322-676-13	Sequence 13, Appl	C 354	9.8	61.3	78	4	US-08-653-648A-47	Sequence 47, Appl
C 282	9.8	61.3	30	2	US-08-600-999-3	Sequence 3, Appl	C 355	9.8	61.3	81	2	US-08-116-778E-26	Sequence 26, Appl
C 283	9.8	61.3	30	3	US-08-898-218-13	Sequence 13, Appl	C 356	9.8	61.3	81	2	US-08-438-562-26	Sequence 26, Appl
C 284	9.8	61.3	30	3	US-08-848-793-13	Sequence 13, Appl	C 357	9.8	61.3	81	2	US-08-438-562-26	Sequence 26, Appl
C 285	9.8	61.3	30	3	US-08-687-421-9	Sequence 9, Appl	C 358	9.8	61.3	81	2	US-08-673-799C-57	Sequence 57, Appl
C 286	9.8	61.3	30	4	US-09-937-832-2	Sequence 2, Appl	C 359	9.8	61.3	81	4	US-09-393-385B-26	Sequence 26, Appl
C 287	9.8	61.3	31	2	US-08-322-678-13	Sequence 13, Appl	C 360	9.8	61.3	82	3	US-08-393-385B-26	Sequence 26, Appl
C 288	9.8	61.3	31	2	US-08-600-999-11	Sequence 11, Appl	C 361	9.8	61.3	84	5	US-08-468-551B-67	Sequence 67, App
C 289	9.8	61.3	31	3	US-08-732-218-10	Sequence 10, Appl	C 362	9.8	61.3	86	5	PCT-US96-00952-13	Sequence 13, Appl
C 290	9.8	61.3	31	3	US-08-523-894-57	Sequence 57, Appl	C 363	9.8	61.3	86	5	PCT-US94-07779-19	Sequence 19, Appl
C 291	9.8	61.3	32	4	US-09-420-819-8	Sequence 8, Appl	C 364	9.8	61.3	87	5	PCT-US95-05600-6	Sequence 6, Appl
C 292	9.8	61.3	35	1	US-08-328-592-9	Sequence 9, Appl	C 365	9.8	61.3	87	5	PCT-US95-05600-11	Sequence 11, Appl
C 293	9.8	61.3	35	3	US-09-439-000-3	Sequence 3, Appl	C 366	9.8	61.3	93	3	US-08-943-731-16	Sequence 16, Appl
C 294	9.8	61.3	36	3	US-08-746-889-9	Sequence 9, Appl	C 367	9.8	61.3	93	3	US-08-943-731-16	Sequence 16, Appl
C 295	9.8	61.3	37	4	US-09-366-009-18	Sequence 18, Appl	C 368	9.8	61.3	94	2	US-08-483-528B-57	Sequence 57, Appl
C 296	9.8	61.3	37	4	US-08-809-156B-18	Sequence 18, Appl	C 369	9.8	61.3	94	3	US-08-673-799C-57	Sequence 57, Appl
C 297	9.8	61.3	39	1	US-08-253-155A-83	Sequence 83, Appl	C 370	9.8	61.3	94	4	US-09-353-385B-57	Sequence 57, Appl
C 298	9.8	61.3	39	1	US-08-625-209A-12	Sequence 12, Appl	C 371	9.8	61.3	99	1	US-08-162-961B-6	Sequence 6, Appl
C 299	9.8	61.3	39	3	US-08-853-733B-12	Sequence 12, Appl	C 372	9.8	61.3	99	4	US-09-007-678B-6	Sequence 6, Appl
C 300	9.8	61.3	39	3	US-07-987-264-37	Sequence 37, Appl	C 373	9.8	61.3	100	4	US-08-706-945D-91	Sequence 91, Appl
C 301	9.8	61.3	39	3	US-07-987-264-37	Sequence 37, Appl	C 374	9.6	60.0	10	3	US-09-581-326-13	Sequence 13, Appl
C 302	9.8	61.3	40	4	US-09-538-709-1193	Sequence 1193, Ap	C 375	9.6	60.0	10	3	US-09-581-326-18	Sequence 18, Appl
C 303	9.8	61.3	41	4	US-08-813-507-115	Sequence 115, App	C 376	9.6	60.0	10	4	US-09-907-074A-13	Sequence 13, Appl
C 304	9.8	61.3	41	4	US-09-464-453-135	Sequence 135, App	C 377	9.6	60.0	10	4	US-09-907-074A-13	Sequence 13, Appl
C 305	9.8	61.3	42	1	US-08-271-880A-52	Sequence 52, Appl	C 378	9.6	60.0	29	4	US-09-304-232A-04	Sequence 204, App
C 306	9.8	61.3	42	2	US-08-910-408-52	Sequence 52, Appl	C 379	9.6	60.0	30	3	US-09-136-605-15	Sequence 15, Appl
C 307	9.8	61.3	42	2	US-09-249-215-52	Sequence 52, Appl	C 380	9.6	60.0	35	3	US-09-026-958-11	Sequence 11, Appl
C 308	9.8	61.3	44	6	5252466-21	Patent No. 5252466	C 381	9.6	60.0	36	4	US-09-390-207-19	Sequence 19, Appl
C 309	9.8	61.3	47	4	US-09-422-978-2991	Sequence 2991, Ap	C 382	9.6	60.0	46	3	US-08-997-918-17	Sequence 17, Appl
C 310	9.8	61.3	47	4	US-09-422-978-3652	Sequence 3652, Ap	C 383	9.6	60.0	47	4	US-09-422-978-3651	Sequence 2615, App
C 311	9.8	61.3	48	4	US-09-063-893A-18	Sequence 18, Appl	C 384	9.6	60.0	50	1	US-08-753-054-6	Sequence 6, Appl
C 312	9.8	61.3	49	4	US-09-061-154-8	Sequence 8, Appl	C 385	9.6	60.0	53	1	US-07-778-233B-68	Sequence 68, Appl
C 313	9.8	61.3	49	4	US-09-538-709-957	Sequence 957, App	C 386	9.6	60.0	53	1	US-07-963-321-68	Sequence 68, Appl
C 314	9.8	61.3	50	2	US-08-832-468-6	Sequence 6, Appl	C 387	9.6	60.0	53	1	US-08-290-641-68	Sequence 68, Appl
C 315	9.8	61.3	51	2	US-08-116-778E-42	Sequence 42, Appl	C 388	9.6	60.0	53	1	US-08-548-540-68	Sequence 68, Appl
C 316	9.8	61.3	51	2	US-08-438-562-42	Sequence 42, Appl	C 389	9.6	60.0	53	5	PCT-US96-09809-68	Sequence 68, Appl
C 317	9.8	61.3	51	2	US-08-483-528B-7	Sequence 7, Appl	C 390	9.6	60.0	80	1	US-08-468-275-1	Sequence 1, Appl
C 318	9.8	61.3	51	3	US-08-673-799C-7	Sequence 7, Appl	C 391	9.6	60.0	80	4	US-09-007-466-1	Sequence 1, Appl
C 319	9.8	61.3	51	3	US-07-987-264-8	Sequence 8, Appl	C 392	9.6	60.0	80	4	US-08-952-980B-1	Sequence 1, Appl

393	9.6	60.0	91	1	US-08-142-551B-129	Sequence 129, App	466	9.4	58.8	27	4	US-09-538-709-179	Sequence 179, App
394	9.6	60.0	91	1	US-08-142-551B-130	Sequence 130, App	467	9.4	58.8	27	5	PCT-US93-08435-38	Sequence 38, App
395	9.6	60.0	96	3	US-08-484-322-35	Sequence 35, App	468	9.4	58.8	28	1	US-07-959-369-18	Sequence 18, App
396	9.4	58.8	17	1	US-08-372-124A-4441	Sequence 1441, App	469	9.4	58.8	29	1	US-07-805-567-24	Sequence 24, App
397	9.4	58.8	17	1	US-08-435-628-1441	Sequence 1441, App	470	9.4	58.8	29	1	US-08-105-483-106	Sequence 106, App
398	9.4	58.8	17	4	US-08-584-040-2621	Sequence 2621, App	471	9.4	58.8	29	1	US-08-220-151-63	Sequence 63, App
399	9.4	58.8	17	4	US-09-371-772B-1145	Sequence 1145, App	472	9.4	58.8	29	1	US-08-413-118-63	Sequence 63, App
400	9.4	58.8	17	4	US-09-371-772B-5482	Sequence 5482, App	473	9.4	58.8	29	1	US-08-224-657-40	Sequence 40, App
401	9.4	58.8	17	6	US-09-371-772B-5482	Sequence 5482, App	474	9.4	58.8	29	1	US-08-709-209-106	Sequence 106, App
402	9.4	58.8	18	1	US-08-468-580-28	Sequence 28, App	475	9.4	58.8	29	1	US-08-458-101-106	Sequence 106, App
403	9.4	58.8	18	3	US-08-643-212-50	Sequence 50, App	476	9.4	58.8	29	2	US-08-184-009-39	Sequence 39, App
404	9.4	58.8	18	4	US-09-242-937-3	Sequence 3, App	477	9.4	58.8	29	2	US-08-486-969-28	Sequence 28, App
405	9.4	58.8	18	4	US-09-422-978-10236	Sequence 10236, A	478	9.4	58.8	29	2	US-08-417-210A-39	Sequence 39, App
406	9.4	58.8	18	5	PCT-US95-03731-28	Sequence 28, App	479	9.4	58.8	29	2	US-08-458-356-33	Sequence 33, App
407	9.4	58.8	19	1	US-08-379-081B-141	Sequence 141, App	480	9.4	58.8	29	2	US-08-471-025-28	Sequence 28, App
408	9.4	58.8	19	1	US-08-379-081B-142	Sequence 142, App	481	9.4	58.8	29	2	US-08-658-665-28	Sequence 28, App
409	9.4	58.8	19	1	US-08-379-081B-143	Sequence 143, App	482	9.4	58.8	29	3	US-08-473-446-63	Sequence 63, App
410	9.4	58.8	19	1	US-08-379-078-141	Sequence 141, App	483	9.4	58.8	29	3	US-08-460-736-39	Sequence 39, App
411	9.4	58.8	19	1	US-08-379-078-142	Sequence 142, App	484	9.4	58.8	29	3	US-09-085-273-28	Sequence 28, App
412	9.4	58.8	19	1	US-08-379-078-143	Sequence 143, App	485	9.4	58.8	29	4	US-09-354-138-40	Sequence 40, App
413	9.4	58.8	19	3	US-08-749-157-8	Sequence 8, App	486	9.4	58.8	29	4	US-09-535-370-39	Sequence 39, App
414	9.4	58.8	19	4	US-09-302-681-79	Sequence 79, App	487	9.4	58.8	29	5	PCT-US96-00547-28	Sequence 28, App
415	9.4	58.8	20	2	US-08-484-985-43	Sequence 43, App	488	9.4	58.8	30	1	US-08-182-530-4	Sequence 4, App
416	9.4	58.8	20	2	US-08-757-653-43	Sequence 43, App	489	9.4	58.8	30	1	US-08-050-058B-4	Sequence 4, App
417	9.4	58.8	20	3	US-09-428-696-52	Sequence 52, App	490	9.4	58.8	30	1	US-08-737-577-5	Sequence 5, App
418	9.4	58.8	20	3	US-09-311-260-183	Sequence 183, App	491	9.4	58.8	30	1	US-08-463-587A-4	Sequence 4, App
419	9.4	58.8	20	3	US-09-171-945-120	Sequence 120, App	492	9.4	58.8	30	2	US-08-463-667-7	Sequence 7, App
420	9.4	58.8	20	4	US-08-520-946-43	Sequence 43, App	493	9.4	58.8	30	2	US-08-663-743-14	Sequence 14, App
421	9.4	58.8	20	4	US-09-332-199A-23	Sequence 23, App	494	9.4	58.8	30	2	US-08-441-871-8	Sequence 8, App
422	9.4	58.8	20	4	US-09-011-768A-76	Sequence 76, App	495	9.4	58.8	30	3	US-08-923-854-4	Sequence 4, App
423	9.4	58.8	20	4	US-09-198-452A-2909	Sequence 2909, App	496	9.4	58.8	30	3	US-09-171-945-121	Sequence 121, App
424	9.4	58.8	20	4	US-09-198-452A-3607	Sequence 3607, App	497	9.4	58.8	30	4	US-09-011-769A-78	Sequence 78, App
425	9.4	58.8	20	4	US-09-198-452A-5879	Sequence 5879, App	498	9.4	58.8	30	5	PCT-US91-09133-4	Sequence 4, App
426	9.4	58.8	20	4	US-09-198-452A-6215	Sequence 6215, App	499	9.4	58.8	31	3	US-08-281-313-3	Sequence 3, App
427	9.4	58.8	20	4	US-09-198-452A-6756	Sequence 6756, App	500	9.4	58.8	31	3	US-09-007-288E-106	Sequence 106, App
428	9.4	58.8	20	4	US-09-460-555-6	Sequence 555, App	501	9.4	58.8	32	4	US-09-443-800-4	Sequence 4, App
429	9.4	58.8	21	1	US-08-598-591-46	Sequence 46, App	502	9.4	58.8	33	4	US-09-587-835B-4	Sequence 4, App
430	9.4	58.8	21	1	US-08-798-691-50	Sequence 50, App	503	9.4	58.8	34	4	US-08-110-161A-14	Sequence 14, App
431	9.4	58.8	21	1	US-08-782-047-12	Sequence 12, App	504	9.4	58.8	34	5	PCT-US94-09350-14	Sequence 14, App
432	9.4	58.8	21	1	US-08-749-431A-12	Sequence 12, App	505	9.4	58.8	35	1	US-08-147-000B-14	Sequence 14, App
433	9.4	58.8	21	2	US-08-600-999-7	Sequence 9, App	506	9.4	58.8	36	2	US-08-792-055-4	Sequence 5, App
434	9.4	58.8	21	2	US-08-825-487A-50	Sequence 50, App	507	9.4	58.8	36	2	US-08-330-888A-3	Sequence 3, App
435	9.4	58.8	21	3	US-08-825-487A-86	Sequence 86, App	508	9.4	58.8	36	2	US-08-657-641-8	Sequence 8, App
436	9.4	58.8	21	3	US-09-074-476-50	Sequence 50, App	509	9.4	58.8	36	2	US-09-892-074-10	Sequence 10, App
437	9.4	58.8	21	3	US-08-924-870A-12	Sequence 12, App	510	9.4	58.8	36	5	PCT-US94-07233-8	Sequence 8, App
438	9.4	58.8	22	1	US-08-111-077-62	Sequence 11, App	511	9.4	58.8	38	3	US-08-930-589A-16	Sequence 16, App
439	9.4	58.8	22	2	US-08-951-718-15	Sequence 15, App	512	9.4	58.8	39	1	US-08-539-781-16	Sequence 16, App
440	9.4	58.8	22	2	US-08-969-813-5	Sequence 5, App	513	9.4	58.8	39	1	US-08-231-342-18	Sequence 18, App
441	9.4	58.8	22	6	5219727-31	Patent No. 5219727	514	9.4	58.8	40	1	US-08-458-067-17	Sequence 17, App
442	9.4	58.8	22	6	US-09-011-600-2	Sequence 2, App	515	9.4	58.8	40	5	PCT-US96-07795-17	Sequence 17, App
443	9.4	58.8	24	3	US-09-722-348-2	Sequence 2, App	516	9.4	58.8	40	5	US-08-980-241-3	Sequence 3, App
444	9.4	58.8	24	4	US-09-600-031-9	Sequence 9, App	517	9.4	58.8	41	4	US-09-713-678-38	Sequence 38, App
445	9.4	58.8	24	4	US-09-538-709-229	Sequence 229, App	518	9.4	58.8	41	4	US-09-132-316-4	Sequence 4, App
446	9.4	58.8	24	4	US-09-216-393B-355	Sequence 359, App	519	9.4	58.8	44	4	US-07-854-603-37	Sequence 37, App
447	9.4	58.8	25	1	US-08-382-933-3	Sequence 3, App	520	9.4	58.8	44	4	US-08-486-137-3	Sequence 3, App
448	9.4	58.8	25	1	US-08-147-000B-7	Sequence 7, App	521	9.4	58.8	45	1	US-08-485-180-3	Sequence 3, App
449	9.4	58.8	25	2	US-08-779-596A-13	Sequence 13, App	522	9.4	58.8	45	1	US-08-419-765-3	Sequence 3, App
450	9.4	58.8	25	2	US-08-726-090-7	Sequence 7, App	523	9.4	58.8	45	1	US-08-753-054-9	Sequence 9, App
451	9.4	58.8	26	1	US-08-094-128A-28	Sequence 28, App	524	9.4	58.8	45	1	US-08-741-881-108	Sequence 108, App
452	9.4	58.8	26	1	US-08-455-674-28	Sequence 34, App	525	9.4	58.8	45	1	US-08-739-158-108	Sequence 108, App
453	9.4	58.8	26	1	US-08-450-257-34	Sequence 34, App	526	9.4	58.8	45	2	US-08-739-167-108	Sequence 108, App
454	9.4	58.8	26	1	US-08-455-992-28	Sequence 28, App	527	9.4	58.8	45	2	US-08-404-796-108	Sequence 108, App
455	9.4	58.8	26	1	US-08-455-992-28	Sequence 28, App	528	9.4	58.8	45	3	US-08-921-869-108	Sequence 108, App
456	9.4	58.8	26	1	US-08-450-246-34	Sequence 34, App	529	9.4	58.8	45	3	US-09-350-359-108	Sequence 108, App
457	9.4	58.8	26	1	US-08-450-098-34	Sequence 34, App	530	9.4	58.8	45	4	US-09-236-140A-108	Sequence 108, App
458	9.4	58.8	26	1	US-08-451-233-34	Sequence 34, App	531	9.4	58.8	46	1	US-07-805-567-22	Sequence 22, App
459	9.4	58.8	26	1	US-08-450-236-34	Sequence 34, App	532	9.4	58.8	46	1	US-08-103-483-107	Sequence 107, App
460	9.4	58.8	26	2	US-08-690-734A-21	Sequence 21, App	533	9.4	58.8	46	1	US-08-073-962-15	Sequence 15, App
461	9.4	58.8	26	3	US-08-742-185-21	Sequence 21, App	534	9.4	58.8	46	1	US-08-220-151-64	Sequence 64, App
462	9.4	58.8	26	3	US-08-742-185-21	Sequence 21, App	535	9.4	58.8	46	1	US-08-413-118-60	Sequence 60, App
463	9.4	58.8	26	5	PCT-US92-00652-28	Sequence 28, App	536	9.4	58.8	46	1	US-08-224-391-60	Sequence 60, App
464	9.4	58.8	27	2	US-08-545-562A-62	Sequence 62, App	537	9.4	58.8	46	1		
465	9.4	58.8	27	2			538	9.4	58.8	46	1		

C 539	9.4	58.8	46 1	US-08-484-304-60	Sequence 60, Appl	C 612	9.4	58.8	70 1	US-08-105-483-457	Sequence 457, App
C 540	9.4	58.8	46 1	US-08-224-657-41	Sequence 41, Appl	C 613	9.4	58.8	70 1	US-08-303-124-13	Sequence 13, Appl
C 541	9.4	58.8	46 1	US-08-487-412-15	Sequence 15, Appl	C 614	9.4	58.8	70 1	US-08-475-063-42	Sequence 42, Appl
C 542	9.4	58.8	46 1	US-08-709-209-107	Sequence 107, App	C 615	9.4	58.8	70 1	US-08-207-792-42	Sequence 42, Appl
C 543	9.4	58.8	46 1	US-08-458-101-107	Sequence 101, App	C 616	9.4	58.8	70 1	US-08-709-209-457	Sequence 457, App
C 544	9.4	58.8	46 2	US-08-184-009-40	Sequence 40, Appl	C 617	9.4	58.8	70 1	US-08-303-275-169	Sequence 169, App
C 545	9.4	58.8	46 2	US-08-486-969-29	Sequence 29, Appl	C 618	9.4	58.8	70 2	US-08-458-101-457	Sequence 457, App
C 546	9.4	58.8	46 2	US-08-417-210A-20	Sequence 40, Appl	C 619	9.4	58.8	70 2	US-08-480-697B-13	Sequence 13, Appl
C 547	9.4	58.8	46 2	US-08-458-356-40	Sequence 40, Appl	C 620	9.4	58.8	71 1	US-08-081-539-43	Sequence 43, Appl
C 548	9.4	58.8	46 2	US-08-471-025-29	Sequence 29, Appl	C 621	9.4	58.8	71 1	US-08-466-647-21	Sequence 41, Appl
C 549	9.4	58.8	46 2	US-08-658-665-29	Sequence 29, Appl	C 622	9.4	58.8	72 1	US-08-105-483-211	Sequence 211, App
C 550	9.4	58.8	46 3	US-08-473-446-64	Sequence 64, Appl	C 623	9.4	58.8	72 1	US-08-105-483-212	Sequence 212, App
C 551	9.4	58.8	46 3	US-08-460-736-40	Sequence 40, Appl	C 624	9.4	58.8	72 1	US-08-303-124-10	Sequence 10, Appl
C 552	9.4	58.8	46 3	US-09-085-273-29	Sequence 29, Appl	C 625	9.4	58.8	72 1	US-08-303-124-11	Sequence 11, Appl
C 553	9.4	58.8	46 4	US-09-354-138-41	Sequence 41, Appl	C 626	9.4	58.8	72 1	US-08-204-729-10	Sequence 10, Appl
C 554	9.4	58.8	46 4	US-09-535-370-40	Sequence 40, Appl	C 627	9.4	58.8	72 1	US-08-204-729-11	Sequence 11, Appl
C 555	9.4	58.8	46 5	PCT-US96-00547-29	Sequence 29, Appl	C 628	9.4	58.8	72 1	US-08-475-063-38	Sequence 28, Appl
C 556	9.4	58.8	47 4	US-09-422-978-1577	Sequence 1577, Ap	C 629	9.4	58.8	72 1	US-08-207-792-28	Sequence 28, Appl
C 557	9.4	58.8	47 4	US-09-422-978-1753	Sequence 1753, Ap	C 630	9.4	58.8	72 1	US-08-709-209-211	Sequence 211, App
C 558	9.4	58.8	47 4	US-09-422-978-1834	Sequence 1834, Ap	C 631	9.4	58.8	72 1	US-08-709-209-212	Sequence 212, App
C 559	9.4	58.8	47 4	US-09-422-978-2810	Sequence 2810, Ap	C 632	9.4	58.8	72 1	US-08-458-101-211	Sequence 211, App
C 560	9.4	58.8	48 1	US-07-842-089B-6	Sequence 6, Appli	C 633	9.4	58.8	72 1	US-08-458-101-212	Sequence 212, App
C 561	9.4	58.8	48 1	US-08-264-485-6	Sequence 6, Appli	C 634	9.4	58.8	72 2	US-08-480-697B-10	Sequence 10, Appl
C 562	9.4	58.8	48 2	US-08-458-067-16	Sequence 16, Appl	C 635	9.4	58.8	72 2	US-08-480-697B-11	Sequence 11, Appl
C 563	9.4	58.8	48 2	US-08-629-039-9	Sequence 9, Appli	C 636	9.4	58.8	72 3	US-09-367-953B-8	Sequence 8, Appli
C 564	9.4	58.8	48 2	US-08-629-039-10	Sequence 10, Appl	C 637	9.4	58.8	73 1	US-08-475-063-39	Sequence 29, Appl
C 565	9.4	58.8	48 5	PCT-US96-07795-16	Sequence 16, Appl	C 638	9.4	58.8	73 1	US-08-207-792-29	Sequence 29, Appl
C 566	9.4	58.8	48 5	PCT-US96-07796-16	Sequence 16, Appl	C 639	9.4	58.8	75 1	US-07-973-333-18	Sequence 18, Appl
C 567	9.4	58.8	50 1	US-07-805-567-23	Sequence 23, Appl	C 640	9.4	58.8	75 1	US-08-081-539-42	Sequence 42, Appl
C 568	9.4	58.8	50 1	US-08-105-483-108	Sequence 108, App	C 641	9.4	58.8	75 1	US-08-466-647-42	Sequence 42, Appl
C 569	9.4	58.8	50 1	US-08-073-962-16	Sequence 16, Appl	C 642	9.4	58.8	75 1	US-08-219-012-18	Sequence 18, Appl
C 570	9.4	58.8	50 1	US-08-220-151-65	Sequence 65, Appl	C 643	9.4	58.8	75 3	US-08-687-421-206	Sequence 206, App
C 571	9.4	58.8	50 1	US-08-413-118-65	Sequence 65, Appl	C 644	9.4	58.8	75 3	US-09-476-239-14	Sequence 14, Appl
C 572	9.4	58.8	50 1	US-08-224-331-61	Sequence 61, Appl	C 645	9.4	58.8	76 1	US-08-430-709-3	Sequence 3, Appli
C 573	9.4	58.8	50 1	US-08-484-304-61	Sequence 61, Appl	C 646	9.4	58.8	76 1	US-08-430-709-4	Sequence 4, Appli
C 574	9.4	58.8	50 1	US-08-224-657-42	Sequence 42, Appl	C 647	9.4	58.8	76 2	US-08-918-304A-3	Sequence 3, Appli
C 575	9.4	58.8	50 1	US-08-487-412-16	Sequence 16, Appl	C 648	9.4	58.8	76 3	US-09-407-234-3	Sequence 3, Appli
C 576	9.4	58.8	50 1	US-08-709-209-108	Sequence 108, App	C 649	9.4	58.8	78 1	US-08-430-709-15	Sequence 15, Appl
C 577	9.4	58.8	50 1	US-08-458-101-108	Sequence 108, App	C 650	9.4	58.8	78 2	US-08-918-304A-15	Sequence 15, Appl
C 578	9.4	58.8	50 2	US-08-184-009-41	Sequence 41, Appl	C 651	9.4	58.8	78 3	US-09-407-234-15	Sequence 15, Appl
C 579	9.4	58.8	50 2	US-08-486-969-30	Sequence 30, Appl	C 652	9.4	58.8	78 4	US-08-653-648A-48	Sequence 48, Appl
C 580	9.4	58.8	50 2	US-08-417-210A-41	Sequence 41, Appl	C 653	9.4	58.8	79 1	US-08-384-708A-210	Sequence 210, App
C 581	9.4	58.8	50 2	US-08-458-356-41	Sequence 41, Appl	C 654	9.4	58.8	79 2	US-08-470-399-8	Sequence 8, Appli
C 582	9.4	58.8	50 2	US-08-471-025-30	Sequence 30, Appl	C 655	9.4	58.8	79 3	US-08-687-421-102	Sequence 302, App
C 583	9.4	58.8	50 2	US-08-658-665-30	Sequence 30, Appl	C 656	9.4	58.8	79 5	PCT-US96-09452-8	Sequence 8, Appli
C 584	9.4	58.8	50 3	US-08-473-446-65	Sequence 65, Appl	C 657	9.4	58.8	80 1	US-08-472-255A-149	Sequence 149, App
C 585	9.4	58.8	50 3	US-09-012-0397A-18	Sequence 18, Appl	C 658	9.4	58.8	80 1	US-08-479-724A-149	Sequence 149, App
C 586	9.4	58.8	50 3	US-08-460-776-41	Sequence 41, Appl	C 659	9.4	58.8	80 3	US-08-472-256B-149	Sequence 149, App
C 587	9.4	58.8	50 3	US-09-085-273-10	Sequence 30, Appl	C 660	9.4	58.8	80 3	US-08-952-793-149	Sequence 149, App
C 588	9.4	58.8	50 3	US-09-390-867A-40	Sequence 40, Appl	C 661	9.4	58.8	80 4	US-09-849-928-149	Sequence 149, App
C 589	9.4	58.8	50 4	US-09-354-138-42	Sequence 42, Appl	C 662	9.4	58.8	80 5	PCT-US96-09455A-149	Sequence 149, App
C 590	9.4	58.8	50 4	US-09-548-260-40	Sequence 40, Appl	C 663	9.4	58.8	81 1	US-08-472-255A-151	Sequence 151, App
C 591	9.4	58.8	50 4	US-09-535-370-41	Sequence 41, Appl	C 664	9.4	58.8	81 1	US-08-479-724A-151	Sequence 151, App
C 592	9.4	58.8	50 5	PCT-US96-00547-30	Sequence 30, Appl	C 665	9.4	58.8	81 3	US-08-472-256B-151	Sequence 151, App
C 593	9.4	58.8	51 3	US-09-367-953B-3	Sequence 3, Appli	C 666	9.4	58.8	81 3	US-08-952-793-151	Sequence 151, App
C 594	9.4	58.8	53 4	US-09-132-316-6	Sequence 6, Appli	C 667	9.4	58.8	81 4	US-09-849-928-151	Sequence 151, App
C 595	9.4	58.8	54 4	US-08-679-645-640	Sequence 640, App	C 668	9.4	58.8	81 5	PCT-US96-09455A-151	Sequence 151, App
C 596	9.4	58.8	57 1	US-07-916-034-18	Sequence 18, Appl	C 669	9.4	58.8	87 1	US-07-842-089B-26	Sequence 26, Appl
C 597	9.4	58.8	60 3	US-08-814-052-35	Sequence 35, Appl	C 670	9.4	58.8	87 1	US-08-264-485-16	Sequence 16, Appl
C 598	9.4	58.8	60 3	US-08-812-829-27	Sequence 27, Appl	C 671	9.4	58.8	89 3	US-09-367-953B-5	Sequence 5, Appli
C 599	9.4	58.8	61 3	US-08-986-727-18	Sequence 18, Appl	C 672	9.4	58.8	91 1	US-07-842-089B-25	Sequence 25, Appl
C 600	9.4	58.8	61 4	US-09-619-213B-83	Sequence 83, Appl	C 673	9.4	58.8	91 1	US-08-264-485-25	Sequence 25, Appl
C 601	9.4	58.8	63 2	US-08-472-171-6	Sequence 6, Appli	C 674	9.4	58.8	94 4	US-09-537-030G-258	Sequence 258, App
C 602	9.4	58.8	63 2	US-08-894-526-6	Sequence 6, Appli	C 675	9.4	57.5	15 1	US-08-182-868A-386	Sequence 386, App
C 603	9.4	58.8	63 2	US-09-013-047-6	Sequence 6, Appli	C 676	9.2	57.5	15 1	US-08-311-886C-580	Sequence 580, App
C 604	9.4	58.8	63 3	US-09-374-597-6	Sequence 6, Appli	C 677	9.2	57.5	15 2	US-08-774-306A-386	Sequence 386, App
C 605	9.4	58.8	68 2	US-08-459-135A-3	Sequence 3, Appli	C 678	9.2	57.5	15 4	US-09-064-156A-386	Sequence 386, App
C 606	9.4	58.8	68 3	US-08-495-559-3	Sequence 3, Appli	C 679	9.2	57.5	18 4	US-09-496-694B-102	Sequence 102, App
C 607	9.4	58.8	68 3	US-09-367-953B-10	Sequence 10, Appli	C 680	9.2	57.5	19 1	US-08-460-853-11	Sequence 11, Appl
C 608	9.4	58.8	69 2	US-08-472-171-13	Sequence 13, Appl	C 681	9.2	57.5	19 2	US-08-639-501-106	Sequence 106, App
C 609	9.4	58.8	69 2	US-08-894-526-13	Sequence 13, Appl	C 682	9.2	57.5	19 3	US-09-044-946-106	Sequence 106, App
C 610	9.4	58.8	69 2	US-09-013-047-13	Sequence 13, Appl	C 683	9.2	57.5	19 3	US-09-044-908-106	Sequence 106, App
C 611	9.4	58.8	69 3	US-09-374-597-13	Sequence 13, Appl	C 684	9.2	57.5	19 4	US-09-358-036-11	Sequence 11, Appl

C 685	9.2	57.5	19	4	US-09-298-745-23	Sequence 23, Appl	C 758	9.2	57.5	26	4	US-09-538-709-34	Sequence 34, Appl
C 686	9.2	57.5	19	4	US-09-097-239-11	Sequence 11, Appl	C 759	9.2	57.5	26	4	US-09-225-201B-1007	Sequence 1007, Ap
C 687	9.2	57.5	19	4	US-09-474-178-29	Sequence 29, Appl	C 760	9.2	57.5	27	1	US-07-566-278-3	Sequence 3, Appl
C 688	9.2	57.5	20	1	US-08-063-632-1	Sequence 1, Appl	C 761	9.2	57.5	27	1	US-08-590-804-8	Sequence 8, Appl
C 689	9.2	57.5	20	1	US-08-471-724-14	Sequence 14, Appl	C 762	9.2	57.5	27	3	US-09-042-353-3	Sequence 3, Appl
C 690	9.2	57.5	20	2	US-08-471-969-14	Sequence 14, Appl	C 763	9.2	57.5	27	4	US-08-758-117A-271	Sequence 271, Ap
C 691	9.2	57.5	20	2	US-08-384-137-14	Sequence 14, Appl	C 764	9.2	57.5	27	4	US-09-020-846-17	Sequence 17, Appl
C 692	9.2	57.5	20	2	US-08-975-211-14	Sequence 14, Appl	C 765	9.2	57.5	28	2	US-08-519-283A-3	Sequence 3, Appl
C 693	9.2	57.5	20	2	US-08-470-006A-14	Sequence 14, Appl	C 766	9.2	57.5	28	2	US-08-788-711-3	Sequence 842, Ap
C 694	9.2	57.5	20	3	US-08-691-563C-14	Sequence 11, Appl	C 767	9.2	57.5	28	2	US-08-859-998-842	Sequence 131, Ap
C 695	9.2	57.5	20	3	US-08-914-961-11	Sequence 226, App	C 768	9.2	57.5	28	4	US-08-544-381B-131	Sequence 842, App
C 696	9.2	57.5	20	3	US-09-009-913-226	Sequence 14, Appl	C 769	9.2	57.5	28	4	US-09-225-928-842	Sequence 842, App
C 697	9.2	57.5	20	3	US-09-200-990-14	Sequence 14, Appl	C 770	9.2	57.5	28	4	US-09-225-201B-842	Sequence 37, Appl
C 698	9.2	57.5	20	3	US-09-282-736-14	Sequence 1, Appl	C 771	9.2	57.5	29	2	US-08-537-402-3	Sequence 3, Appl
C 699	9.2	57.5	20	4	US-09-384-749-1	Sequence 2, Appl	C 772	9.2	57.5	29	2	US-08-716-317-25	Sequence 25, Appl
C 700	9.2	57.5	20	4	US-09-555-778-2	Sequence 14, Appl	C 773	9.2	57.5	29	2	US-08-232-016-13	Sequence 13, Appl
C 701	9.2	57.5	20	4	US-09-133-411-14	Sequence 14, Appl	C 774	9.2	57.5	30	1	US-08-479-487-24	Sequence 24, Appl
C 702	9.2	57.5	20	4	US-09-167-109-50	Sequence 90, Appl	C 775	9.2	57.5	30	1	US-08-647-584-100	Sequence 100, App
C 703	9.2	57.5	20	4	US-09-657-452A-90	Sequence 90, Appl	C 776	9.2	57.5	30	2	US-08-544-332-76	Sequence 76, Appl
C 704	9.2	57.5	20	4	US-09-088-274-21	Sequence 21, Appl	C 777	9.2	57.5	30	3	US-08-852-629-3	Sequence 3, Appl
C 705	9.2	57.5	20	4	US-09-422-978-5781	Sequence 5781, Ap	C 778	9.2	57.5	30	3	US-08-321-831-9	Sequence 9, Appl
C 706	9.2	57.5	20	4	US-09-180-570A-17	Sequence 17, Appl	C 779	9.2	57.5	30	3	US-09-321-831-11	Sequence 11, Appl
C 707	9.2	57.5	20	4	US-09-198-452A-2494	Sequence 3222, Ap	C 780	9.2	57.5	30	3	US-09-374-038-9	Sequence 9, Appl
C 708	9.2	57.5	20	4	US-09-198-452A-3222	Sequence 3712, Ap	C 781	9.2	57.5	30	4	US-09-370-861A-72	Sequence 72, Appl
C 709	9.2	57.5	20	4	US-09-198-452A-3712	Sequence 5936, Ap	C 782	9.2	57.5	30	4	US-09-529-279-23	Sequence 23, Appl
C 710	9.2	57.5	20	4	US-09-198-452A-5936	Sequence 2, Appl	C 783	9.2	57.5	30	4	US-09-538-709-20	Sequence 20, Appl
C 711	9.2	57.5	20	4	US-09-649-728-2	Sequence 14, Appl	C 784	9.2	57.5	30	4	US-08-948-113D-8	Sequence 8, Appl
C 712	9.2	57.5	20	4	US-09-374-766-14	Sequence 14, Appl	C 785	9.2	57.5	30	4	US-10-158-895-23	Sequence 23, Appl
C 713	9.2	57.5	20	4	US-08-979-847B-14	Sequence 11, Appl	C 786	9.2	57.5	30	4	US-08-948-113D-8	Sequence 8, Appl
C 714	9.2	57.5	21	2	US-08-669-284B-11	Sequence 70, Appl	C 787	9.2	57.5	30	4	US-10-158-895-23	Sequence 23, Appl
C 715	9.2	57.5	21	3	US-08-258-287B-70	Sequence 68, Appl	C 788	9.2	57.5	30	5	PCT-US95-01944-5	Sequence 5, Appl
C 716	9.2	57.5	22	1	US-08-368-704C-68	Sequence 15, Appl	C 789	9.2	57.5	31	4	PCT-US95-01944-5	Sequence 16, Appl
C 717	9.2	57.5	22	1	US-08-357-565-15	Sequence 695, App	C 790	9.2	57.5	31	4	US-09-916-510A-16	Sequence 4, Appl
C 718	9.2	57.5	22	1	US-08-379-078-695	Sequence 697, App	C 791	9.2	57.5	32	1	PCT-US93-04301-1	Sequence 25, Appl
C 719	9.2	57.5	22	1	US-08-379-078-697	Sequence 25, Appl	C 792	9.2	57.5	32	1	US-07-977-666C-25	Sequence 25, Appl
C 720	9.2	57.5	22	1	US-08-332-420-25	Sequence 15, Appl	C 793	9.2	57.5	32	2	US-08-129-920B-25	Sequence 107, App
C 721	9.2	57.5	22	3	US-08-434-720A-15	Sequence 43, Appl	C 794	9.2	57.5	32	2	US-07-673-661B-14	Sequence 107, App
C 722	9.2	57.5	22	3	US-08-867-381A-45	Sequence 260, App	C 795	9.2	57.5	32	3	US-08-783-853A-107	Sequence 8, Appl
C 723	9.2	57.5	22	4	US-07-974-409C-260	Sequence 264, App	C 796	9.2	57.5	32	3	US-09-075-272-8	Sequence 9, Appl
C 724	9.2	57.5	22	4	US-07-974-409C-264	Sequence 43, Appl	C 797	9.2	57.5	32	3	US-09-075-272-8	Sequence 9, Appl
C 725	9.2	57.5	22	5	US-09-521-144-43	Sequence 260, App	C 798	9.2	57.5	32	4	US-08-134-346A-12	Sequence 12, Appl
C 726	9.2	57.5	22	5	PCT-US93-00977-260	Sequence 264, App	C 799	9.2	57.5	32	4	US-08-976-288A-25	Sequence 25, Appl
C 727	9.2	57.5	23	2	PCT-US93-00977-264	Sequence 27, Appl	C 800	9.2	57.5	33	1	US-08-452-129A-14	Sequence 107, App
C 728	9.2	57.5	23	2	US-08-985-908-27	Sequence 27, Appl	C 801	9.2	57.5	33	1	US-07-988-154A-37	Sequence 37, Appl
C 729	9.2	57.5	23	3	US-09-339-775-3	Sequence 3, Appl	C 802	9.2	57.5	33	1	US-08-102-567-5	Sequence 5, Appl
C 730	9.2	57.5	23	3	US-09-163-162-4	Sequence 4, Appl	C 803	9.2	57.5	33	1	US-08-258-152-3	Sequence 3, Appl
C 731	9.2	57.5	23	3	US-09-286-407-4	Sequence 6, Appl	C 804	9.2	57.5	33	2	US-08-076-289A-3	Sequence 3, Appl
C 732	9.2	57.5	23	3	US-09-496-694B-6	Sequence 38, Appl	C 805	9.2	57.5	33	2	US-08-438-582-3	Sequence 5, Appl
C 733	9.2	57.5	23	4	US-09-502-357-38	Sequence 1, Appl	C 806	9.2	57.5	33	2	US-08-717-123-13	Sequence 13, Appl
C 734	9.2	57.5	24	1	US-08-324-243-1	Sequence 1, Appl	C 807	9.2	57.5	33	3	US-08-462-947-5	Sequence 5, Appl
C 735	9.2	57.5	24	1	US-08-532-390-1	Sequence 157, App	C 808	9.2	57.5	33	3	US-09-026-673-5	Sequence 3, Appl
C 736	9.2	57.5	24	3	US-08-835-728B-53	Sequence 53, Appl	C 809	9.2	57.5	33	3	US-09-266-596-3	Sequence 36, Appl
C 737	9.2	57.5	24	3	US-08-835-728B-157	Sequence 1, Appl	C 810	9.2	57.5	33	4	US-08-479-737-38	Sequence 38, Appl
C 738	9.2	57.5	24	3	US-08-526-136-6	Sequence 6, Appl	C 811	9.2	57.5	33	4	US-08-475-442A-38	Sequence 13, Appl
C 739	9.2	57.5	24	3	US-08-117-294-1	Sequence 1, Appl	C 812	9.2	57.5	33	4	US-09-375-257-13	Sequence 13, Appl
C 740	9.2	57.5	24	3	US-09-490-558-53	Sequence 53, Appl	C 813	9.2	57.5	33	4	US-09-944-411-3	Sequence 3, Appl
C 741	9.2	57.5	24	3	US-09-490-558-157	Sequence 157, App	C 814	9.2	57.5	33	4	US-08-846-762-31	Sequence 31, Appl
C 742	9.2	57.5	24	3	US-08-948-113D-4	Sequence 4, Appl	C 815	9.2	57.5	34	2	US-08-956-182-37	Sequence 37, Appl
C 743	9.2	57.5	24	4	PCT-US95-11511-1	Sequence 8, Appl	C 816	9.2	57.5	34	2	US-08-973-131-67	Sequence 67, Appl
C 744	9.2	57.5	25	1	US-08-056-200-8	Sequence 20, Appl	C 817	9.2	57.5	34	4	US-09-842-164A-22	Sequence 22, Appl
C 745	9.2	57.5	25	1	US-08-244-269-20	Sequence 500, App	C 818	9.2	57.5	35	1	US-07-992-827D-4	Sequence 4, Appl
C 746	9.2	57.5	25	2	US-08-117-952-500	Sequence 1, Appl	C 819	9.2	57.5	35	1	US-08-686-609-12	Sequence 12, Appl
C 747	9.2	57.5	25	2	US-08-519-283A-1	Sequence 8, Appl	C 820	9.2	57.5	36	1	US-08-975-902-55	Sequence 55, Appl
C 748	9.2	57.5	25	2	US-08-117-952-500	Sequence 1, Appl	C 821	9.2	57.5	36	2	US-09-002-832-12	Sequence 12, Appl
C 749	9.2	57.5	25	2	US-08-788-711-1	Sequence 1, Appl	C 822	9.2	57.5	36	2	US-09-455-960-13	Sequence 13, Appl
C 750	9.2	57.5	25	2	US-08-400-644-8	Sequence 50, Appl	C 823	9.2	57.5	36	4	US-07-937-609-7	Sequence 7, Appl
C 751	9.2	57.5	25	4	US-08-982-285-50	Sequence 51, Appl	C 824	9.2	57.5	37	1	US-08-261-670-13	Sequence 13, Appl
C 752	9.2	57.5	26	1	US-08-982-285-51	Sequence 53, Appl	C 825	9.2	57.5	37	1	US-08-029-170-7	Sequence 7, Appl
C 753	9.2	57.5	26	1	US-08-093-741-53	Sequence 1007, Ap	C 826	9.2	57.5	37	1	US-09-842-164A-19	Sequence 19, Appl
C 754	9.2	57.5	26	1	US-08-720-012-53	Sequence 1007, Ap	C 827	9.2	57.5	37	4	US-09-842-164A-23	Sequence 23, Appl
C 755	9.2	57.5	26	4	US-09-225-928-1007	Sequence 27, Appl	C 828	9.2	57.5	37	4		
C 756	9.2	57.5	26	4			C 829	9.2	57.5	37	4		
C 757	9.2	57.5	26	4			C 830	9.2	57.5	37	4		

C 831	9.2	57.5	37	5	PCT-US93-02115-13	Sequence 13, Appl	C 904	9.2	57.5	50	3	US-08-463-903-65	Sequence 65, Appl
C 832	9.2	57.5	38	4	US-09-556-877-201	Sequence 201, App	C 905	9.2	57.5	50	3	US-09-262-142-19	Sequence 19, Appl
C 833	9.2	57.5	38	4	US-09-620-412C-201	Sequence 201, App	C 906	9.2	57.5	50	3	US-09-315-886C-12	Sequence 12, Appl
C 834	9.2	57.5	38	4	US-09-598-419-201	Sequence 201, App	C 907	9.2	57.5	50	3	US-09-282-147-43	Sequence 43, Appl
C 835	9.2	57.5	39	1	US-08-723-896-9	Sequence 9, Appl1	C 908	9.2	57.5	50	4	US-08-849-567A-19	Sequence 19, Appl
C 836	9.2	57.5	39	1	US-08-464-531-105	Sequence 105, App	C 909	9.2	57.5	50	4	US-07-935-695-64	Sequence 64, Appl
C 837	9.2	57.5	39	2	US-08-461-598-105	Sequence 105, App	C 910	9.2	57.5	50	4	US-07-935-695-65	Sequence 65, Appl
C 838	9.2	57.5	39	3	US-08-322-137-105	Sequence 105, App	C 911	9.2	57.5	50	4	US-08-961-309-13	Sequence 33, Appl
C 839	9.2	57.5	39	3	US-08-717-294-47	Sequence 47, Appl	C 912	9.2	57.5	50	4	US-08-961-309-34	Sequence 34, Appl
C 840	9.2	57.5	39	3	US-08-732-708C-27	Sequence 27, Appl	C 913	9.2	57.5	50	4	US-09-354-929-69	Sequence 69, Appl
C 841	9.2	57.5	39	3	US-08-582-333A-41	Sequence 41, Appl	C 914	9.2	57.5	50	5	PCT-US95-11405-17	Sequence 17, Appl
C 842	9.2	57.5	39	4	US-08-424-797A-7	Sequence 7, Appl1	C 915	9.2	57.5	51	1	US-08-688-609-13	Sequence 13, Appl
C 843	9.2	57.5	39	4	US-09-381-847-3	Sequence 3, Appl1	C 916	9.2	57.5	51	3	US-09-002-932-13	Sequence 13, Appl
C 844	9.2	57.5	39	6	5256648-32	Patent No. 5256648	C 917	9.2	57.5	51	3	US-08-889-502-10	Sequence 30, Appl
C 845	9.2	57.5	39	6	5519127-31	Patent No. 5519127	C 918	9.2	57.5	52	3	US-08-889-502-29	Sequence 29, Appl
C 846	9.2	57.5	40	1	US-08-443-957-25	Sequence 25, Appl	C 919	9.2	57.5	53	2	US-08-657-392-32	Sequence 32, Appl
C 847	9.2	57.5	40	1	US-08-454-097-36	Sequence 36, Appl	C 920	9.2	57.5	53	5	PCT-US94-02539-32	Sequence 32, Appl
C 848	9.2	57.5	40	1	US-08-454-097-38	Sequence 38, Appl	C 921	9.2	57.5	54	2	US-08-832-535-8	Sequence 8, Appl1
C 849	9.2	57.5	40	3	US-08-185-359-36	Sequence 36, Appl	C 922	9.2	57.5	54	2	US-08-540-804-14	Sequence 34, Appl
C 850	9.2	57.5	40	3	US-08-185-359-38	Sequence 38, Appl	C 923	9.2	57.5	54	2	US-08-218-265-14	Sequence 34, Appl
C 851	9.2	57.5	40	4	US-09-842-164A-20	Sequence 20, Appl	C 924	9.2	57.5	54	3	US-08-521-872-34	Sequence 34, Appl
C 852	9.2	57.5	41	1	US-08-696-026A-3	Sequence 3, Appl1	C 925	9.2	57.5	54	3	US-09-019-485-15	Sequence 15, Appl
C 853	9.2	57.5	41	1	US-09-066-597-14	Sequence 14, Appl	C 926	9.2	57.5	54	3	US-08-590-399-14	Sequence 34, Appl
C 854	9.2	57.5	41	4	US-09-812-042A-3	Sequence 3, Appl1	C 927	9.2	57.5	54	4	US-09-479-645A-218	Sequence 218, App
C 855	9.2	57.5	42	1	US-07-867-106-8	Sequence 8, Appl1	C 928	9.2	57.5	54	4	US-09-528-436B-14	Sequence 14, Appl
C 856	9.2	57.5	42	1	US-08-468-036-24	Sequence 24, Appl	C 929	9.2	57.5	55	4	US-09-672-603A-29	Sequence 29, Appl
C 857	9.2	57.5	42	1	US-08-468-036-39	Sequence 39, Appl	C 930	9.2	57.5	55	4	US-08-025-403A-29	Sequence 29, Appl
C 858	9.2	57.5	42	1	US-08-376-843-24	Sequence 24, Appl	C 931	9.2	57.5	56	1	US-08-221-662-5	Sequence 5, Appl1
C 859	9.2	57.5	42	2	US-08-376-843-39	Sequence 39, Appl	C 932	9.2	57.5	56	1	US-08-221-662-6	Sequence 6, Appl1
C 860	9.2	57.5	42	2	US-08-466-860-41	Sequence 41, Appl	C 933	9.2	57.5	60	1	US-08-460-853-6	Sequence 6, Appl1
C 861	9.2	57.5	42	3	US-08-472-040A-41	Sequence 41, Appl	C 934	9.2	57.5	60	1	US-08-460-853-12	Sequence 12, Appl
C 862	9.2	57.5	42	3	US-09-105-678A-20	Sequence 20, Appl	C 935	9.2	57.5	60	1	US-08-460-853-13	Sequence 13, Appl
C 863	9.2	57.5	42	3	US-08-276-776-41	Sequence 41, Appl	C 936	9.2	57.5	60	4	US-09-339-913B-15	Sequence 15, Appl
C 864	9.2	57.5	42	3	US-08-471-209-41	Sequence 41, Appl	C 937	9.2	57.5	60	4	US-09-339-913B-45	Sequence 45, Appl
C 865	9.2	57.5	42	3	US-08-872-056-15	Sequence 15, Appl	C 938	9.2	57.5	60	4	US-09-339-904A-15	Sequence 15, Appl
C 866	9.2	57.5	42	3	US-09-421-208-20	Sequence 20, Appl	C 939	9.2	57.5	60	4	US-09-339-904A-45	Sequence 45, Appl
C 867	9.2	57.5	42	4	US-09-387-300-24	Sequence 24, Appl	C 940	9.2	57.5	60	4	US-08-769-062B-15	Sequence 15, Appl
C 868	9.2	57.5	43	1	US-08-330-638D-4	Sequence 4, Appl1	C 941	9.2	57.5	60	4	US-08-769-062B-45	Sequence 45, Appl
C 869	9.2	57.5	43	2	US-08-906-746A-4	Sequence 4, Appl1	C 942	9.2	57.5	60	4	US-09-344-002B-15	Sequence 15, Appl
C 870	9.2	57.5	43	3	US-08-833-985-42	Sequence 42, Appl	C 943	9.2	57.5	60	4	US-09-344-002B-45	Sequence 45, Appl
C 871	9.2	57.5	43	4	US-09-410-903-23	Sequence 23, Appl	C 944	9.2	57.5	60	4	US-09-559-565C-15	Sequence 15, Appl
C 872	9.2	57.5	43	4	US-08-835-159-42	Sequence 42, Appl	C 945	9.2	57.5	60	4	US-09-559-565C-45	Sequence 45, Appl
C 873	9.2	57.5	45	1	US-08-089-862-8	Sequence 8, Appl1	C 946	9.2	57.5	60	4	US-09-693-350-15	Sequence 15, Appl
C 874	9.2	57.5	45	5	PCT-US94-07776-13	Sequence 13, Appl	C 947	9.2	57.5	60	4	US-09-693-350-45	Sequence 45, Appl
C 875	9.2	57.5	46	1	US-08-171-389-23	Sequence 23, Appl	C 948	9.2	57.5	60	4	US-09-693-389-15	Sequence 15, Appl
C 876	9.2	57.5	46	1	US-08-123-936-23	Sequence 23, Appl	C 949	9.2	57.5	60	4	US-09-693-389-45	Sequence 45, Appl
C 877	9.2	57.5	46	2	US-08-475-228A-23	Sequence 23, Appl	C 950	9.2	57.5	61	4	US-09-549-848B-66	Sequence 66, Appl
C 878	9.2	57.5	46	3	US-08-482-080A-23	Sequence 23, Appl	C 951	9.2	57.5	62	1	US-08-366-783-13	Sequence 13, Appl
C 879	9.2	57.5	46	3	US-09-171-945-102	Sequence 102, App	C 952	9.2	57.5	62	2	US-08-846-021A-17	Sequence 17, Appl
C 880	9.2	57.5	46	4	US-09-354-947-23	Sequence 23, Appl	C 953	9.2	57.5	62	3	US-08-956-182-25	Sequence 25, Appl
C 881	9.2	57.5	47	5	PCT-US93-12388-23	Sequence 23, Appl	C 954	9.2	57.5	63	1	US-07-807-529A-16	Sequence 16, Appl
C 882	9.2	57.5	47	1	US-08-171-389-103	Sequence 103, App	C 955	9.2	57.5	63	1	US-08-530-92-6	Sequence 6, Appl1
C 883	9.2	57.5	47	1	US-08-171-389-125	Sequence 125, App	C 956	9.2	57.5	63	3	US-08-300-928C-65	Sequence 65, Appl
C 884	9.2	57.5	47	1	US-08-123-936-103	Sequence 103, App	C 957	9.2	57.5	63	3	US-08-430-944D-65	Sequence 65, Appl
C 885	9.2	57.5	47	1	US-08-475-228A-125	Sequence 125, App	C 958	9.2	57.5	63	3	US-08-430-944-65	Sequence 65, Appl
C 886	9.2	57.5	47	2	US-08-475-228A-103	Sequence 103, App	C 959	9.2	57.5	63	3	US-08-431-184-65	Sequence 65, Appl
C 887	9.2	57.5	47	2	US-08-475-228A-125	Sequence 125, App	C 960	9.2	57.5	63	3	US-08-906-517-6	Sequence 6, Appl1
C 888	9.2	57.5	47	2	US-09-081-731-4	Sequence 4, Appl1	C 961	9.2	57.5	64	1	US-08-318-193-19	Sequence 19, Appl
C 889	9.2	57.5	47	3	US-08-482-080A-103	Sequence 103, App	C 962	9.2	57.5	66	2	US-08-500-635A-14	Sequence 14, Appl
C 890	9.2	57.5	47	3	US-08-482-080A-125	Sequence 125, App	C 963	9.2	57.5	66	3	US-09-167-151-14	Sequence 14, Appl
C 891	9.2	57.5	47	4	US-09-361-727-4	Sequence 4, Appl1	C 964	9.2	57.5	67	3	US-09-014-416-15	Sequence 15, Appl
C 892	9.2	57.5	47	4	US-09-354-947-103	Sequence 103, App	C 965	9.2	57.5	69	1	US-07-959-284-18	Sequence 18, Appl
C 893	9.2	57.5	47	4	US-09-354-947-125	Sequence 125, App	C 966	9.2	57.5	69	1	US-08-184-009-101	Sequence 101, App
C 894	9.2	57.5	47	4	US-09-641-638-1061	Sequence 1061, App	C 967	9.2	57.5	69	2	US-08-308-136A-18	Sequence 18, Appl
C 895	9.2	57.5	47	4	US-09-671-317-977	Sequence 977, App	C 968	9.2	57.5	69	2	US-08-458-356-101	Sequence 101, App
C 896	9.2	57.5	47	4	US-09-422-978-858	Sequence 858, App	C 969	9.2	57.5	69	3	US-08-460-736-101	Sequence 101, App
C 897	9.2	57.5	47	4	US-09-423-978-1642	Sequence 1642, App	C 970	9.2	57.5	69	4	US-08-645-107A-18	Sequence 18, Appl
C 898	9.2	57.5	47	4	US-09-423-978-3426	Sequence 3426, App	C 971	9.2	57.5	69	4	US-09-197-349-18	Sequence 18, Appl
C 899	9.2	57.5	47	4	US-09-546-934-34	Sequence 34, Appl	C 972	9.2	57.5	69	4	US-09-031-693-18	Sequence 18, Appl
C 900	9.2	57.5	47	5	PCT-US93-12388-103	Sequence 103, App	C 973	9.2	57.5	69	4	US-09-535-370-101	Sequence 101, App
C 901	9.2	57.5	47	5	PCT-US93-12388-125	Sequence 125, App	C 974	9.2	57.5	69	5	PCT-US93-09649A-18	Sequence 18, Appl
C 902	9.2	57.5	50	1	US-08-472-194A-19	Sequence 19, Appl	C 975	9.2	57.5	69	5	PCT-US93-09649-18	Sequence 18, Appl
C 903	9.2	57.5	50	3	US-08-463-903-64	Sequence 64, Appl	C 976	9.2	57.5	72	1	US-08-318-193-78	Sequence 78, Appl

977 9.2 57.5 73 1 US-07-982-712-12 Sequence 12, Appl
 C 978 9.2 57.5 74 3 US-09-389-341-64 Sequence 64, Appl
 C 979 9.2 57.5 75 1 US-08-219-012-84 Sequence 84, Appl
 C 980 9.2 57.5 75 3 US-08-687-421-272 Sequence 272, App
 C 981 9.2 57.5 75 4 US-09-397-787-4 Sequence 4, Appl
 C 982 9.2 57.5 77 3 US-08-956-307B-5 Sequence 5, Appl
 C 983 9.2 57.5 78 3 US-08-918-288-63 Sequence 6, Appl
 C 984 9.2 57.5 78 3 US-08-918-288-63 Sequence 63, Appl
 C 985 9.2 57.5 78 3 US-09-282-357-63 Sequence 139, Appl
 C 986 9.2 57.5 79 1 US-08-472-255A-139 Sequence 139, App
 C 987 9.2 57.5 79 1 US-08-472-255A-139 Sequence 165, App
 C 988 9.2 57.5 79 1 US-08-479-724A-139 Sequence 139, App
 C 989 9.2 57.5 79 1 US-08-479-724A-139 Sequence 165, App
 C 990 9.2 57.5 79 3 US-08-472-256B-139 Sequence 139, App
 C 991 9.2 57.5 79 3 US-08-472-256B-139 Sequence 165, App
 C 992 9.2 57.5 79 3 US-09-023-228B-7 Sequence 7, Appl
 C 993 9.2 57.5 79 3 US-08-952-793-139 Sequence 139, App
 C 994 9.2 57.5 79 3 US-08-952-793-139 Sequence 165, App
 C 995 9.2 57.5 79 4 US-09-163-025B-7 Sequence 7, Appl
 C 996 9.2 57.5 79 4 US-09-849-928-139 Sequence 139, App
 C 997 9.2 57.5 79 4 US-09-849-928-139 Sequence 165, App
 C 998 9.2 57.5 79 4 US-10-037-282-7 Sequence 7, Appl
 C 999 9.2 57.5 79 5 PCT-US96-09455A-139 Sequence 139, App
 1000 9.2 57.5 79 5 PCT-US96-09455A-165 Sequence 165, App

ALIGNMENTS

RESULT 1
 US-09-536-393-19
 ; Sequence 19, Application US/09536393
 ; Patent No. 6562570
 ; GENERAL INFORMATION:
 ; APPLICANT: Rossi, John J.
 ; APPLICANT: Scherr, Michaela
 ; APPLICANT: R1998, Arthur D.
 ; TITLE OF INVENTION: Method for Identifying Accessible Binding Sites on RNA
 ; FILE REFERENCE: 1954-285
 ; CURRENT APPLICATION NUMBER: US/09/536,393
 ; CURRENT FILING DATE: 2000-03-28
 ; EARLIER APPLICATION NUMBER: 60/127,529
 ; EARLIER FILING DATE: 1999-04-02
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 19
 ; LENGTH: 16
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: DNazyme core
 US-09-536-393-19
 Query Match 97.5%; Score 15.6; DB 4; Length 16;
 Best Local Similarity 93.8%; Pred. No. 4;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGGCTAGCTACAACGA 16
 Db 1 AGGCTAGCTACAACGA 16
 RESULT 2
 US-09-536-393-20
 ; Sequence 20, Application US/09536393
 ; Patent No. 6562570
 ; GENERAL INFORMATION:
 ; APPLICANT: Rossi, John J.
 ; APPLICANT: Scherr, Michaela
 ; APPLICANT: R1998, Arthur D.
 ; TITLE OF INVENTION: Method for Identifying Accessible Binding Sites on RNA
 ; FILE REFERENCE: 1954-285
 ; CURRENT APPLICATION NUMBER: US/09/536,393

CURRENT FILING DATE: 2000-03-28
 ; EARLIER APPLICATION NUMBER: 60/127,529
 ; EARLIER FILING DATE: 1999-04-02
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 20
 ; LENGTH: 16
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: DNazyme core
 US-09-536-393-20
 Query Match 97.5%; Score 15.6; DB 4; Length 16;
 Best Local Similarity 93.8%; Pred. No. 4;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACAACGA 16
 Db 1 AGGCTAGCTACAACGA 16

RESULT 3
 US-09-270-140A-23
 ; Sequence 23, Application US/09270140A
 ; Patent No. 6361941
 ; GENERAL INFORMATION:
 ; APPLICANT: Todd, Alison
 ; APPLICANT: Fuery, Caroline
 ; APPLICANT: Fuery, Murray
 ; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
 ; FILE REFERENCE: J61799
 ; CURRENT APPLICATION NUMBER: US/09/270,140A
 ; CURRENT FILING DATE: 1999-03-16
 ; PRIOR APPLICATION NUMBER: 60/079,651
 ; PRIOR FILING DATE: 1998-03-27
 ; NUMBER OF SEQ ID NOS: 96
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 23
 ; LENGTH: 29
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: DNazyme for
 ; OTHER INFORMATION: N-ras codon 61 position 1 - mutant (C to A, G or
 ; OTHER INFORMATION: U)
 US-09-270-140A-23
 Query Match 97.5%; Score 15.6; DB 4; Length 29;
 Best Local Similarity 93.8%; Pred. No. 4.2;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGGCTAGCTACAACGA 16
 Db 8 AGGCTAGCTACAACGA 23
 RESULT 4
 US-09-270-140A-25
 ; Sequence 25, Application US/09270140A
 ; Patent No. 6361941
 ; GENERAL INFORMATION:
 ; APPLICANT: Todd, Alison
 ; APPLICANT: Fuery, Caroline
 ; APPLICANT: Fuery, Murray
 ; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
 ; FILE REFERENCE: J61799
 ; CURRENT APPLICATION NUMBER: US/09/270,140A
 ; CURRENT FILING DATE: 1999-03-16
 ; PRIOR APPLICATION NUMBER: 60/079,651
 ; PRIOR FILING DATE: 1998-03-27
 ; NUMBER OF SEQ ID NOS: 96
 ; SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 25
LENGTH: 29
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for
OTHER INFORMATION: N-ras codon 61, position 1
US-09-270-140A-25

Query Match 97.5%; Score 15.6; DB 4; Length 29;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
: |||||
DB 9 AGGCTAGCTACACGA 24

RESULT 5
US-09-270-140A-55
Sequence 55, Application US/09270140A
Patent No. 6361941
GENERAL INFORMATION:
APPLICANT: Todd, Alison
APPLICANT: Fuery, Caroline
APPLICANT: Cairns, Murray
TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
FILE REFERENCE: J6J1799
CURRENT APPLICATION NUMBER: US/09/270,140A
CURRENT FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 60/079,651
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 55
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for
OTHER INFORMATION: codon 508 - mutant (CTT deletion) for Cystic
US-09-270-140A-55

Query Match 97.5%; Score 15.6; DB 4; Length 30;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
: |||||
DB 8 AGGCTAGCTACACGA 23

RESULT 6
US-09-253-955-5
Sequence 5, Application US/09253955
Patent No. 6140055
GENERAL INFORMATION:
APPLICANT: Todd, Alison V
APPLICANT: Fuery, Caroline J
APPLICANT: Cairns, Murray J
TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
TITLE OF INVENTION: Molecules And Kits
FILE REFERENCE: J01770SequenceListing
CURRENT APPLICATION NUMBER: US/09/253,955
CURRENT FILING DATE: 1999-02-22
PRIOR APPLICATION NUMBER: 60/076,899
PRIOR FILING DATE: 1998-03-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 31
TYPE: DNA

ORGANISM: synthetic construct
US-09-253-955-5

Query Match 97.5%; Score 15.6; DB 3; Length 31;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
: |||||
DB 8 AGGCTAGCTACACGA 23

RESULT 7
US-09-637-405-5
Sequence 5, Application US/09637405
Patent No. 620113
GENERAL INFORMATION:
APPLICANT: Todd, Alison V
APPLICANT: Fuery, Caroline J
APPLICANT: Cairns, Murray J
TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
TITLE OF INVENTION: Molecules And Kits
FILE REFERENCE: J01770SequenceListing
CURRENT APPLICATION NUMBER: US/09/637,405
CURRENT FILING DATE: 2000-08-11
EARLIER APPLICATION NUMBER: 09/253,955
EARLIER FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 31
TYPE: DNA
ORGANISM: synthetic construct
US-09-637-405-5

Query Match 97.5%; Score 15.6; DB 3; Length 31;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
: |||||
DB 8 AGGCTAGCTACACGA 23

RESULT 8
US-09-270-140A-42
Sequence 42, Application US/09270140A
Patent No. 6361941
GENERAL INFORMATION:
APPLICANT: Todd, Alison
APPLICANT: Fuery, Caroline
APPLICANT: Cairns, Murray
TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
FILE REFERENCE: J6J1799
CURRENT APPLICATION NUMBER: US/09/270,140A
CURRENT FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 60/079,651
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 42
LENGTH: 31
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for
OTHER INFORMATION: codon 542 - Cystic Fibrosis
US-09-270-140A-42

Query Match 97.5%; Score 15.6; DB 4; Length 31;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16
: |||||
DB 10 AGGCTAGCTACACGA 25

RESULT 9
US-09-270-140A-45
; Sequence 45, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Fuary, Allison
; APPLICANT: Todd, Allison
; APPLICANT: Fuary, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J6J1799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 45
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for
; OTHER INFORMATION: cystic Fibrosis Codon 542 - mutant (G to U)
US-09-270-140A-45

Query Match 97.5%; Score 15.6; DB 4; Length 31;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16
: |||||
DB 10 AGGCTAGCTACACGA 25

RESULT 10
US-09-270-140A-48
; Sequence 48, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Allison
; APPLICANT: Fuary, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J6J1799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 48
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for
; OTHER INFORMATION: Codon 551 - wildtype
US-09-270-140A-48

Query Match 97.5%; Score 15.6; DB 4; Length 31;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16
: |||||
DB 9 GGGCTAGCTACACGA 24

RESULT 11
US-09-270-140A-51
; Sequence 51, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Allison
; APPLICANT: Fuary, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J6J1799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 51
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for
; OTHER INFORMATION: Codon 51 - mutant (G to A)
US-09-270-140A-51

Query Match 97.5%; Score 15.6; DB 4; Length 31;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16
: |||||
DB 9 AGGCTAGCTACACGA 24

RESULT 12
US-09-746-985B-5
; Sequence 5, Application US/09746985B
; Patent No. 6365724
; GENERAL INFORMATION:
; APPLICANT: Todd, Allison V
; APPLICANT: Fuary, Caroline J
; APPLICANT: Cairns, Murray J
; TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
; FILE REFERENCE: Sequencelisting
; CURRENT APPLICATION NUMBER: US/09/746,985B
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/076,899
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-746-985B-5

Query Match 97.5%; Score 15.6; DB 4; Length 31;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16
: |||||
DB 8 AGGCTAGCTACACGA 23

RESULT 13
US-09-270-140A-12
; Sequence 12, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:

```

; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J611799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNazyme for
; OTHER INFORMATION: H-ras codon 61, position 1-mutant
US-09-270-140A-12
```

```

Query Match          97.5%; Score 15.6; DB 4; Length 32;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1  RGCTAGCTACACGA 16
      : |||||
Db      10 GGGCTAGCTACACGA 25
```

```

RESULT 14
US-09-270-140A-15
; Sequence 15, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J611799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNazyme for
; OTHER INFORMATION: H-ras codon 61
US-09-270-140A-15
```

```

Query Match          97.5%; Score 15.6; DB 4; Length 32;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1  RGCTAGCTACACGA 16
      : |||||
Db      12 GGGCTAGCTACACGA 27
```

```

RESULT 15
US-09-270-140A-19
; Sequence 19, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J611799
```

```

; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNazyme for
; OTHER INFORMATION: H-ras codon 61, position 3
US-09-270-140A-19
```

```

Query Match          97.5%; Score 15.6; DB 4; Length 32;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1  RGCTAGCTACACGA 16
      : |||||
Db      11 AGGCTAGCTACACGA 26
```

```

RESULT 16
US-09-270-140A-28
; Sequence 28, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J611799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNazyme
; OTHER INFORMATION: H-ras codon 61
US-09-270-140A-28
```

```

Query Match          97.5%; Score 15.6; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1  RGCTAGCTACACGA 16
      : |||||
Db      9  RGCTAGCTACACGA 24
```

```

RESULT 17
US-09-270-140A-58
; Sequence 58, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J611799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
```

```

; SEQ ID NO 58
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNazyme for
; US-09-270-140A-58
Query Match          97.5%; Score 15.6; DB 4; Length 32;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 RGGCTAGCTACACGA 16
Db      9 GGGCTAGCTACACGA 24

RESULT 18
US-09-270-140A-9
; Sequence 9, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jc01799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNazyme for
; US-09-270-140A-9
Query Match          97.5%; Score 15.6; DB 4; Length 34;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 RGGCTAGCTACACGA 16
Db      13 AGGCTAGCTACACGA 28

RESULT 19
US-09-270-140A-53
; Sequence 53, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jc01799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```

; OTHER INFORMATION: Description of Artificial Sequence: DNazyme for
; US-09-270-140A-53
Query Match          97.5%; Score 15.6; DB 4; Length 34;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 RGGCTAGCTACACGA 16
Db      11 AGGCTAGCTACACGA 26

RESULT 20
US-09-270-140A-3
; Sequence 3, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jc01799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNazyme for
; US-09-270-140A-3
Query Match          97.5%; Score 15.6; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 RGGCTAGCTACACGA 16
Db      11 RGGCTAGCTACACGA 26

RESULT 21
US-09-270-140A-6
; Sequence 6, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jc01799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNazyme
; US-09-270-140A-6
Query Match          97.5%; Score 15.6; DB 4; Length 35;
Best Local Similarity 93.8%; Pred. No. 4.2;
```

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16
:|||||
Db 11 AGGCTAGCTACACGA 26

RESULT 22

US-09-270-140A-31
; Sequence 31, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jc11799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; PRIOR FILING DATE: 1999-03-16
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for
; OTHER INFORMATION: Codon 70 HIV-1 AZT resistant mutant
US-09-270-140A-31

Query Match 97.5%; Score 15.6; DB 4; Length 35;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16
:|||||
Db 9 AGGCTAGCTACACGA 24

RESULT 23

US-09-270-140A-39
; Sequence 39, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jc11799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; PRIOR FILING DATE: 1999-03-16
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for
; OTHER INFORMATION: codon 74
US-09-270-140A-39

Query Match 97.5%; Score 15.6; DB 4; Length 35;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16
:|||||
Db 8 AGGCTAGCTACACGA 23

RESULT 24
US-09-270-140A-34
; Sequence 34, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jc11799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; PRIOR FILING DATE: 1999-03-16
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for
; OTHER INFORMATION: codon 215 - mutant (C to U or A)
US-09-270-140A-34

Query Match 97.5%; Score 15.6; DB 4; Length 38;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16
:|||||
Db 11 AGGCTAGCTACACGA 26

RESULT 25

US-09-270-140A-36
; Sequence 36, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jc11799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; PRIOR FILING DATE: 1999-03-16
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme for
; OTHER INFORMATION: codon 215 - mutant
US-09-270-140A-36

Query Match 97.5%; Score 15.6; DB 4; Length 38;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16
:|||||
Db 10 GGGCTAGCTACACGA 25

RESULT 26

US-09-270-140A-91
; Sequence 91, Application US/09270140A

```
Patent No. 6361941
GENERAL INFORMATION:
APPLICANT: Todd, Alison
APPLICANT: Fuery, Caroline
TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
FILE REFERENCE: Jc11799
CURRENT APPLICATION NUMBER: US/09/270,140A
CURRENT FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 60/079,651
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 91
LENGTH: 39
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: D21 DNazyme
US-09-270-140A-91

Query Match          97.5%; Score 15.6; DB 4; Length 39;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACAACGA 16
   :|||||
   8 GGGCTAGCTACAACGA 23

RESULT 27
US-09-270-140A-94
Sequence 94, Application US/09270140A
Patent No. 6361941
GENERAL INFORMATION:
APPLICANT: Todd, Alison
APPLICANT: Fuery, Caroline
TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
FILE REFERENCE: Jc11799
CURRENT APPLICATION NUMBER: US/09/270,140A
CURRENT FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 60/079,651
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 94
LENGTH: 39
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: D23 DNazyme
US-09-270-140A-94

Query Match          97.5%; Score 15.6; DB 4; Length 39;
Best Local Similarity 93.8%; Pred. No. 4.2;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACAACGA 16
   :|||||
   8 AGGCTAGCTACAACGA 23

RESULT 28
US-08-849-567A-85
Sequence 85, Application US/08849567A
Patent No. 6326174
GENERAL INFORMATION:
APPLICANT: Joyce, Gerald F.
APPLICANT: Breaker, Ronald R.
TITLE OF INVENTION: ENZYMATIC DNA MOLECULES
FILE REFERENCE: SCR19435
CURRENT APPLICATION NUMBER: US/08/849,567A
CURRENT FILING DATE: 1997-08-25
```

```
CURRENT FILING DATE: 1997-08-25
PRIOR APPLICATION NUMBER: PCT/US95/15580
PRIOR FILING DATE: 1995-12-01
PRIOR APPLICATION NUMBER: 08/472,194
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/349,023
PRIOR FILING DATE: 1994-12-02
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 85
LENGTH: 47
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNA enzyme
US-08-849-567A-85

Query Match          97.5%; Score 15.6; DB 4; Length 47;
Best Local Similarity 93.8%; Pred. No. 4.3;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACAACGA 16
   :|||||
   11 AGGCTAGCTACAACGA 26

RESULT 29
US-08-849-567A-87
Sequence 87, Application US/08849567A
Patent No. 6326174
GENERAL INFORMATION:
APPLICANT: Joyce, Gerald F.
APPLICANT: Breaker, Ronald R.
TITLE OF INVENTION: ENZYMATIC DNA MOLECULES
FILE REFERENCE: SCR19435
CURRENT APPLICATION NUMBER: US/08/849,567A
CURRENT FILING DATE: 1997-08-25
PRIOR APPLICATION NUMBER: PCT/US95/15580
PRIOR FILING DATE: 1995-12-01
PRIOR APPLICATION NUMBER: 08/472,194
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/349,023
PRIOR FILING DATE: 1994-12-02
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 87
LENGTH: 48
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNA enzyme
US-08-849-567A-87

Query Match          97.5%; Score 15.6; DB 4; Length 48;
Best Local Similarity 93.8%; Pred. No. 4.3;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACAACGA 16
   :|||||
   10 AGGCTAGCTACAACGA 25

RESULT 30
US-08-849-567A-81
Sequence 81, Application US/08849567A
Patent No. 6326174
GENERAL INFORMATION:
APPLICANT: Joyce, Gerald F.
APPLICANT: Breaker, Ronald R.
TITLE OF INVENTION: ENZYMATIC DNA MOLECULES
FILE REFERENCE: SCR19435
CURRENT APPLICATION NUMBER: US/08/849,567A
CURRENT FILING DATE: 1997-08-25
```



```

; PRIOR APPLICATION NUMBER: PCT/US95/15580
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 08/472,194
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/349,023
; PRIOR FILING DATE: 1994-12-02
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA enzyme
US-08-849-567A-81

```

Query Match	97.5%	Score 15.6	DB 4	Length 49
Best Local Similarity	93.8%	Pred. No. 4.3		
Matches 15; Conservative	1	Mismatches 0	Indels 0	Gaps 0

QY 1 RGGCTAGCTACACGA 16
: |||||
Db 10 AGGCTAGCTACACGA 25

```

RESULT 31
US-09-253-955-8/c
; Sequence 8, Application US/09253955
; Patent No. 6140055
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison V
; APPLICANT: Fuery, Caroline J
; APPLICANT: Cairns, Murray J
; TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
; TITLE OF INVENTION: Molecules And Kits
; FILE REFERENCE: J01770sequence1sting
; CURRENT APPLICATION NUMBER: US/09/253,955
; CURRENT FILING DATE: 1999-02-22
; EARLIER APPLICATION NUMBER: 60/076,899
; EARLIER FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 50
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-253-955-8

```

Query Match	97.5%	Score 15.6	DB 3	length 50
Best Local Similarity	93.8%	Pred. No. 4.3		
Matches 15, Conservative	1	Mismatches 0	Indels 0	Gaps 0

```
QY      1  RGCTAGCTACAACGA  1
          : |||||
Db      22  AGGCTAGCTACAACGA  7
```

```

, RESULT 32
, US-09-637-405-8/C
, Sequence 8, Application US/09637405
, Patent No. 6201113
, GENERAL INFORMATION:
, APPLICANT: Todd, Alison V
, APPLICANT: Fuery, Caroline J
, APPLICANT: Cairns, Murray J
, TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
, TITLE OF INVENTION: Molecules And Kits
, FILE REFERENCE: J0170sequence1isting
, CURRENT APPLICATION NUMBER: US/09/637,405
, CURRENT FILING DATE: 2000-08-11
, EARLIER APPLICATION NUMBER: 09/253,955
, EARLIER FILING DATE: 1999-02-22
, NUMBER OF SEQ ID NOS: 11

```

```

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 50
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-637-405-8

```

Query Match	97.5%	Score 15.6	DB 3	Length 50
Best Local Similarity	93.8%	Pred. No. 4.3		
Matches 15, Conservative	1	Mismatches 0	Indels 0	Gaps 0

Qy	1	RGGCTAGCTACAACGA	16
	:		
Db	22	AGGCTAGCTACAACGA	7

```

RESULT 33
US-09-746-985B-8/c
: Sequence 8, Application US/09746985B
: Patent No. 6365724
: GENERAL INFORMATION:
: APPLICANT: Todd, Alison V
: APPLICANT: Fuery, Caroline J
: APPLICANT: Cairns, Murray J
: TITLE OF INVENTION: Mammalian Nucleic Acid Detection Methods, And Related
: TITLE OF INVENTION: Molecules And Kits
: FILE REFERENCE: SequenceListing
: CURRENT APPLICATION NUMBER: US/09/746,985B
: CURRENT FILING DATE: 2000-12-21
: PRIOR APPLICATION NUMBER: 60/076,899
: PRIOR FILING DATE: 1998-03-05
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 8
: LENGTH: 50
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: PCR primer
US-09-746-985B-8

```

Query Match	97.5%	Score 15.6	DB 4	Length 50
Best Local Similarity	93.8%	Score 15.4	3	
Matches 15, Conservative	1	Mismatches	0	Gaps 0

```
QY      1 RGGCTAGCTACAACGA 16
          :|||||
Db      22 AGGCTAGCTACAACGA 7
```

```

/ RESULT 34
/ US-08-849-567A-86
/ Sequence 86, Application US/08849567A
/ Patent No. 6326174
/
/ GENERAL INFORMATION:
/
/ APPLICANT: Joyce, Gerald F.
/ APPLICANT: Breaker, Ronald R.
/ TITLE OF INVENTION: ENZYMATIC DNA MOLECULES
/ FILE REFERENCE: SCR1943S
/ CURRENT APPLICATION NUMBER: US/08/849,567A
/ CURRENT FILING DATE: 1997-08-25
/ PRIOR APPLICATION NUMBER: PCT/US95/15580
/ PRIOR FILING DATE: 1995-12-01
/ PRIOR APPLICATION NUMBER: 08/472,194
/ PRIOR FILING DATE: 1995-06-07
/ PRIOR APPLICATION NUMBER: 08/349,023
/ PRIOR FILING DATE: 1994-12-02
/ NUMBER OF SEQ ID NOS: 101
/
/ SOFTWARE: PatentIn Ver. 2.1
/
/ SEQ ID NO 86
/
/ LENGTH: 51
/
/ TYPE: DNA
/
/ ORGANISM: Artificial Sequence

```

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNA enzyme
US-08-849-567A-86

Query Match
Best Local Similarity 97.5%; Score 15.6; DB 4; Length 51;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACACGA 16
DB 11 AGGCTAGCTACACGA 26

RESULT 35
US-09-253-955-2/c
Sequence 2, Application US/09253955
Patent No. 6140055
GENERAL INFORMATION:
APPLICANT: Todd, Alison V
APPLICANT: Fuery, Caroline J
TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
FILE REFERENCE: J1170SequenceListing
CURRENT APPLICATION NUMBER: US/09/253,955
CURRENT FILING DATE: 1999-02-22
EARLIER APPLICATION NUMBER: 60/076,899
EARLIER FILING DATE: 1998-03-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 59
TYPE: DNA
ORGANISM: synthetic construct
US-09-253-955-2

Query Match
Best Local Similarity 97.5%; Score 15.6; DB 3; Length 59;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACACGA 16
DB 28 AGGCTAGCTACACGA 13

RESULT 36
US-09-637-405-2/c
Sequence 2, Application US/09637405
Patent No. 6201113
GENERAL INFORMATION:
APPLICANT: Todd, Alison V
APPLICANT: Fuery, Caroline J
APPLICANT: Cairns, Murray J
TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
FILE REFERENCE: J1170SequenceListing
CURRENT APPLICATION NUMBER: US/09/637,405
CURRENT FILING DATE: 2000-08-11
EARLIER APPLICATION NUMBER: 09/253,955
EARLIER FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 59
TYPE: DNA
ORGANISM: synthetic construct
US-09-637-405-2

Query Match
Best Local Similarity 97.5%; Score 15.6; DB 3; Length 59;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACACGA 16

DB 28 AGGCTAGCTACACGA 13

RESULT 37
US-09-746-985B-2/c
Sequence 2, Application US/09746985B
Patent No. 6365724
GENERAL INFORMATION:
APPLICANT: Todd, Alison V
APPLICANT: Fuery, Caroline J
APPLICANT: Cairns, Murray J
TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
FILE REFERENCE: SequenceListing
CURRENT APPLICATION NUMBER: US/09/746,985B
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/076,899
PRIOR FILING DATE: 1998-03-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 59
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR primer
US-09-746-985B-2

Query Match
Best Local Similarity 97.5%; Score 15.6; DB 4; Length 59;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACACGA 16
DB 28 AGGCTAGCTACACGA 13

RESULT 38
US-09-253-955-10/c
Sequence 10, Application US/09253955
Patent No. 6140055
GENERAL INFORMATION:
APPLICANT: Todd, Alison V
APPLICANT: Fuery, Caroline J
APPLICANT: Cairns, Murray J
TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
FILE REFERENCE: J1170SequenceListing
CURRENT APPLICATION NUMBER: US/09/253,955
CURRENT FILING DATE: 1999-02-22
EARLIER APPLICATION NUMBER: 60/076,899
EARLIER FILING DATE: 1998-03-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 60
TYPE: DNA
ORGANISM: synthetic construct
US-09-253-955-10

Query Match
Best Local Similarity 97.5%; Score 15.6; DB 3; Length 60;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACACGA 16
DB 32 GGGCTAGCTACACGA 17

RESULT 39
US-09-637-405-10/c
Sequence 10, Application US/09637405

; Patent No. 620113
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison V
; APPLICANT: Fuery, Caroline J
; APPLICANT: Cairns, Murray J
; TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
; TITLE OF INVENTION: Molecules And Kits
; FILE REFERENCE: j3170SequenceListing
; CURRENT APPLICATION NUMBER: US/09/637,405
; CURRENT FILING DATE: 2000-08-11
; EARLIER APPLICATION NUMBER: 09/253,955
; EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 60
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-637-405-10

Query Match 97.5%; Score 15.6; DB 3; Length 60;
Best Local Similarity 93.8%; Pred. No. 4.4;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCTACACGA 16
: |||||
Db 32 GGGCTAGCTACACGA 17

RESULT 40
US-09-270-140A-95/c
; Sequence 95, Application US/09270140A
; Patent No. 6361941

; GENERAL INFORMATION:
; APPLICANT: Fuery, Alison
; APPLICANT: Todd, Alison
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: Jc31799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 3' zymogene
; OTHER INFORMATION: primer ek42b22
US-09-270-140A-95

Query Match 97.5%; Score 15.6; DB 4; Length 60;
Best Local Similarity 93.8%; Pred. No. 4.4;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCTACACGA 16
: |||||
Db 32 GGGCTAGCTACACGA 17

Search completed: January 21, 2004, 08:17:05
Job time : 60 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model1

Run on: January 21, 2004, 06:47:52 : Search time 154 Seconds
(without alignments)
366.209 Million cell updates/sec

Title: US-09-423-035B-121

Perfect score: 16

Sequence: 1 rgcgtactacacga 16

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2324096 seqs, 1762381658 residues

Total number of hits satisfying chosen parameters: 1462038

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.6	97.5	16	10	US-09-877-526A-21
2	15.6	97.5	16	10	US-09-864-116B-15
3	15.6	97.5	16	10	US-09-864-785-3928
4	15.6	97.5	16	11	US-09-992-160-21
5	15.6	97.5	16	11	US-09-730-289B-3896
6	15.6	97.5	16	11	US-09-780-533A-6679
7	15.6	97.5	16	11	US-09-877-478-6585
8	15.6	97.5	16	11	US-09-848-754A-9645
9	15.6	97.5	16	11	US-09-776-474-2991
10	15.6	97.5	16	11	US-09-930-423-4543
11	15.6	97.5	16	11	US-09-780-164-2602
12	15.6	97.5	16	11	US-09-827-395A-2617
13	15.6	97.5	16	12	US-10-366-191-14
14	15.6	97.5	16	12	US-10-435-044A-19
15	15.6	97.5	16	12	US-10-435-044A-20

16	15.6	97.5	16	13	US-09-745-237A-4549	Sequence 4549, Ap
17	15.6	97.5	16	13	US-09-792-818-2304	Sequence 2304, Ap
18	15.6	97.5	16	13	US-10-279-401-11	Sequence 11, Appl
19	15.6	97.5	16	13	US-10-201-389A-13	Sequence 13, Appl
20	15.6	97.5	16	13	US-10-238-700-4666	Sequence 4666, Ap
21	15.6	97.5	16	13	US-10-277-494-445	Sequence 445, Appl
22	15.6	97.5	16	13	US-10-230-006-2677	Sequence 2677, Ap
23	15.6	97.5	16	13	US-10-306-747A-11	Sequence 11, Appl
24	15.6	97.5	16	15	US-10-151-116-12	Sequence 12, Appl
25	15.6	97.5	16	15	US-10-163-552-1997	Sequence 1997, Ap
26	15.6	97.5	16	15	US-10-156-306-8013	Sequence 8013, Ap
27	15.6	97.5	16	16	US-10-157-580A-170	Sequence 170, Appl
28	15.6	97.5	16	16	US-10-201-394A-13	Sequence 13, Appl
29	15.6	97.5	23	13	US-10-277-494-334	Sequence 334, Appl
30	15.6	97.5	23	13	US-10-277-494-335	Sequence 335, Appl
31	15.6	97.5	23	13	US-10-277-494-336	Sequence 336, Appl
32	15.6	97.5	23	13	US-10-277-494-337	Sequence 337, Appl
33	15.6	97.5	23	13	US-10-277-494-338	Sequence 338, Appl
34	15.6	97.5	23	13	US-10-277-494-339	Sequence 339, Appl
35	15.6	97.5	23	13	US-10-277-494-340	Sequence 340, Appl
36	15.6	97.5	23	13	US-10-277-494-341	Sequence 341, Appl
37	15.6	97.5	23	13	US-10-277-494-342	Sequence 342, Appl
38	15.6	97.5	23	13	US-10-277-494-343	Sequence 343, Appl
39	15.6	97.5	23	13	US-10-277-494-344	Sequence 344, Appl
40	15.6	97.5	23	13	US-10-277-494-345	Sequence 345, Appl
41	15.6	97.5	23	13	US-10-277-494-346	Sequence 346, Appl
42	15.6	97.5	23	13	US-10-277-494-347	Sequence 347, Appl
43	15.6	97.5	23	13	US-10-277-494-348	Sequence 348, Appl
44	15.6	97.5	23	13	US-10-277-494-349	Sequence 349, Appl
45	15.6	97.5	23	13	US-10-277-494-350	Sequence 350, Appl
46	15.6	97.5	23	13	US-10-277-494-351	Sequence 351, Appl
47	15.6	97.5	23	13	US-10-277-494-352	Sequence 352, Appl
48	15.6	97.5	23	13	US-10-277-494-353	Sequence 353, Appl
49	15.6	97.5	23	13	US-10-277-494-354	Sequence 354, Appl
50	15.6	97.5	23	13	US-10-277-494-355	Sequence 355, Appl
51	15.6	97.5	23	13	US-10-277-494-356	Sequence 356, Appl
52	15.6	97.5	23	13	US-10-277-494-357	Sequence 357, Appl
53	15.6	97.5	24	13	US-10-277-494-332	Sequence 332, Appl
54	15.6	97.5	25	13	US-10-277-494-327	Sequence 327, Appl
55	15.6	97.5	25	13	US-10-277-494-328	Sequence 328, Appl
56	15.6	97.5	25	13	US-10-277-494-329	Sequence 329, Appl
57	15.6	97.5	26	13	US-10-277-494-326	Sequence 326, Appl
58	15.6	97.5	27	13	US-10-277-494-322	Sequence 322, Appl
59	15.6	97.5	27	13	US-10-277-494-323	Sequence 323, Appl
60	15.6	97.5	28	15	US-10-163-552-1982	Sequence 1982, Ap
61	15.6	97.5	28	15	US-10-163-552-1984	Sequence 1984, Ap
62	15.6	97.5	29	12	US-10-420-194-706	Sequence 706, Appl
63	15.6	97.5	29	12	US-10-420-194-710	Sequence 710, Appl
64	15.6	97.5	29	12	US-10-420-194-711	Sequence 711, Appl
65	15.6	97.5	29	12	US-10-420-194-712	Sequence 712, Appl
66	15.6	97.5	29	12	US-10-420-194-713	Sequence 713, Appl
67	15.6	97.5	29	12	US-10-420-194-715	Sequence 715, Appl
68	15.6	97.5	29	12	US-10-420-194-716	Sequence 716, Appl
69	15.6	97.5	29	12	US-10-420-194-717	Sequence 717, Appl
70	15.6	97.5	29	12	US-10-420-194-718	Sequence 718, Appl
71	15.6	97.5	29	12	US-10-420-194-732	Sequence 732, Appl
72	15.6	97.5	29	12	US-10-420-194-734	Sequence 734, Appl
73	15.6	97.5	29	12	US-10-420-194-741	Sequence 741, Appl
74	15.6	97.5	29	12	US-10-420-194-742	Sequence 742, Appl
75	15.6	97.5	29	12	US-10-420-194-744	Sequence 744, Appl
76	15.6	97.5	29	12	US-10-420-194-747	Sequence 747, Appl
77	15.6	97.5	29	12	US-10-420-194-748	Sequence 748, Appl
78	15.6	97.5	29	12	US-10-420-194-749	Sequence 749, Appl
79	15.6	97.5	29	12	US-10-420-194-750	Sequence 750, Appl
80	15.6	97.5	29	12	US-10-420-194-751	Sequence 751, Appl
81	15.6	97.5	29	12	US-10-420-194-755	Sequence 755, Appl
82	15.6	97.5	29	12	US-10-420-194-756	Sequence 756, Appl
83	15.6	97.5	29	12	US-10-420-194-757	Sequence 757, Appl
84	15.6	97.5	29	12	US-10-420-194-760	Sequence 760, Appl
85	15.6	97.5	29	12	US-10-420-194-761	Sequence 761, Appl
86	15.6	97.5	29	12	US-10-420-194-763	Sequence 763, Appl
87	15.6	97.5	29	12	US-10-420-194-767	Sequence 767, Appl
88	15.6	97.5	29	12	US-10-420-194-771	Sequence 771, Appl

89	15.6	97.5	29	12	US-10-420-194-774	Sequence 774, App	162	15.6	97.5	30	13	US-09-792-818-2291	Sequence 2291, App
90	15.6	97.5	29	12	US-10-420-194-777	Sequence 777, App	163	15.6	97.5	30	13	US-09-817-879-9597	Sequence 9597, App
91	15.6	97.5	29	12	US-10-420-194-779	Sequence 779, App	164	15.6	97.5	30	13	US-09-817-879-9598	Sequence 9598, App
92	15.6	97.5	29	12	US-10-420-194-781	Sequence 781, App	165	15.6	97.5	30	13	US-09-817-879-9599	Sequence 9599, App
93	15.6	97.5	29	12	US-10-420-194-786	Sequence 786, App	166	15.6	97.5	30	13	US-09-817-879-9600	Sequence 9600, App
94	15.6	97.5	29	12	US-10-420-194-788	Sequence 788, App	167	15.6	97.5	30	13	US-09-817-879-9601	Sequence 9601, App
95	15.6	97.5	29	12	US-10-420-194-792	Sequence 792, App	168	15.6	97.5	30	13	US-09-817-879-9602	Sequence 9602, App
96	15.6	97.5	29	12	US-10-420-194-795	Sequence 795, App	169	15.6	97.5	30	13	US-09-817-879-9603	Sequence 9603, App
97	15.6	97.5	29	12	US-10-420-194-799	Sequence 799, App	170	15.6	97.5	30	13	US-09-817-879-9604	Sequence 9604, App
98	15.6	97.5	29	12	US-10-420-194-804	Sequence 804, App	171	15.6	97.5	30	13	US-09-817-879-9605	Sequence 9605, App
99	15.6	97.5	29	12	US-10-277-494-302	Sequence 302, App	172	15.6	97.5	30	13	US-09-817-879-9606	Sequence 9606, App
100	15.6	97.5	29	13	US-10-277-494-303	Sequence 303, App	173	15.6	97.5	30	15	US-10-122-013-14	Sequence 14, Appl
101	15.6	97.5	29	13	US-10-277-494-304	Sequence 304, App	174	15.6	97.5	30	15	US-10-163-552-1983	Sequence 1983, App
102	15.6	97.5	29	13	US-10-277-494-305	Sequence 305, App	175	15.6	97.5	30	15	US-10-163-552-1985	Sequence 1985, App
103	15.6	97.5	29	13	US-10-277-494-306	Sequence 306, App	176	15.6	97.5	30	15	US-10-163-552-1986	Sequence 1986, App
104	15.6	97.5	29	13	US-10-277-494-307	Sequence 307, App	177	15.6	97.5	30	15	US-10-156-306-7919	Sequence 7919, App
105	15.6	97.5	29	13	US-10-277-494-308	Sequence 308, App	178	15.6	97.5	30	15	US-10-156-306-7920	Sequence 7920, App
106	15.6	97.5	29	13	US-10-277-494-309	Sequence 309, App	179	15.6	97.5	30	15	US-10-156-306-7921	Sequence 7921, App
107	15.6	97.5	29	13	US-10-277-494-310	Sequence 310, App	180	15.6	97.5	30	15	US-10-156-306-7922	Sequence 7922, App
108	15.6	97.5	29	13	US-10-277-494-311	Sequence 311, App	181	15.6	97.5	30	15	US-10-156-306-7923	Sequence 7923, App
109	15.6	97.5	29	13	US-10-277-494-312	Sequence 312, App	182	15.6	97.5	30	15	US-10-156-306-7924	Sequence 7924, App
110	15.6	97.5	29	13	US-10-277-494-313	Sequence 313, App	183	15.6	97.5	30	15	US-10-156-306-7925	Sequence 7925, App
111	15.6	97.5	29	13	US-10-277-494-314	Sequence 314, App	184	15.6	97.5	30	15	US-10-156-306-7926	Sequence 7926, App
112	15.6	97.5	29	13	US-10-277-494-315	Sequence 315, App	185	15.6	97.5	30	15	US-10-156-306-7927	Sequence 7927, App
113	15.6	97.5	29	13	US-10-277-494-316	Sequence 316, App	186	15.6	97.5	30	15	US-10-156-306-7928	Sequence 7928, App
114	15.6	97.5	29	13	US-10-277-494-317	Sequence 317, App	187	15.6	97.5	31	9	US-09-813-380-9	Sequence 9, Appl
115	15.6	97.5	29	13	US-10-277-494-318	Sequence 318, App	188	15.6	97.5	31	10	US-09-864-785-2151	Sequence 2151, App
116	15.6	97.5	29	13	US-10-277-494-319	Sequence 319, App	189	15.6	97.5	31	10	US-09-864-785-2152	Sequence 2152, App
117	15.6	97.5	29	13	US-10-277-494-320	Sequence 320, App	190	15.6	97.5	31	10	US-09-864-785-2153	Sequence 2153, App
118	15.6	97.5	29	15	US-10-122-013-2	Sequence 2, Appl	191	15.6	97.5	31	10	US-09-864-785-2154	Sequence 2154, App
119	15.6	97.5	29	15	US-10-122-013-3	Sequence 3, Appl	192	15.6	97.5	31	10	US-09-864-785-2155	Sequence 2155, App
120	15.6	97.5	29	15	US-10-122-013-4	Sequence 4, Appl	193	15.6	97.5	31	10	US-09-864-785-2156	Sequence 2156, App
121	15.6	97.5	29	15	US-10-122-013-5	Sequence 5, Appl	194	15.6	97.5	31	10	US-09-864-785-2157	Sequence 2157, App
122	15.6	97.5	29	15	US-10-122-013-6	Sequence 6, Appl	195	15.6	97.5	31	10	US-09-864-785-2158	Sequence 2158, App
123	15.6	97.5	29	15	US-10-122-013-7	Sequence 7, Appl	196	15.6	97.5	31	10	US-09-864-785-2159	Sequence 2159, App
124	15.6	97.5	29	15	US-10-122-013-8	Sequence 8, Appl	197	15.6	97.5	31	10	US-09-864-785-2160	Sequence 2160, App
125	15.6	97.5	29	15	US-10-122-013-9	Sequence 9, Appl	198	15.6	97.5	31	10	US-09-864-785-2161	Sequence 2161, App
126	15.6	97.5	29	15	US-10-122-013-10	Sequence 10, Appl	199	15.6	97.5	31	10	US-09-864-785-2162	Sequence 2162, App
127	15.6	97.5	29	15	US-10-122-013-11	Sequence 11, Appl	200	15.6	97.5	31	10	US-09-864-785-2163	Sequence 2163, App
128	15.6	97.5	29	15	US-10-122-013-12	Sequence 12, Appl	201	15.6	97.5	31	10	US-09-864-785-2164	Sequence 2164, App
129	15.6	97.5	29	15	US-10-122-013-13	Sequence 13, Appl	202	15.6	97.5	31	10	US-09-864-785-2165	Sequence 2165, App
130	15.6	97.5	29	15	US-10-122-013-15	Sequence 15, Appl	203	15.6	97.5	31	10	US-09-864-785-2166	Sequence 2166, App
131	15.6	97.5	29	15	US-10-122-013-16	Sequence 16, Appl	204	15.6	97.5	31	10	US-09-864-785-2167	Sequence 2167, App
132	15.6	97.5	29	15	US-10-157-580A-149	Sequence 149, App	205	15.6	97.5	31	10	US-09-864-785-2168	Sequence 2168, App
133	15.6	97.5	29	15	US-10-157-580A-150	Sequence 150, App	206	15.6	97.5	31	10	US-09-864-785-2169	Sequence 2169, App
134	15.6	97.5	29	15	US-10-157-580A-151	Sequence 151, App	207	15.6	97.5	31	10	US-09-864-785-2170	Sequence 2170, App
135	15.6	97.5	29	15	US-10-157-580A-152	Sequence 152, App	208	15.6	97.5	31	10	US-09-864-785-2171	Sequence 2171, App
136	15.6	97.5	29	15	US-10-157-580A-153	Sequence 153, App	209	15.6	97.5	31	10	US-09-864-785-2172	Sequence 2172, App
137	15.6	97.5	30	10	US-09-864-785-3908	Sequence 3908, App	210	15.6	97.5	31	10	US-09-864-785-2173	Sequence 2173, App
138	15.6	97.5	30	10	US-09-864-785-3909	Sequence 3909, App	211	15.6	97.5	31	10	US-09-864-785-2174	Sequence 2174, App
139	15.6	97.5	30	10	US-09-864-785-3910	Sequence 3910, App	212	15.6	97.5	31	10	US-09-864-785-2175	Sequence 2175, App
140	15.6	97.5	30	10	US-09-864-785-3911	Sequence 3911, App	213	15.6	97.5	31	10	US-09-864-785-2176	Sequence 2176, App
141	15.6	97.5	30	10	US-09-864-785-3912	Sequence 3912, App	214	15.6	97.5	31	10	US-09-864-785-2177	Sequence 2177, App
142	15.6	97.5	30	11	US-09-725-926A-7	Sequence 7, Appl	215	15.6	97.5	31	10	US-09-864-785-2178	Sequence 2178, App
143	15.6	97.5	30	11	US-09-877-478-6567	Sequence 6567, App	216	15.6	97.5	31	10	US-09-864-785-2179	Sequence 2179, App
144	15.6	97.5	30	11	US-09-877-478-6568	Sequence 6568, App	217	15.6	97.5	31	10	US-09-864-785-2180	Sequence 2180, App
145	15.6	97.5	30	11	US-09-877-478-6569	Sequence 6569, App	218	15.6	97.5	31	10	US-09-864-785-2181	Sequence 2181, App
146	15.6	97.5	30	11	US-09-877-478-6570	Sequence 6570, App	219	15.6	97.5	31	10	US-09-864-785-2182	Sequence 2182, App
147	15.6	97.5	30	11	US-09-877-478-6571	Sequence 6571, App	220	15.6	97.5	31	10	US-09-864-785-2183	Sequence 2183, App
148	15.6	97.5	30	11	US-09-740-332-9597	Sequence 9597, App	221	15.6	97.5	31	10	US-09-864-785-2184	Sequence 2184, App
149	15.6	97.5	30	11	US-09-740-332-9598	Sequence 9598, App	222	15.6	97.5	31	10	US-09-864-785-2185	Sequence 2185, App
150	15.6	97.5	30	11	US-09-740-332-9599	Sequence 9599, App	223	15.6	97.5	31	10	US-09-864-785-2186	Sequence 2186, App
151	15.6	97.5	30	11	US-09-740-332-9600	Sequence 9600, App	224	15.6	97.5	31	10	US-09-864-785-2187	Sequence 2187, App
152	15.6	97.5	30	11	US-09-740-332-9601	Sequence 9601, App	225	15.6	97.5	31	10	US-09-864-785-2188	Sequence 2188, App
153	15.6	97.5	30	11	US-09-740-332-9602	Sequence 9602, App	226	15.6	97.5	31	10	US-09-864-785-2189	Sequence 2189, App
154	15.6	97.5	30	11	US-09-740-332-9603	Sequence 9603, App	227	15.6	97.5	31	10	US-09-864-785-2190	Sequence 2190, App
155	15.6	97.5	30	11	US-09-740-332-9604	Sequence 9604, App	228	15.6	97.5	31	10	US-09-864-785-2191	Sequence 2191, App
156	15.6	97.5	30	11	US-09-740-332-9605	Sequence 9605, App	229	15.6	97.5	31	10	US-09-864-785-2192	Sequence 2192, App
157	15.6	97.5	30	11	US-09-740-332-9606	Sequence 9606, App	230	15.6	97.5	31	10	US-09-864-785-2193	Sequence 2193, App
158	15.6	97.5	30	13	US-09-792-818-2287	Sequence 2287, App	231	15.6	97.5	31	10	US-09-864-785-2194	Sequence 2194, App
159	15.6	97.5	30	13	US-09-792-818-2288	Sequence 2288, App	232	15.6	97.5	31	10	US-09-864-785-2195	Sequence 2195, App
160	15.6	97.5	30	13	US-09-792-818-2289	Sequence 2289, App	233	15.6	97.5	31	10	US-09-864-785-2196	Sequence 2196, App
161	15.6	97.5	30	13	US-09-792-818-2290	Sequence 2290, App	234	15.6	97.5	31	10	US-09-864-785-2197	Sequence 2197, App

235	15.6	97.5	31	10	US-09-864-785-2198	Sequence 2198, Ap	308	15.6	97.5	31	10	US-09-864-785-2271	Sequence 2271, Ap
236	15.6	97.5	31	10	US-09-864-785-2199	Sequence 2199, Ap	309	15.6	97.5	31	10	US-09-864-785-2272	Sequence 2272, Ap
237	15.6	97.5	31	10	US-09-864-785-2200	Sequence 2200, Ap	310	15.6	97.5	31	10	US-09-864-785-2273	Sequence 2273, Ap
238	15.6	97.5	31	10	US-09-864-785-2201	Sequence 2201, Ap	311	15.6	97.5	31	10	US-09-864-785-2274	Sequence 2274, Ap
239	15.6	97.5	31	10	US-09-864-785-2202	Sequence 2202, Ap	312	15.6	97.5	31	10	US-09-864-785-2275	Sequence 2275, Ap
240	15.6	97.5	31	10	US-09-864-785-2203	Sequence 2203, Ap	313	15.6	97.5	31	10	US-09-864-785-2276	Sequence 2276, Ap
241	15.6	97.5	31	10	US-09-864-785-2204	Sequence 2204, Ap	314	15.6	97.5	31	10	US-09-864-785-2277	Sequence 2277, Ap
242	15.6	97.5	31	10	US-09-864-785-2205	Sequence 2205, Ap	315	15.6	97.5	31	10	US-09-864-785-2278	Sequence 2278, Ap
243	15.6	97.5	31	10	US-09-864-785-2206	Sequence 2206, Ap	316	15.6	97.5	31	10	US-09-864-785-2279	Sequence 2279, Ap
244	15.6	97.5	31	10	US-09-864-785-2207	Sequence 2207, Ap	317	15.6	97.5	31	10	US-09-864-785-2280	Sequence 2280, Ap
245	15.6	97.5	31	10	US-09-864-785-2208	Sequence 2208, Ap	318	15.6	97.5	31	10	US-09-864-785-2281	Sequence 2281, Ap
246	15.6	97.5	31	10	US-09-864-785-2209	Sequence 2209, Ap	319	15.6	97.5	31	10	US-09-864-785-2282	Sequence 2282, Ap
247	15.6	97.5	31	10	US-09-864-785-2210	Sequence 2210, Ap	320	15.6	97.5	31	10	US-09-864-785-2283	Sequence 2283, Ap
248	15.6	97.5	31	10	US-09-864-785-2211	Sequence 2211, Ap	321	15.6	97.5	31	10	US-09-864-785-2284	Sequence 2284, Ap
249	15.6	97.5	31	10	US-09-864-785-2212	Sequence 2212, Ap	322	15.6	97.5	31	10	US-09-864-785-2285	Sequence 2285, Ap
250	15.6	97.5	31	10	US-09-864-785-2213	Sequence 2213, Ap	323	15.6	97.5	31	10	US-09-864-785-2286	Sequence 2286, Ap
251	15.6	97.5	31	10	US-09-864-785-2214	Sequence 2214, Ap	324	15.6	97.5	31	10	US-09-864-785-2287	Sequence 2287, Ap
252	15.6	97.5	31	10	US-09-864-785-2215	Sequence 2215, Ap	325	15.6	97.5	31	10	US-09-864-785-2288	Sequence 2288, Ap
253	15.6	97.5	31	10	US-09-864-785-2216	Sequence 2216, Ap	326	15.6	97.5	31	10	US-09-864-785-2289	Sequence 2289, Ap
254	15.6	97.5	31	10	US-09-864-785-2217	Sequence 2217, Ap	327	15.6	97.5	31	10	US-09-864-785-2290	Sequence 2290, Ap
255	15.6	97.5	31	10	US-09-864-785-2218	Sequence 2218, Ap	328	15.6	97.5	31	10	US-09-864-785-2291	Sequence 2291, Ap
256	15.6	97.5	31	10	US-09-864-785-2219	Sequence 2219, Ap	329	15.6	97.5	31	10	US-09-864-785-2292	Sequence 2292, Ap
257	15.6	97.5	31	10	US-09-864-785-2220	Sequence 2220, Ap	330	15.6	97.5	31	10	US-09-864-785-2293	Sequence 2293, Ap
258	15.6	97.5	31	10	US-09-864-785-2221	Sequence 2221, Ap	331	15.6	97.5	31	10	US-09-864-785-2294	Sequence 2294, Ap
259	15.6	97.5	31	10	US-09-864-785-2222	Sequence 2222, Ap	332	15.6	97.5	31	10	US-09-864-785-2295	Sequence 2295, Ap
260	15.6	97.5	31	10	US-09-864-785-2223	Sequence 2223, Ap	333	15.6	97.5	31	10	US-09-864-785-2296	Sequence 2296, Ap
261	15.6	97.5	31	10	US-09-864-785-2224	Sequence 2224, Ap	334	15.6	97.5	31	10	US-09-864-785-2297	Sequence 2297, Ap
262	15.6	97.5	31	10	US-09-864-785-2225	Sequence 2225, Ap	335	15.6	97.5	31	10	US-09-864-785-2298	Sequence 2298, Ap
263	15.6	97.5	31	10	US-09-864-785-2226	Sequence 2226, Ap	336	15.6	97.5	31	10	US-09-864-785-2299	Sequence 2299, Ap
264	15.6	97.5	31	10	US-09-864-785-2227	Sequence 2227, Ap	337	15.6	97.5	31	10	US-09-864-785-2300	Sequence 2300, Ap
265	15.6	97.5	31	10	US-09-864-785-2228	Sequence 2228, Ap	338	15.6	97.5	31	10	US-09-864-785-2301	Sequence 2301, Ap
266	15.6	97.5	31	10	US-09-864-785-2229	Sequence 2229, Ap	339	15.6	97.5	31	10	US-09-864-785-2302	Sequence 2302, Ap
267	15.6	97.5	31	10	US-09-864-785-2230	Sequence 2230, Ap	340	15.6	97.5	31	10	US-09-864-785-2303	Sequence 2303, Ap
268	15.6	97.5	31	10	US-09-864-785-2231	Sequence 2231, Ap	341	15.6	97.5	31	10	US-09-864-785-2304	Sequence 2304, Ap
269	15.6	97.5	31	10	US-09-864-785-2232	Sequence 2232, Ap	342	15.6	97.5	31	10	US-09-864-785-2305	Sequence 2305, Ap
270	15.6	97.5	31	10	US-09-864-785-2233	Sequence 2233, Ap	343	15.6	97.5	31	10	US-09-864-785-2306	Sequence 2306, Ap
271	15.6	97.5	31	10	US-09-864-785-2234	Sequence 2234, Ap	344	15.6	97.5	31	10	US-09-864-785-2307	Sequence 2307, Ap
272	15.6	97.5	31	10	US-09-864-785-2235	Sequence 2235, Ap	345	15.6	97.5	31	10	US-09-864-785-2308	Sequence 2308, Ap
273	15.6	97.5	31	10	US-09-864-785-2236	Sequence 2236, Ap	346	15.6	97.5	31	10	US-09-864-785-2309	Sequence 2309, Ap
274	15.6	97.5	31	10	US-09-864-785-2237	Sequence 2237, Ap	347	15.6	97.5	31	10	US-09-864-785-2310	Sequence 2310, Ap
275	15.6	97.5	31	10	US-09-864-785-2238	Sequence 2238, Ap	348	15.6	97.5	31	10	US-09-864-785-2311	Sequence 2311, Ap
276	15.6	97.5	31	10	US-09-864-785-2239	Sequence 2239, Ap	349	15.6	97.5	31	10	US-09-864-785-2312	Sequence 2312, Ap
277	15.6	97.5	31	10	US-09-864-785-2240	Sequence 2240, Ap	350	15.6	97.5	31	10	US-09-864-785-2313	Sequence 2313, Ap
278	15.6	97.5	31	10	US-09-864-785-2241	Sequence 2241, Ap	351	15.6	97.5	31	10	US-09-864-785-2314	Sequence 2314, Ap
279	15.6	97.5	31	10	US-09-864-785-2242	Sequence 2242, Ap	352	15.6	97.5	31	10	US-09-864-785-2315	Sequence 2315, Ap
280	15.6	97.5	31	10	US-09-864-785-2243	Sequence 2243, Ap	353	15.6	97.5	31	10	US-09-864-785-2316	Sequence 2316, Ap
281	15.6	97.5	31	10	US-09-864-785-2244	Sequence 2244, Ap	354	15.6	97.5	31	10	US-09-864-785-2317	Sequence 2317, Ap
282	15.6	97.5	31	10	US-09-864-785-2245	Sequence 2245, Ap	355	15.6	97.5	31	10	US-09-864-785-2318	Sequence 2318, Ap
283	15.6	97.5	31	10	US-09-864-785-2246	Sequence 2246, Ap	356	15.6	97.5	31	10	US-09-864-785-2319	Sequence 2319, Ap
284	15.6	97.5	31	10	US-09-864-785-2247	Sequence 2247, Ap	357	15.6	97.5	31	10	US-09-864-785-2320	Sequence 2320, Ap
285	15.6	97.5	31	10	US-09-864-785-2248	Sequence 2248, Ap	358	15.6	97.5	31	10	US-09-864-785-2321	Sequence 2321, Ap
286	15.6	97.5	31	10	US-09-864-785-2249	Sequence 2249, Ap	359	15.6	97.5	31	10	US-09-864-785-2322	Sequence 2322, Ap
287	15.6	97.5	31	10	US-09-864-785-2250	Sequence 2250, Ap	360	15.6	97.5	31	10	US-09-864-785-2323	Sequence 2323, Ap
288	15.6	97.5	31	10	US-09-864-785-2251	Sequence 2251, Ap	361	15.6	97.5	31	10	US-09-864-785-2324	Sequence 2324, Ap
289	15.6	97.5	31	10	US-09-864-785-2252	Sequence 2252, Ap	362	15.6	97.5	31	10	US-09-864-785-2325	Sequence 2325, Ap
290	15.6	97.5	31	10	US-09-864-785-2253	Sequence 2253, Ap	363	15.6	97.5	31	10	US-09-864-785-2326	Sequence 2326, Ap
291	15.6	97.5	31	10	US-09-864-785-2254	Sequence 2254, Ap	364	15.6	97.5	31	10	US-09-864-785-2327	Sequence 2327, Ap
292	15.6	97.5	31	10	US-09-864-785-2255	Sequence 2255, Ap	365	15.6	97.5	31	10	US-09-864-785-2328	Sequence 2328, Ap
293	15.6	97.5	31	10	US-09-864-785-2256	Sequence 2256, Ap	366	15.6	97.5	31	10	US-09-864-785-2329	Sequence 2329, Ap
294	15.6	97.5	31	10	US-09-864-785-2257	Sequence 2257, Ap	367	15.6	97.5	31	10	US-09-864-785-2330	Sequence 2330, Ap
295	15.6	97.5	31	10	US-09-864-785-2258	Sequence 2258, Ap	368	15.6	97.5	31	10	US-09-864-785-2331	Sequence 2331, Ap
296	15.6	97.5	31	10	US-09-864-785-2259	Sequence 2259, Ap	369	15.6	97.5	31	10	US-09-864-785-2332	Sequence 2332, Ap
297	15.6	97.5	31	10	US-09-864-785-2260	Sequence 2260, Ap	370	15.6	97.5	31	10	US-09-864-785-2333	Sequence 2333, Ap
298	15.6	97.5	31	10	US-09-864-785-2261	Sequence 2261, Ap	371	15.6	97.5	31	10	US-09-864-785-2334	Sequence 2334, Ap
299	15.6	97.5	31	10	US-09-864-785-2262	Sequence 2262, Ap	372	15.6	97.5	31	10	US-09-864-785-2335	Sequence 2335, Ap
300	15.6	97.5	31	10	US-09-864-785-2263	Sequence 2263, Ap	373	15.6	97.5	31	10	US-09-864-785-2336	Sequence 2336, Ap
301	15.6	97.5	31	10	US-09-864-785-2264	Sequence 2264, Ap	374	15.6	97.5	31	10	US-09-864-785-2337	Sequence 2337, Ap
302	15.6	97.5	31	10	US-09-864-785-2265	Sequence 2265, Ap	375	15.6	97.5	31	10	US-09-864-785-2338	Sequence 2338, Ap
303	15.6	97.5	31	10	US-09-864-785-2266	Sequence 2266, Ap	376	15.6	97.5	31	10	US-09-864-785-2339	Sequence 2339, Ap
304	15.6	97.5	31	10	US-09-864-785-2267	Sequence 2267, Ap	377	15.6	97.5	31	10	US-09-864-785-2340	Sequence 2340, Ap
305	15.6	97.5	31	10	US-09-864-785-2268	Sequence 2268, Ap	378	15.6	97.5	31	10	US-09-864-785-2341	Sequence 2341, Ap
306	15.6	97.5	31	10	US-09-864-785-2269	Sequence 2269, Ap	379	15.6	97.5	31	10	US-09-864-785-2342	Sequence 2342, Ap
307	15.6	97.5	31	10	US-09-864-785-2270	Sequence 2270, Ap	380	15.6	97.5	31	10	US-09-864-785-2343	Sequence 2343, Ap

381	15.6	97.5	31	10	US-09-864-785-2344	Sequence 2344, Ap	454	15.6	97.5	31	10	US-09-864-785-2417	Sequence 2417, Ap
382	15.6	97.5	31	10	US-09-864-785-2345	Sequence 2345, Ap	455	15.6	97.5	31	10	US-09-864-785-2418	Sequence 2418, Ap
383	15.6	97.5	31	10	US-09-864-785-2346	Sequence 2346, Ap	456	15.6	97.5	31	10	US-09-864-785-2419	Sequence 2419, Ap
384	15.6	97.5	31	10	US-09-864-785-2347	Sequence 2347, Ap	457	15.6	97.5	31	10	US-09-864-785-2420	Sequence 2420, Ap
385	15.6	97.5	31	10	US-09-864-785-2348	Sequence 2348, Ap	458	15.6	97.5	31	10	US-09-864-785-2421	Sequence 2421, Ap
386	15.6	97.5	31	10	US-09-864-785-2349	Sequence 2349, Ap	459	15.6	97.5	31	10	US-09-864-785-2422	Sequence 2422, Ap
387	15.6	97.5	31	10	US-09-864-785-2350	Sequence 2350, Ap	460	15.6	97.5	31	10	US-09-864-785-2423	Sequence 2423, Ap
388	15.6	97.5	31	10	US-09-864-785-2351	Sequence 2351, Ap	461	15.6	97.5	31	10	US-09-864-785-2424	Sequence 2424, Ap
389	15.6	97.5	31	10	US-09-864-785-2352	Sequence 2352, Ap	462	15.6	97.5	31	10	US-09-864-785-2425	Sequence 2425, Ap
390	15.6	97.5	31	10	US-09-864-785-2353	Sequence 2353, Ap	463	15.6	97.5	31	10	US-09-864-785-2426	Sequence 2426, Ap
391	15.6	97.5	31	10	US-09-864-785-2354	Sequence 2354, Ap	464	15.6	97.5	31	10	US-09-864-785-2427	Sequence 2427, Ap
392	15.6	97.5	31	10	US-09-864-785-2355	Sequence 2355, Ap	465	15.6	97.5	31	10	US-09-864-785-2428	Sequence 2428, Ap
393	15.6	97.5	31	10	US-09-864-785-2356	Sequence 2356, Ap	466	15.6	97.5	31	10	US-09-864-785-2429	Sequence 2429, Ap
394	15.6	97.5	31	10	US-09-864-785-2357	Sequence 2357, Ap	467	15.6	97.5	31	10	US-09-864-785-2430	Sequence 2430, Ap
395	15.6	97.5	31	10	US-09-864-785-2358	Sequence 2358, Ap	468	15.6	97.5	31	10	US-09-864-785-2431	Sequence 2431, Ap
396	15.6	97.5	31	10	US-09-864-785-2359	Sequence 2359, Ap	469	15.6	97.5	31	10	US-09-864-785-2432	Sequence 2432, Ap
397	15.6	97.5	31	10	US-09-864-785-2360	Sequence 2360, Ap	470	15.6	97.5	31	10	US-09-864-785-2433	Sequence 2433, Ap
398	15.6	97.5	31	10	US-09-864-785-2361	Sequence 2361, Ap	471	15.6	97.5	31	10	US-09-864-785-2434	Sequence 2434, Ap
399	15.6	97.5	31	10	US-09-864-785-2362	Sequence 2362, Ap	472	15.6	97.5	31	10	US-09-864-785-2435	Sequence 2435, Ap
400	15.6	97.5	31	10	US-09-864-785-2363	Sequence 2363, Ap	473	15.6	97.5	31	10	US-09-864-785-2436	Sequence 2436, Ap
401	15.6	97.5	31	10	US-09-864-785-2364	Sequence 2364, Ap	474	15.6	97.5	31	10	US-09-864-785-2437	Sequence 2437, Ap
402	15.6	97.5	31	10	US-09-864-785-2365	Sequence 2365, Ap	475	15.6	97.5	31	10	US-09-864-785-2438	Sequence 2438, Ap
403	15.6	97.5	31	10	US-09-864-785-2366	Sequence 2366, Ap	476	15.6	97.5	31	10	US-09-864-785-2439	Sequence 2439, Ap
404	15.6	97.5	31	10	US-09-864-785-2367	Sequence 2367, Ap	477	15.6	97.5	31	10	US-09-864-785-2440	Sequence 2440, Ap
405	15.6	97.5	31	10	US-09-864-785-2368	Sequence 2368, Ap	478	15.6	97.5	31	10	US-09-864-785-2441	Sequence 2441, Ap
406	15.6	97.5	31	10	US-09-864-785-2369	Sequence 2369, Ap	479	15.6	97.5	31	10	US-09-864-785-2442	Sequence 2442, Ap
407	15.6	97.5	31	10	US-09-864-785-2370	Sequence 2370, Ap	480	15.6	97.5	31	10	US-09-864-785-2443	Sequence 2443, Ap
408	15.6	97.5	31	10	US-09-864-785-2371	Sequence 2371, Ap	481	15.6	97.5	31	10	US-09-864-785-2444	Sequence 2444, Ap
409	15.6	97.5	31	10	US-09-864-785-2372	Sequence 2372, Ap	482	15.6	97.5	31	10	US-09-864-785-2445	Sequence 2445, Ap
410	15.6	97.5	31	10	US-09-864-785-2373	Sequence 2373, Ap	483	15.6	97.5	31	10	US-09-864-785-2446	Sequence 2446, Ap
411	15.6	97.5	31	10	US-09-864-785-2374	Sequence 2374, Ap	484	15.6	97.5	31	10	US-09-864-785-2447	Sequence 2447, Ap
412	15.6	97.5	31	10	US-09-864-785-2375	Sequence 2375, Ap	485	15.6	97.5	31	10	US-09-864-785-2448	Sequence 2448, Ap
413	15.6	97.5	31	10	US-09-864-785-2376	Sequence 2376, Ap	486	15.6	97.5	31	10	US-09-864-785-2449	Sequence 2449, Ap
414	15.6	97.5	31	10	US-09-864-785-2377	Sequence 2377, Ap	487	15.6	97.5	31	10	US-09-864-785-2450	Sequence 2450, Ap
415	15.6	97.5	31	10	US-09-864-785-2378	Sequence 2378, Ap	488	15.6	97.5	31	10	US-09-864-785-2451	Sequence 2451, Ap
416	15.6	97.5	31	10	US-09-864-785-2379	Sequence 2379, Ap	489	15.6	97.5	31	10	US-09-864-785-2452	Sequence 2452, Ap
417	15.6	97.5	31	10	US-09-864-785-2380	Sequence 2380, Ap	490	15.6	97.5	31	10	US-09-864-785-2453	Sequence 2453, Ap
418	15.6	97.5	31	10	US-09-864-785-2381	Sequence 2381, Ap	491	15.6	97.5	31	10	US-09-864-785-2454	Sequence 2454, Ap
419	15.6	97.5	31	10	US-09-864-785-2382	Sequence 2382, Ap	492	15.6	97.5	31	10	US-09-864-785-2455	Sequence 2455, Ap
420	15.6	97.5	31	10	US-09-864-785-2383	Sequence 2383, Ap	493	15.6	97.5	31	10	US-09-864-785-2456	Sequence 2456, Ap
421	15.6	97.5	31	10	US-09-864-785-2384	Sequence 2384, Ap	494	15.6	97.5	31	10	US-09-864-785-2457	Sequence 2457, Ap
422	15.6	97.5	31	10	US-09-864-785-2385	Sequence 2385, Ap	495	15.6	97.5	31	10	US-09-864-785-2458	Sequence 2458, Ap
423	15.6	97.5	31	10	US-09-864-785-2386	Sequence 2386, Ap	496	15.6	97.5	31	10	US-09-864-785-2459	Sequence 2459, Ap
424	15.6	97.5	31	10	US-09-864-785-2387	Sequence 2387, Ap	497	15.6	97.5	31	10	US-09-864-785-2460	Sequence 2460, Ap
425	15.6	97.5	31	10	US-09-864-785-2388	Sequence 2388, Ap	498	15.6	97.5	31	10	US-09-864-785-2461	Sequence 2461, Ap
426	15.6	97.5	31	10	US-09-864-785-2389	Sequence 2389, Ap	499	15.6	97.5	31	10	US-09-864-785-2462	Sequence 2462, Ap
427	15.6	97.5	31	10	US-09-864-785-2390	Sequence 2390, Ap	500	15.6	97.5	31	10	US-09-864-785-2463	Sequence 2463, Ap
428	15.6	97.5	31	10	US-09-864-785-2391	Sequence 2391, Ap	501	15.6	97.5	31	10	US-09-864-785-2464	Sequence 2464, Ap
429	15.6	97.5	31	10	US-09-864-785-2392	Sequence 2392, Ap	502	15.6	97.5	31	10	US-09-864-785-2465	Sequence 2465, Ap
430	15.6	97.5	31	10	US-09-864-785-2393	Sequence 2393, Ap	503	15.6	97.5	31	10	US-09-864-785-2466	Sequence 2466, Ap
431	15.6	97.5	31	10	US-09-864-785-2394	Sequence 2394, Ap	504	15.6	97.5	31	10	US-09-864-785-2467	Sequence 2467, Ap
432	15.6	97.5	31	10	US-09-864-785-2395	Sequence 2395, Ap	505	15.6	97.5	31	10	US-09-864-785-2468	Sequence 2468, Ap
433	15.6	97.5	31	10	US-09-864-785-2396	Sequence 2396, Ap	506	15.6	97.5	31	10	US-09-864-785-2469	Sequence 2469, Ap
434	15.6	97.5	31	10	US-09-864-785-2397	Sequence 2397, Ap	507	15.6	97.5	31	10	US-09-864-785-2470	Sequence 2470, Ap
435	15.6	97.5	31	10	US-09-864-785-2398	Sequence 2398, Ap	508	15.6	97.5	31	10	US-09-864-785-2471	Sequence 2471, Ap
436	15.6	97.5	31	10	US-09-864-785-2399	Sequence 2399, Ap	509	15.6	97.5	31	10	US-09-864-785-2472	Sequence 2472, Ap
437	15.6	97.5	31	10	US-09-864-785-2400	Sequence 2400, Ap	510	15.6	97.5	31	10	US-09-864-785-2473	Sequence 2473, Ap
438	15.6	97.5	31	10	US-09-864-785-2401	Sequence 2401, Ap	511	15.6	97.5	31	10	US-09-864-785-2474	Sequence 2474, Ap
439	15.6	97.5	31	10	US-09-864-785-2402	Sequence 2402, Ap	512	15.6	97.5	31	10	US-09-864-785-2475	Sequence 2475, Ap
440	15.6	97.5	31	10	US-09-864-785-2403	Sequence 2403, Ap	513	15.6	97.5	31	10	US-09-864-785-2476	Sequence 2476, Ap
441	15.6	97.5	31	10	US-09-864-785-2404	Sequence 2404, Ap	514	15.6	97.5	31	10	US-09-864-785-2477	Sequence 2477, Ap
442	15.6	97.5	31	10	US-09-864-785-2405	Sequence 2405, Ap	515	15.6	97.5	31	10	US-09-864-785-2478	Sequence 2478, Ap
443	15.6	97.5	31	10	US-09-864-785-2406	Sequence 2406, Ap	516	15.6	97.5	31	10	US-09-864-785-2479	Sequence 2479, Ap
444	15.6	97.5	31	10	US-09-864-785-2407	Sequence 2407, Ap	517	15.6	97.5	31	10	US-09-864-785-2480	Sequence 2480, Ap
445	15.6	97.5	31	10	US-09-864-785-2408	Sequence 2408, Ap	518	15.6	97.5	31	10	US-09-864-785-2481	Sequence 2481, Ap
446	15.6	97.5	31	10	US-09-864-785-2409	Sequence 2409, Ap	519	15.6	97.5	31	10	US-09-864-785-2482	Sequence 2482, Ap
447	15.6	97.5	31	10	US-09-864-785-2410	Sequence 2410, Ap	520	15.6	97.5	31	10	US-09-864-785-2483	Sequence 2483, Ap
448	15.6	97.5	31	10	US-09-864-785-2411	Sequence 2411, Ap	521	15.6	97.5	31	10	US-09-864-785-2484	Sequence 2484, Ap
449	15.6	97.5	31	10	US-09-864-785-2412	Sequence 2412, Ap	522	15.6	97.5	31	10	US-09-864-785-2485	Sequence 2485, Ap
450	15.6	97.5	31	10	US-09-864-785-2413	Sequence 2413, Ap	523	15.6	97.5	31	10	US-09-864-785-2486	Sequence 2486, Ap
451	15.6	97.5	31	10	US-09-864-785-2414	Sequence 2414, Ap	524	15.6	97.5	31	10	US-09-864-785-2487	Sequence 2487, Ap
452	15.6	97.5	31	10	US-09-864-785-2415	Sequence 2415, Ap	525	15.6	97.5	31	10	US-09-864-785-2488	Sequence 2488, Ap
453	15.6	97.5	31	10	US-09-864-785-2416	Sequence 2416, Ap	526	15.6	97.5	31	10	US-09-864-785-2489	Sequence 2489, Ap

527	15.6	97.5	31	10	US-09-864-785-2490	Sequence 2490, Ap	600	15.6	97.5	31	10	US-09-864-785-2563	Sequence 2563, Ap
528	15.6	97.5	31	10	US-09-864-785-2491	Sequence 2491, Ap	601	15.6	97.5	31	10	US-09-864-785-2564	Sequence 2564, Ap
529	15.6	97.5	31	10	US-09-864-785-2492	Sequence 2492, Ap	602	15.6	97.5	31	10	US-09-864-785-2565	Sequence 2565, Ap
530	15.6	97.5	31	10	US-09-864-785-2493	Sequence 2493, Ap	603	15.6	97.5	31	10	US-09-864-785-2566	Sequence 2566, Ap
531	15.6	97.5	31	10	US-09-864-785-2494	Sequence 2494, Ap	604	15.6	97.5	31	10	US-09-864-785-2567	Sequence 2567, Ap
532	15.6	97.5	31	10	US-09-864-785-2495	Sequence 2495, Ap	605	15.6	97.5	31	10	US-09-864-785-2568	Sequence 2568, Ap
533	15.6	97.5	31	10	US-09-864-785-2496	Sequence 2496, Ap	606	15.6	97.5	31	10	US-09-864-785-2569	Sequence 2569, Ap
534	15.6	97.5	31	10	US-09-864-785-2497	Sequence 2497, Ap	607	15.6	97.5	31	10	US-09-864-785-2570	Sequence 2570, Ap
535	15.6	97.5	31	10	US-09-864-785-2498	Sequence 2498, Ap	608	15.6	97.5	31	10	US-09-864-785-2571	Sequence 2571, Ap
536	15.6	97.5	31	10	US-09-864-785-2499	Sequence 2499, Ap	609	15.6	97.5	31	10	US-09-864-785-2572	Sequence 2572, Ap
537	15.6	97.5	31	10	US-09-864-785-2500	Sequence 2500, Ap	610	15.6	97.5	31	10	US-09-864-785-2573	Sequence 2573, Ap
538	15.6	97.5	31	10	US-09-864-785-2501	Sequence 2501, Ap	611	15.6	97.5	31	10	US-09-864-785-2574	Sequence 2574, Ap
539	15.6	97.5	31	10	US-09-864-785-2502	Sequence 2502, Ap	612	15.6	97.5	31	10	US-09-864-785-2575	Sequence 2575, Ap
540	15.6	97.5	31	10	US-09-864-785-2503	Sequence 2503, Ap	613	15.6	97.5	31	10	US-09-864-785-2576	Sequence 2576, Ap
541	15.6	97.5	31	10	US-09-864-785-2504	Sequence 2504, Ap	614	15.6	97.5	31	10	US-09-864-785-2577	Sequence 2577, Ap
542	15.6	97.5	31	10	US-09-864-785-2505	Sequence 2505, Ap	615	15.6	97.5	31	10	US-09-864-785-2578	Sequence 2578, Ap
543	15.6	97.5	31	10	US-09-864-785-2506	Sequence 2506, Ap	616	15.6	97.5	31	10	US-09-864-785-2579	Sequence 2579, Ap
544	15.6	97.5	31	10	US-09-864-785-2507	Sequence 2507, Ap	617	15.6	97.5	31	10	US-09-864-785-2580	Sequence 2580, Ap
545	15.6	97.5	31	10	US-09-864-785-2508	Sequence 2508, Ap	618	15.6	97.5	31	10	US-09-864-785-2581	Sequence 2581, Ap
546	15.6	97.5	31	10	US-09-864-785-2509	Sequence 2509, Ap	619	15.6	97.5	31	10	US-09-864-785-2582	Sequence 2582, Ap
547	15.6	97.5	31	10	US-09-864-785-2510	Sequence 2510, Ap	620	15.6	97.5	31	10	US-09-864-785-2583	Sequence 2583, Ap
548	15.6	97.5	31	10	US-09-864-785-2511	Sequence 2511, Ap	621	15.6	97.5	31	10	US-09-864-785-2584	Sequence 2584, Ap
549	15.6	97.5	31	10	US-09-864-785-2512	Sequence 2512, Ap	622	15.6	97.5	31	10	US-09-864-785-2585	Sequence 2585, Ap
550	15.6	97.5	31	10	US-09-864-785-2513	Sequence 2513, Ap	623	15.6	97.5	31	10	US-09-864-785-2586	Sequence 2586, Ap
551	15.6	97.5	31	10	US-09-864-785-2514	Sequence 2514, Ap	624	15.6	97.5	31	10	US-09-864-785-2587	Sequence 2587, Ap
552	15.6	97.5	31	10	US-09-864-785-2515	Sequence 2515, Ap	625	15.6	97.5	31	10	US-09-864-785-2588	Sequence 2588, Ap
553	15.6	97.5	31	10	US-09-864-785-2516	Sequence 2516, Ap	626	15.6	97.5	31	10	US-09-864-785-2589	Sequence 2589, Ap
554	15.6	97.5	31	10	US-09-864-785-2517	Sequence 2517, Ap	627	15.6	97.5	31	10	US-09-864-785-2590	Sequence 2590, Ap
555	15.6	97.5	31	10	US-09-864-785-2518	Sequence 2518, Ap	628	15.6	97.5	31	10	US-09-864-785-2591	Sequence 2591, Ap
556	15.6	97.5	31	10	US-09-864-785-2519	Sequence 2519, Ap	629	15.6	97.5	31	10	US-09-864-785-2592	Sequence 2592, Ap
557	15.6	97.5	31	10	US-09-864-785-2520	Sequence 2520, Ap	630	15.6	97.5	31	10	US-09-864-785-2593	Sequence 2593, Ap
558	15.6	97.5	31	10	US-09-864-785-2521	Sequence 2521, Ap	631	15.6	97.5	31	10	US-09-864-785-2594	Sequence 2594, Ap
559	15.6	97.5	31	10	US-09-864-785-2522	Sequence 2522, Ap	632	15.6	97.5	31	10	US-09-864-785-2595	Sequence 2595, Ap
560	15.6	97.5	31	10	US-09-864-785-2523	Sequence 2523, Ap	633	15.6	97.5	31	10	US-09-864-785-2596	Sequence 2596, Ap
561	15.6	97.5	31	10	US-09-864-785-2524	Sequence 2524, Ap	634	15.6	97.5	31	10	US-09-864-785-2597	Sequence 2597, Ap
562	15.6	97.5	31	10	US-09-864-785-2525	Sequence 2525, Ap	635	15.6	97.5	31	10	US-09-864-785-2598	Sequence 2598, Ap
563	15.6	97.5	31	10	US-09-864-785-2526	Sequence 2526, Ap	636	15.6	97.5	31	10	US-09-864-785-2599	Sequence 2599, Ap
564	15.6	97.5	31	10	US-09-864-785-2527	Sequence 2527, Ap	637	15.6	97.5	31	10	US-09-864-785-2600	Sequence 2600, Ap
565	15.6	97.5	31	10	US-09-864-785-2528	Sequence 2528, Ap	638	15.6	97.5	31	10	US-09-864-785-2601	Sequence 2601, Ap
566	15.6	97.5	31	10	US-09-864-785-2529	Sequence 2529, Ap	639	15.6	97.5	31	10	US-09-864-785-2602	Sequence 2602, Ap
567	15.6	97.5	31	10	US-09-864-785-2530	Sequence 2530, Ap	640	15.6	97.5	31	10	US-09-864-785-2603	Sequence 2603, Ap
568	15.6	97.5	31	10	US-09-864-785-2531	Sequence 2531, Ap	641	15.6	97.5	31	10	US-09-864-785-2604	Sequence 2604, Ap
569	15.6	97.5	31	10	US-09-864-785-2532	Sequence 2532, Ap	642	15.6	97.5	31	10	US-09-864-785-2605	Sequence 2605, Ap
570	15.6	97.5	31	10	US-09-864-785-2533	Sequence 2533, Ap	643	15.6	97.5	31	10	US-09-864-785-2606	Sequence 2606, Ap
571	15.6	97.5	31	10	US-09-864-785-2534	Sequence 2534, Ap	644	15.6	97.5	31	10	US-09-864-785-2607	Sequence 2607, Ap
572	15.6	97.5	31	10	US-09-864-785-2535	Sequence 2535, Ap	645	15.6	97.5	31	10	US-09-864-785-2608	Sequence 2608, Ap
573	15.6	97.5	31	10	US-09-864-785-2536	Sequence 2536, Ap	646	15.6	97.5	31	10	US-09-864-785-2609	Sequence 2609, Ap
574	15.6	97.5	31	10	US-09-864-785-2537	Sequence 2537, Ap	647	15.6	97.5	31	10	US-09-864-785-2610	Sequence 2610, Ap
575	15.6	97.5	31	10	US-09-864-785-2538	Sequence 2538, Ap	648	15.6	97.5	31	10	US-09-864-785-2611	Sequence 2611, Ap
576	15.6	97.5	31	10	US-09-864-785-2539	Sequence 2539, Ap	649	15.6	97.5	31	10	US-09-864-785-2612	Sequence 2612, Ap
577	15.6	97.5	31	10	US-09-864-785-2540	Sequence 2540, Ap	650	15.6	97.5	31	10	US-09-864-785-2613	Sequence 2613, Ap
578	15.6	97.5	31	10	US-09-864-785-2541	Sequence 2541, Ap	651	15.6	97.5	31	10	US-09-864-785-2614	Sequence 2614, Ap
579	15.6	97.5	31	10	US-09-864-785-2542	Sequence 2542, Ap	652	15.6	97.5	31	10	US-09-864-785-2615	Sequence 2615, Ap
580	15.6	97.5	31	10	US-09-864-785-2543	Sequence 2543, Ap	653	15.6	97.5	31	10	US-09-864-785-2616	Sequence 2616, Ap
581	15.6	97.5	31	10	US-09-864-785-2544	Sequence 2544, Ap	654	15.6	97.5	31	10	US-09-864-785-2617	Sequence 2617, Ap
582	15.6	97.5	31	10	US-09-864-785-2545	Sequence 2545, Ap	655	15.6	97.5	31	10	US-09-864-785-2618	Sequence 2618, Ap
583	15.6	97.5	31	10	US-09-864-785-2546	Sequence 2546, Ap	656	15.6	97.5	31	10	US-09-864-785-2619	Sequence 2619, Ap
584	15.6	97.5	31	10	US-09-864-785-2547	Sequence 2547, Ap	657	15.6	97.5	31	10	US-09-864-785-2620	Sequence 2620, Ap
585	15.6	97.5	31	10	US-09-864-785-2548	Sequence 2548, Ap	658	15.6	97.5	31	10	US-09-864-785-2621	Sequence 2621, Ap
586	15.6	97.5	31	10	US-09-864-785-2549	Sequence 2549, Ap	659	15.6	97.5	31	10	US-09-864-785-2622	Sequence 2622, Ap
587	15.6	97.5	31	10	US-09-864-785-2550	Sequence 2550, Ap	660	15.6	97.5	31	10	US-09-864-785-2623	Sequence 2623, Ap
588	15.6	97.5	31	10	US-09-864-785-2551	Sequence 2551, Ap	661	15.6	97.5	31	10	US-09-864-785-2624	Sequence 2624, Ap
589	15.6	97.5	31	10	US-09-864-785-2552	Sequence 2552, Ap	662	15.6	97.5	31	10	US-09-864-785-2625	Sequence 2625, Ap
590	15.6	97.5	31	10	US-09-864-785-2553	Sequence 2553, Ap	663	15.6	97.5	31	10	US-09-864-785-2626	Sequence 2626, Ap
591	15.6	97.5	31	10	US-09-864-785-2554	Sequence 2554, Ap	664	15.6	97.5	31	10	US-09-864-785-2627	Sequence 2627, Ap
592	15.6	97.5	31	10	US-09-864-785-2555	Sequence 2555, Ap	665	15.6	97.5	31	10	US-09-864-785-2628	Sequence 2628, Ap
593	15.6	97.5	31	10	US-09-864-785-2556	Sequence 2556, Ap	666	15.6	97.5	31	10	US-09-864-785-2629	Sequence 2629, Ap
594	15.6	97.5	31	10	US-09-864-785-2557	Sequence 2557, Ap	667	15.6	97.5	31	10	US-09-864-785-2630	Sequence 2630, Ap
595	15.6	97.5	31	10	US-09-864-785-2558	Sequence 2558, Ap	668	15.6	97.5	31	10	US-09-864-785-2631	Sequence 2631, Ap
596	15.6	97.5	31	10	US-09-864-785-2559	Sequence 2559, Ap	669	15.6	97.5	31	10	US-09-864-785-2632	Sequence 2632, Ap
597	15.6	97.5	31	10	US-09-864-785-2560	Sequence 2560, Ap	670	15.6	97.5	31	10	US-09-864-785-2633	Sequence 2633, Ap
598	15.6	97.5	31	10	US-09-864-785-2561	Sequence 2561, Ap	671	15.6	97.5	31	10	US-09-864-785-2634	Sequence 2634, Ap
599	15.6	97.5	31	10	US-09-864-785-2562	Sequence 2562, Ap	672	15.6	97.5	31	10	US-09-864-785-2635	Sequence 2635, Ap

673	15.6	97.5	31	10	US-09-864-785-2636	Sequence 2636, Ap	746	15.6	97.5	31	11	US-09-730-2898-2952	Sequence 2952, Ap
674	15.6	97.5	31	10	US-09-864-785-2637	Sequence 2637, Ap	747	15.6	97.5	31	11	US-09-730-2898-2953	Sequence 2953, Ap
675	15.6	97.5	31	10	US-09-864-785-2638	Sequence 2638, Ap	748	15.6	97.5	31	11	US-09-730-2898-2954	Sequence 2954, Ap
676	15.6	97.5	31	10	US-09-864-785-2639	Sequence 2639, Ap	749	15.6	97.5	31	11	US-09-730-2898-2955	Sequence 2955, Ap
677	15.6	97.5	31	10	US-09-864-785-2640	Sequence 2640, Ap	750	15.6	97.5	31	11	US-09-730-2898-2956	Sequence 2956, Ap
678	15.6	97.5	31	10	US-09-864-785-2641	Sequence 2641, Ap	751	15.6	97.5	31	11	US-09-730-2898-2957	Sequence 2957, Ap
679	15.6	97.5	31	10	US-09-864-785-2642	Sequence 2642, Ap	752	15.6	97.5	31	11	US-09-730-2898-2958	Sequence 2958, Ap
680	15.6	97.5	31	10	US-09-864-785-2643	Sequence 2643, Ap	753	15.6	97.5	31	11	US-09-730-2898-2959	Sequence 2959, Ap
681	15.6	97.5	31	10	US-09-864-785-2644	Sequence 2644, Ap	754	15.6	97.5	31	11	US-09-730-2898-2960	Sequence 2960, Ap
682	15.6	97.5	31	10	US-09-864-785-2645	Sequence 2645, Ap	755	15.6	97.5	31	11	US-09-730-2898-2961	Sequence 2961, Ap
683	15.6	97.5	31	10	US-09-864-785-2646	Sequence 2646, Ap	756	15.6	97.5	31	11	US-09-730-2898-2962	Sequence 2962, Ap
684	15.6	97.5	31	10	US-09-864-785-2647	Sequence 2647, Ap	757	15.6	97.5	31	11	US-09-730-2898-2963	Sequence 2963, Ap
685	15.6	97.5	31	10	US-09-864-785-2648	Sequence 2648, Ap	758	15.6	97.5	31	11	US-09-730-2898-2964	Sequence 2964, Ap
686	15.6	97.5	31	10	US-09-864-785-2649	Sequence 2649, Ap	759	15.6	97.5	31	11	US-09-730-2898-2965	Sequence 2965, Ap
687	15.6	97.5	31	10	US-09-864-785-2650	Sequence 2650, Ap	760	15.6	97.5	31	11	US-09-730-2898-2966	Sequence 2966, Ap
688	15.6	97.5	31	10	US-09-864-785-2651	Sequence 2651, Ap	761	15.6	97.5	31	11	US-09-730-2898-2967	Sequence 2967, Ap
689	15.6	97.5	31	10	US-09-864-785-2652	Sequence 2652, Ap	762	15.6	97.5	31	11	US-09-730-2898-2968	Sequence 2968, Ap
690	15.6	97.5	31	10	US-09-864-785-2653	Sequence 2653, Ap	763	15.6	97.5	31	11	US-09-730-2898-2969	Sequence 2969, Ap
691	15.6	97.5	31	10	US-09-864-785-2654	Sequence 2654, Ap	764	15.6	97.5	31	11	US-09-730-2898-2970	Sequence 2970, Ap
692	15.6	97.5	31	10	US-09-864-785-2655	Sequence 2655, Ap	765	15.6	97.5	31	11	US-09-730-2898-2971	Sequence 2971, Ap
693	15.6	97.5	31	11	US-09-864-785-2656	Sequence 2656, Ap	766	15.6	97.5	31	11	US-09-730-2898-2972	Sequence 2972, Ap
694	15.6	97.5	31	11	US-09-730-2898-2900	Sequence 2900, Ap	767	15.6	97.5	31	11	US-09-730-2898-2973	Sequence 2973, Ap
695	15.6	97.5	31	11	US-09-730-2898-2901	Sequence 2901, Ap	768	15.6	97.5	31	11	US-09-730-2898-2974	Sequence 2974, Ap
696	15.6	97.5	31	11	US-09-730-2898-2902	Sequence 2902, Ap	769	15.6	97.5	31	11	US-09-730-2898-2975	Sequence 2975, Ap
697	15.6	97.5	31	11	US-09-730-2898-2903	Sequence 2903, Ap	770	15.6	97.5	31	11	US-09-730-2898-2976	Sequence 2976, Ap
698	15.6	97.5	31	11	US-09-730-2898-2904	Sequence 2904, Ap	771	15.6	97.5	31	11	US-09-730-2898-2977	Sequence 2977, Ap
699	15.6	97.5	31	11	US-09-730-2898-2905	Sequence 2905, Ap	772	15.6	97.5	31	11	US-09-730-2898-2978	Sequence 2978, Ap
700	15.6	97.5	31	11	US-09-730-2898-2906	Sequence 2906, Ap	773	15.6	97.5	31	11	US-09-730-2898-2979	Sequence 2979, Ap
701	15.6	97.5	31	11	US-09-730-2898-2907	Sequence 2907, Ap	774	15.6	97.5	31	11	US-09-730-2898-2980	Sequence 2980, Ap
702	15.6	97.5	31	11	US-09-730-2898-2908	Sequence 2908, Ap	775	15.6	97.5	31	11	US-09-730-2898-2981	Sequence 2981, Ap
703	15.6	97.5	31	11	US-09-730-2898-2909	Sequence 2909, Ap	776	15.6	97.5	31	11	US-09-730-2898-2982	Sequence 2982, Ap
704	15.6	97.5	31	11	US-09-730-2898-2910	Sequence 2910, Ap	777	15.6	97.5	31	11	US-09-730-2898-2983	Sequence 2983, Ap
705	15.6	97.5	31	11	US-09-730-2898-2911	Sequence 2911, Ap	778	15.6	97.5	31	11	US-09-730-2898-2984	Sequence 2984, Ap
706	15.6	97.5	31	11	US-09-730-2898-2912	Sequence 2912, Ap	779	15.6	97.5	31	11	US-09-730-2898-2985	Sequence 2985, Ap
707	15.6	97.5	31	11	US-09-730-2898-2913	Sequence 2913, Ap	780	15.6	97.5	31	11	US-09-730-2898-2986	Sequence 2986, Ap
708	15.6	97.5	31	11	US-09-730-2898-2914	Sequence 2914, Ap	781	15.6	97.5	31	11	US-09-730-2898-2987	Sequence 2987, Ap
709	15.6	97.5	31	11	US-09-730-2898-2915	Sequence 2915, Ap	782	15.6	97.5	31	11	US-09-730-2898-2988	Sequence 2988, Ap
710	15.6	97.5	31	11	US-09-730-2898-2916	Sequence 2916, Ap	783	15.6	97.5	31	11	US-09-730-2898-2989	Sequence 2989, Ap
711	15.6	97.5	31	11	US-09-730-2898-2917	Sequence 2917, Ap	784	15.6	97.5	31	11	US-09-730-2898-2990	Sequence 2990, Ap
712	15.6	97.5	31	11	US-09-730-2898-2918	Sequence 2918, Ap	785	15.6	97.5	31	11	US-09-730-2898-2991	Sequence 2991, Ap
713	15.6	97.5	31	11	US-09-730-2898-2919	Sequence 2919, Ap	786	15.6	97.5	31	11	US-09-730-2898-2992	Sequence 2992, Ap
714	15.6	97.5	31	11	US-09-730-2898-2920	Sequence 2920, Ap	787	15.6	97.5	31	11	US-09-730-2898-2993	Sequence 2993, Ap
715	15.6	97.5	31	11	US-09-730-2898-2921	Sequence 2921, Ap	788	15.6	97.5	31	11	US-09-730-2898-2994	Sequence 2994, Ap
716	15.6	97.5	31	11	US-09-730-2898-2922	Sequence 2922, Ap	789	15.6	97.5	31	11	US-09-730-2898-2995	Sequence 2995, Ap
717	15.6	97.5	31	11	US-09-730-2898-2923	Sequence 2923, Ap	790	15.6	97.5	31	11	US-09-730-2898-2996	Sequence 2996, Ap
718	15.6	97.5	31	11	US-09-730-2898-2924	Sequence 2924, Ap	791	15.6	97.5	31	11	US-09-730-2898-2997	Sequence 2997, Ap
719	15.6	97.5	31	11	US-09-730-2898-2925	Sequence 2925, Ap	792	15.6	97.5	31	11	US-09-730-2898-2998	Sequence 2998, Ap
720	15.6	97.5	31	11	US-09-730-2898-2926	Sequence 2926, Ap	793	15.6	97.5	31	11	US-09-730-2898-2999	Sequence 2999, Ap
721	15.6	97.5	31	11	US-09-730-2898-2927	Sequence 2927, Ap	794	15.6	97.5	31	11	US-09-730-2898-3000	Sequence 3000, Ap
722	15.6	97.5	31	11	US-09-730-2898-2928	Sequence 2928, Ap	795	15.6	97.5	31	11	US-09-730-2898-3001	Sequence 3001, Ap
723	15.6	97.5	31	11	US-09-730-2898-2929	Sequence 2929, Ap	796	15.6	97.5	31	11	US-09-730-2898-3002	Sequence 3002, Ap
724	15.6	97.5	31	11	US-09-730-2898-2930	Sequence 2930, Ap	797	15.6	97.5	31	11	US-09-730-2898-3003	Sequence 3003, Ap
725	15.6	97.5	31	11	US-09-730-2898-2931	Sequence 2931, Ap	798	15.6	97.5	31	11	US-09-730-2898-3004	Sequence 3004, Ap
726	15.6	97.5	31	11	US-09-730-2898-2932	Sequence 2932, Ap	799	15.6	97.5	31	11	US-09-730-2898-3005	Sequence 3005, Ap
727	15.6	97.5	31	11	US-09-730-2898-2933	Sequence 2933, Ap	800	15.6	97.5	31	11	US-09-730-2898-3006	Sequence 3006, Ap
728	15.6	97.5	31	11	US-09-730-2898-2934	Sequence 2934, Ap	801	15.6	97.5	31	11	US-09-730-2898-3007	Sequence 3007, Ap
729	15.6	97.5	31	11	US-09-730-2898-2935	Sequence 2935, Ap	802	15.6	97.5	31	11	US-09-730-2898-3008	Sequence 3008, Ap
730	15.6	97.5	31	11	US-09-730-2898-2936	Sequence 2936, Ap	803	15.6	97.5	31	11	US-09-730-2898-3009	Sequence 3009, Ap
731	15.6	97.5	31	11	US-09-730-2898-2937	Sequence 2937, Ap	804	15.6	97.5	31	11	US-09-730-2898-3010	Sequence 3010, Ap
732	15.6	97.5	31	11	US-09-730-2898-2938	Sequence 2938, Ap	805	15.6	97.5	31	11	US-09-730-2898-3011	Sequence 3011, Ap
733	15.6	97.5	31	11	US-09-730-2898-2939	Sequence 2939, Ap	806	15.6	97.5	31	11	US-09-730-2898-3012	Sequence 3012, Ap
734	15.6	97.5	31	11	US-09-730-2898-2940	Sequence 2940, Ap	807	15.6	97.5	31	11	US-09-730-2898-3013	Sequence 3013, Ap
735	15.6	97.5	31	11	US-09-730-2898-2941	Sequence 2941, Ap	808	15.6	97.5	31	11	US-09-730-2898-3014	Sequence 3014, Ap
736	15.6	97.5	31	11	US-09-730-2898-2942	Sequence 2942, Ap	809	15.6	97.5	31	11	US-09-730-2898-3015	Sequence 3015, Ap
737	15.6	97.5	31	11	US-09-730-2898-2943	Sequence 2943, Ap	810	15.6	97.5	31	11	US-09-730-2898-3016	Sequence 3016, Ap
738	15.6	97.5	31	11	US-09-730-2898-2944	Sequence 2944, Ap	811	15.6	97.5	31	11	US-09-730-2898-3017	Sequence 3017, Ap
739	15.6	97.5	31	11	US-09-730-2898-2945	Sequence 2945, Ap	812	15.6	97.5	31	11	US-09-730-2898-3018	Sequence 3018, Ap
740	15.6	97.5	31	11	US-09-730-2898-2946	Sequence 2946, Ap	813	15.6	97.5	31	11	US-09-730-2898-3019	Sequence 3019, Ap
741	15.6	97.5	31	11	US-09-730-2898-2947	Sequence 2947, Ap	814	15.6	97.5	31	11	US-09-730-2898-3020	Sequence 3020, Ap
742	15.6	97.5	31	11	US-09-730-2898-2948	Sequence 2948, Ap	815	15.6	97.5	31	11	US-09-730-2898-3021	Sequence 3021, Ap
743	15.6	97.5	31	11	US-09-730-2898-2949	Sequence 2949, Ap	816	15.6	97.5	31	11	US-09-730-2898-3022	Sequence 3022, Ap
744	15.6	97.5	31	11	US-09-730-2898-2950	Sequence 2950, Ap	817	15.6	97.5	31	11	US-09-730-2898-3023	Sequence 3023, Ap
745	15.6	97.5	31	11	US-09-730-2898-2951	Sequence 2951, Ap	818	15.6	97.5	31	11	US-09-730-2898-3024	Sequence 3024, Ap

819	15.6	97.5	31	11	US-09-730-2898B-3025	Sequence 3025, Ap	892	15.6	97.5	31	11	US-09-730-2898B-3098	Sequence 3098, Ap
820	15.6	97.5	31	11	US-09-730-2898B-3026	Sequence 3026, Ap	893	15.6	97.5	31	11	US-09-730-2898B-3099	Sequence 3100, Ap
821	15.6	97.5	31	11	US-09-730-2898B-3027	Sequence 3027, Ap	894	15.6	97.5	31	11	US-09-730-2898B-3100	Sequence 3101, Ap
822	15.6	97.5	31	11	US-09-730-2898B-3028	Sequence 3028, Ap	895	15.6	97.5	31	11	US-09-730-2898B-3101	Sequence 3102, Ap
823	15.6	97.5	31	11	US-09-730-2898B-3029	Sequence 3029, Ap	896	15.6	97.5	31	11	US-09-730-2898B-3102	Sequence 3103, Ap
824	15.6	97.5	31	11	US-09-730-2898B-3030	Sequence 3030, Ap	897	15.6	97.5	31	11	US-09-730-2898B-3103	Sequence 3104, Ap
825	15.6	97.5	31	11	US-09-730-2898B-3031	Sequence 3031, Ap	898	15.6	97.5	31	11	US-09-730-2898B-3104	Sequence 3105, Ap
826	15.6	97.5	31	11	US-09-730-2898B-3032	Sequence 3032, Ap	899	15.6	97.5	31	11	US-09-730-2898B-3105	Sequence 3106, Ap
827	15.6	97.5	31	11	US-09-730-2898B-3033	Sequence 3033, Ap	900	15.6	97.5	31	11	US-09-730-2898B-3106	Sequence 3107, Ap
828	15.6	97.5	31	11	US-09-730-2898B-3034	Sequence 3034, Ap	901	15.6	97.5	31	11	US-09-730-2898B-3107	Sequence 3108, Ap
829	15.6	97.5	31	11	US-09-730-2898B-3035	Sequence 3035, Ap	902	15.6	97.5	31	11	US-09-730-2898B-3108	Sequence 3109, Ap
830	15.6	97.5	31	11	US-09-730-2898B-3036	Sequence 3036, Ap	903	15.6	97.5	31	11	US-09-730-2898B-3109	Sequence 3110, Ap
831	15.6	97.5	31	11	US-09-730-2898B-3037	Sequence 3037, Ap	904	15.6	97.5	31	11	US-09-730-2898B-3110	Sequence 3111, Ap
832	15.6	97.5	31	11	US-09-730-2898B-3038	Sequence 3038, Ap	905	15.6	97.5	31	11	US-09-730-2898B-3111	Sequence 3112, Ap
833	15.6	97.5	31	11	US-09-730-2898B-3039	Sequence 3039, Ap	906	15.6	97.5	31	11	US-09-730-2898B-3112	Sequence 3113, Ap
834	15.6	97.5	31	11	US-09-730-2898B-3040	Sequence 3040, Ap	907	15.6	97.5	31	11	US-09-730-2898B-3113	Sequence 3114, Ap
835	15.6	97.5	31	11	US-09-730-2898B-3041	Sequence 3041, Ap	908	15.6	97.5	31	11	US-09-730-2898B-3114	Sequence 3115, Ap
836	15.6	97.5	31	11	US-09-730-2898B-3042	Sequence 3042, Ap	909	15.6	97.5	31	11	US-09-730-2898B-3115	Sequence 3116, Ap
837	15.6	97.5	31	11	US-09-730-2898B-3043	Sequence 3043, Ap	910	15.6	97.5	31	11	US-09-730-2898B-3116	Sequence 3117, Ap
838	15.6	97.5	31	11	US-09-730-2898B-3044	Sequence 3044, Ap	911	15.6	97.5	31	11	US-09-730-2898B-3117	Sequence 3118, Ap
839	15.6	97.5	31	11	US-09-730-2898B-3045	Sequence 3045, Ap	912	15.6	97.5	31	11	US-09-730-2898B-3118	Sequence 3119, Ap
840	15.6	97.5	31	11	US-09-730-2898B-3046	Sequence 3046, Ap	913	15.6	97.5	31	11	US-09-730-2898B-3119	Sequence 3120, Ap
841	15.6	97.5	31	11	US-09-730-2898B-3047	Sequence 3047, Ap	914	15.6	97.5	31	11	US-09-730-2898B-3120	Sequence 3121, Ap
842	15.6	97.5	31	11	US-09-730-2898B-3048	Sequence 3048, Ap	915	15.6	97.5	31	11	US-09-730-2898B-3121	Sequence 3122, Ap
843	15.6	97.5	31	11	US-09-730-2898B-3049	Sequence 3049, Ap	916	15.6	97.5	31	11	US-09-730-2898B-3122	Sequence 3123, Ap
844	15.6	97.5	31	11	US-09-730-2898B-3050	Sequence 3050, Ap	917	15.6	97.5	31	11	US-09-730-2898B-3123	Sequence 3124, Ap
845	15.6	97.5	31	11	US-09-730-2898B-3051	Sequence 3051, Ap	918	15.6	97.5	31	11	US-09-730-2898B-3124	Sequence 3125, Ap
846	15.6	97.5	31	11	US-09-730-2898B-3052	Sequence 3052, Ap	919	15.6	97.5	31	11	US-09-730-2898B-3125	Sequence 3126, Ap
847	15.6	97.5	31	11	US-09-730-2898B-3053	Sequence 3053, Ap	920	15.6	97.5	31	11	US-09-730-2898B-3126	Sequence 3127, Ap
848	15.6	97.5	31	11	US-09-730-2898B-3054	Sequence 3054, Ap	921	15.6	97.5	31	11	US-09-730-2898B-3127	Sequence 3128, Ap
849	15.6	97.5	31	11	US-09-730-2898B-3055	Sequence 3055, Ap	922	15.6	97.5	31	11	US-09-730-2898B-3128	Sequence 3129, Ap
850	15.6	97.5	31	11	US-09-730-2898B-3056	Sequence 3056, Ap	923	15.6	97.5	31	11	US-09-730-2898B-3129	Sequence 3130, Ap
851	15.6	97.5	31	11	US-09-730-2898B-3057	Sequence 3057, Ap	924	15.6	97.5	31	11	US-09-730-2898B-3130	Sequence 3131, Ap
852	15.6	97.5	31	11	US-09-730-2898B-3058	Sequence 3058, Ap	925	15.6	97.5	31	11	US-09-730-2898B-3131	Sequence 3132, Ap
853	15.6	97.5	31	11	US-09-730-2898B-3059	Sequence 3059, Ap	926	15.6	97.5	31	11	US-09-730-2898B-3132	Sequence 3133, Ap
854	15.6	97.5	31	11	US-09-730-2898B-3060	Sequence 3060, Ap	927	15.6	97.5	31	11	US-09-730-2898B-3133	Sequence 3134, Ap
855	15.6	97.5	31	11	US-09-730-2898B-3061	Sequence 3061, Ap	928	15.6	97.5	31	11	US-09-730-2898B-3134	Sequence 3135, Ap
856	15.6	97.5	31	11	US-09-730-2898B-3062	Sequence 3062, Ap	929	15.6	97.5	31	11	US-09-730-2898B-3135	Sequence 3136, Ap
857	15.6	97.5	31	11	US-09-730-2898B-3063	Sequence 3063, Ap	930	15.6	97.5	31	11	US-09-730-2898B-3136	Sequence 3137, Ap
858	15.6	97.5	31	11	US-09-730-2898B-3064	Sequence 3064, Ap	931	15.6	97.5	31	11	US-09-730-2898B-3137	Sequence 3138, Ap
859	15.6	97.5	31	11	US-09-730-2898B-3065	Sequence 3065, Ap	932	15.6	97.5	31	11	US-09-730-2898B-3138	Sequence 3139, Ap
860	15.6	97.5	31	11	US-09-730-2898B-3066	Sequence 3066, Ap	933	15.6	97.5	31	11	US-09-730-2898B-3139	Sequence 3140, Ap
861	15.6	97.5	31	11	US-09-730-2898B-3067	Sequence 3067, Ap	934	15.6	97.5	31	11	US-09-730-2898B-3140	Sequence 3141, Ap
862	15.6	97.5	31	11	US-09-730-2898B-3068	Sequence 3068, Ap	935	15.6	97.5	31	11	US-09-730-2898B-3141	Sequence 3142, Ap
863	15.6	97.5	31	11	US-09-730-2898B-3069	Sequence 3069, Ap	936	15.6	97.5	31	11	US-09-730-2898B-3142	Sequence 3143, Ap
864	15.6	97.5	31	11	US-09-730-2898B-3070	Sequence 3070, Ap	937	15.6	97.5	31	11	US-09-730-2898B-3143	Sequence 3144, Ap
865	15.6	97.5	31	11	US-09-730-2898B-3071	Sequence 3071, Ap	938	15.6	97.5	31	11	US-09-730-2898B-3144	Sequence 3145, Ap
866	15.6	97.5	31	11	US-09-730-2898B-3072	Sequence 3072, Ap	939	15.6	97.5	31	11	US-09-730-2898B-3145	Sequence 3146, Ap
867	15.6	97.5	31	11	US-09-730-2898B-3073	Sequence 3073, Ap	940	15.6	97.5	31	11	US-09-730-2898B-3146	Sequence 3147, Ap
868	15.6	97.5	31	11	US-09-730-2898B-3074	Sequence 3074, Ap	941	15.6	97.5	31	11	US-09-730-2898B-3147	Sequence 3148, Ap
869	15.6	97.5	31	11	US-09-730-2898B-3075	Sequence 3075, Ap	942	15.6	97.5	31	11	US-09-730-2898B-3148	Sequence 3149, Ap
870	15.6	97.5	31	11	US-09-730-2898B-3076	Sequence 3076, Ap	943	15.6	97.5	31	11	US-09-730-2898B-3149	Sequence 3150, Ap
871	15.6	97.5	31	11	US-09-730-2898B-3077	Sequence 3077, Ap	944	15.6	97.5	31	11	US-09-730-2898B-3150	Sequence 3151, Ap
872	15.6	97.5	31	11	US-09-730-2898B-3078	Sequence 3078, Ap	945	15.6	97.5	31	11	US-09-730-2898B-3151	Sequence 3152, Ap
873	15.6	97.5	31	11	US-09-730-2898B-3079	Sequence 3079, Ap	946	15.6	97.5	31	11	US-09-730-2898B-3152	Sequence 3153, Ap
874	15.6	97.5	31	11	US-09-730-2898B-3080	Sequence 3080, Ap	947	15.6	97.5	31	11	US-09-730-2898B-3153	Sequence 3154, Ap
875	15.6	97.5	31	11	US-09-730-2898B-3081	Sequence 3081, Ap	948	15.6	97.5	31	11	US-09-730-2898B-3154	Sequence 3155, Ap
876	15.6	97.5	31	11	US-09-730-2898B-3082	Sequence 3082, Ap	949	15.6	97.5	31	11	US-09-730-2898B-3155	Sequence 3156, Ap
877	15.6	97.5	31	11	US-09-730-2898B-3083	Sequence 3083, Ap	950	15.6	97.5	31	11	US-09-730-2898B-3156	Sequence 3157, Ap
878	15.6	97.5	31	11	US-09-730-2898B-3084	Sequence 3084, Ap	951	15.6	97.5	31	11	US-09-730-2898B-3157	Sequence 3158, Ap
879	15.6	97.5	31	11	US-09-730-2898B-3085	Sequence 3085, Ap	952	15.6	97.5	31	11	US-09-730-2898B-3158	Sequence 3159, Ap
880	15.6	97.5	31	11	US-09-730-2898B-3086	Sequence 3086, Ap	953	15.6	97.5	31	11	US-09-730-2898B-3159	Sequence 3160, Ap
881	15.6	97.5	31	11	US-09-730-2898B-3087	Sequence 3087, Ap	954	15.6	97.5	31	11	US-09-730-2898B-3160	Sequence 3161, Ap
882	15.6	97.5	31	11	US-09-730-2898B-3088	Sequence 3088, Ap	955	15.6	97.5	31	11	US-09-730-2898B-3161	Sequence 3162, Ap
883	15.6	97.5	31	11	US-09-730-2898B-3089	Sequence 3089, Ap	956	15.6	97.5	31	11	US-09-730-2898B-3162	Sequence 3163, Ap
884	15.6	97.5	31	11	US-09-730-2898B-3090	Sequence 3090, Ap	957	15.6	97.5	31	11	US-09-730-2898B-3163	Sequence 3164, Ap
885	15.6	97.5	31	11	US-09-730-2898B-3091	Sequence 3091, Ap	958	15.6	97.5	31	11	US-09-730-2898B-3164	Sequence 3165, Ap
886	15.6	97.5	31	11	US-09-730-2898B-3092	Sequence 3092, Ap	959	15.6	97.5	31	11	US-09-730-2898B-3165	Sequence 3166, Ap
887	15.6	97.5	31	11	US-09-730-2898B-3093	Sequence 3093, Ap	960	15.6	97.5	31	11	US-09-730-2898B-3166	Sequence 3167, Ap
888	15.6	97.5	31	11	US-09-730-2898B-3094	Sequence 3094, Ap	961	15.6	97.5	31	11	US-09-730-2898B-3167	Sequence 3168, Ap
889	15.6	97.5	31	11	US-09-730-2898B-3095	Sequence 3095, Ap	962	15.6	97.5	31	11	US-09-730-2898B-3168	Sequence 3169, Ap
890	15.6	97.5	31	11	US-09-730-2898B-3096	Sequence 3096, Ap	963	15.6	97.5	31	11	US-09-730-2898B-3169	Sequence 3170, Ap
891	15.6	97.5	31	11	US-09-730-2898B-3097	Sequence 3097, Ap	964	15.6	97.5	31	11	US-09-730-2898B-3170	Sequence 3171, Ap

965 15.6 97.5 31 11 US-09-730-289B-3171 Sequence 3171, Ap
966 15.6 97.5 31 11 US-09-730-289B-3172 Sequence 3172, Ap
967 15.6 97.5 31 11 US-09-730-289B-3173 Sequence 3173, Ap
968 15.6 97.5 31 11 US-09-730-289B-3174 Sequence 3174, Ap
969 15.6 97.5 31 11 US-09-730-289B-3175 Sequence 3175, Ap
970 15.6 97.5 31 11 US-09-730-289B-3176 Sequence 3176, Ap
971 15.6 97.5 31 11 US-09-730-289B-3177 Sequence 3177, Ap
972 15.6 97.5 31 11 US-09-730-289B-3178 Sequence 3178, Ap
973 15.6 97.5 31 11 US-09-730-289B-3179 Sequence 3179, Ap
974 15.6 97.5 31 11 US-09-730-289B-3180 Sequence 3180, Ap
975 15.6 97.5 31 11 US-09-730-289B-3181 Sequence 3181, Ap
976 15.6 97.5 31 11 US-09-730-289B-3182 Sequence 3182, Ap
977 15.6 97.5 31 11 US-09-730-289B-3183 Sequence 3183, Ap
978 15.6 97.5 31 11 US-09-730-289B-3184 Sequence 3184, Ap
979 15.6 97.5 31 11 US-09-730-289B-3185 Sequence 3185, Ap
980 15.6 97.5 31 11 US-09-730-289B-3186 Sequence 3186, Ap
981 15.6 97.5 31 11 US-09-730-289B-3187 Sequence 3187, Ap
982 15.6 97.5 31 11 US-09-730-289B-3188 Sequence 3188, Ap
983 15.6 97.5 31 11 US-09-730-289B-3189 Sequence 3189, Ap
984 15.6 97.5 31 11 US-09-730-289B-3190 Sequence 3190, Ap
985 15.6 97.5 31 11 US-09-730-289B-3191 Sequence 3191, Ap
986 15.6 97.5 31 11 US-09-730-289B-3192 Sequence 3192, Ap
987 15.6 97.5 31 11 US-09-730-289B-3193 Sequence 3193, Ap
988 15.6 97.5 31 11 US-09-730-289B-3194 Sequence 3194, Ap
989 15.6 97.5 31 11 US-09-730-289B-3195 Sequence 3195, Ap
990 15.6 97.5 31 11 US-09-730-289B-3196 Sequence 3196, Ap
991 15.6 97.5 31 11 US-09-730-289B-3197 Sequence 3197, Ap
992 15.6 97.5 31 11 US-09-730-289B-3198 Sequence 3198, Ap
993 15.6 97.5 31 11 US-09-730-289B-3199 Sequence 3199, Ap
994 15.6 97.5 31 11 US-09-730-289B-3200 Sequence 3200, Ap
995 15.6 97.5 31 11 US-09-730-289B-3201 Sequence 3201, Ap
996 15.6 97.5 31 11 US-09-730-289B-3202 Sequence 3202, Ap
997 15.6 97.5 31 11 US-09-730-289B-3203 Sequence 3203, Ap
998 15.6 97.5 31 11 US-09-730-289B-3204 Sequence 3204, Ap
999 15.6 97.5 31 11 US-09-730-289B-3205 Sequence 3205, Ap
1000 15.6 97.5 31 11 US-09-730-289B-3206 Sequence 3206, Ap

ALIGNMENTS

RESULT 1

US-09-877-526A-21

Sequence 21, Application US/09877526A

Patent No. US20020102568A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc

APPLICANT: Ushman, Nassim

APPLICANT: McSwigen, Jim

APPLICANT: Zinnen, Shawn

APPLICANT: Seiwert, Scott

APPLICANT: Haebertl, Pete

APPLICANT: Chowritza, Bharat

APPLICANT: Blact, Larry

APPLICANT: Valsh, Narendra

TITLE OF INVENTION: A Process for the Detection of Nucleic Acid Using Nucleic Acid Ca

FILE REFERENCE: MBH00-816-C (700/002)

CURRENT APPLICATION NUMBER: US/09/877,526A

CURRENT FILING DATE: 2001-03-06

PRIOR APPLICATION NUMBER: 60/187,128

PRIOR FILING DATE: 2000-03-06

NUMBER OF SEQ ID NOS: 49

SOFTWARE: PatentIn version 3.0

SEQ ID NO 21

LENGTH: 16

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Motif

US-09-877-526A-21

Query Match 97.5%; Score 15.6; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 23;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RGGCTAGCTACACGA 16
Db 1 RGGCTAGCTACACGA 16

RESULT 2

US-09-866-316B-15

Sequence 15, Application US/09866316B

Patent No. US20020142980A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Thompson, Jim

APPLICANT: McSwigen, Jim

APPLICANT: Haebertl, Pete

APPLICANT: Belgelesky, Alex

APPLICANT: Belton, Lauren

APPLICANT: Reynolds, Mark

APPLICANT: Zwack, Michael

APPLICANT: Jarvis, Thale

APPLICANT: Woolf, Todd

APPLICANT: Maculic-Adamic, Jasenka

TITLE OF INVENTION: Nucleic Acid Molecules with No. US20020142980A1el Chemical Compos

FILE REFERENCE: MBH00,873-H 500/004

CURRENT APPLICATION NUMBER: US/09/866,316B

CURRENT FILING DATE: 2002-03-05

PRIOR APPLICATION NUMBER: US 09/103,656

PRIOR FILING DATE: 1998-06-23

PRIOR APPLICATION NUMBER: US 60/082,404

PRIOR FILING DATE: 1998-04-20

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn version 3.0

SEQ ID NO 15

LENGTH: 16

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: DNazyme Motif

US-09-866-316B-15

Query Match 97.5%; Score 15.6; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCTACACGA 16
Db 1 RGGCTAGCTACACGA 16

RESULT 3

US-09-864-785-3928

Sequence 3928, Application US/09864785

Patent No. US2002017568A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Slinchcomb, Dan

APPLICANT: Draper, Ken

APPLICANT: McSwigen, Jim

TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related

FILE REFERENCE: 400/022 (MBH00-812-D)

CURRENT APPLICATION NUMBER: US/09/864,785

CURRENT FILING DATE: 2001-05-23

NUMBER OF SEQ ID NOS: 3928

SOFTWARE: PatentIn version 3.0

SEQ ID NO 3928

LENGTH: 16

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-3928

Query Match 97.5%; Score 15.6; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACACGA 16
|||||
DB 1 RGCTAGCTACACGA 16

RESULT 4
US-09-992-160-21
Sequence 21, Application US/09992160
Publication No. US2003008295A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc

APPLICANT: Usman, Nassim

APPLICANT: McSwigen, Jim

APPLICANT: Zinnen, Shawn

APPLICANT: Seiwert, Scott

APPLICANT: Haebertl, Pete

APPLICANT: Chowrira, Bharat

APPLICANT: Blatt, Larry

TITLE OF INVENTION: Nucleic Acid Sensor Molecules

FILE REFERENCE: MBH00-816-D (700/004)

CURRENT APPLICATION NUMBER: US/09/992,160

CURRENT FILING DATE: 2001-11-05

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PatentIn version 3.0

SEQ ID NO 21

LENGTH: 16

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Motif

Query Match 97.5%; Score 15.6; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACACGA 16
|||||
DB 1 RGCTAGCTACACGA 16

RESULT 5
US-09-730-289B-3896
Sequence 3896, Application US/09730289B
Publication No. US20030050259A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Blatt, Larry

APPLICANT: McSwigen, Jim

TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease

FILE REFERENCE: MBH00-864-A (400/006)

CURRENT APPLICATION NUMBER: US/09/730,289B

CURRENT FILING DATE: 2000-12-05

PRIOR APPLICATION NUMBER: US 60/169,100

PRIOR FILING DATE: 1999-12-06

NUMBER OF SEQ ID NOS: 3897

SOFTWARE: PatentIn version 3.0

SEQ ID NO 3896

LENGTH: 16

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence

US-09-730-289B-3896

Query Match 97.5%; Score 15.6; DB 11; Length 16;

Best Local Similarity 100.0%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACACGA 16
|||||
DB 1 RGCTAGCTACACGA 16

RESULT 6
US-09-780-533A-6679
Sequence 6679, Application US/09780533A
Publication No. US2003006011A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Blatt, Larry

APPLICANT: McSwigen, Jim

APPLICANT: Chowrira, Bharat

APPLICANT: Haebertl, Pete

TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene

FILE REFERENCE: MBH00-878-A (400/011)

CURRENT APPLICATION NUMBER: US/09/780,533A

CURRENT FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: US 60/181,797

PRIOR FILING DATE: 2000-02-11

NUMBER OF SEQ ID NOS: 6679

SOFTWARE: PatentIn version 3.0

SEQ ID NO 6679

LENGTH: 16

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

Query Match 97.5%; Score 15.6; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACACGA 16
|||||
DB 1 RGCTAGCTACACGA 16

RESULT 7
US-09-877-478-6585
Sequence 6585, Application US/09877478
Publication No. US20030068301A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Draper, Kenneth

APPLICANT: Blatt, Larry

APPLICANT: McSwigen, Jim

TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication

FILE REFERENCE: MBH00-845-H (400/029)

CURRENT APPLICATION NUMBER: US/09/877,478

CURRENT FILING DATE: 2001-12-31

PRIOR APPLICATION NUMBER: US 07/882,712

PRIOR FILING DATE: 1992-05-14

PRIOR APPLICATION NUMBER: US 09/531,025

PRIOR FILING DATE: 2000-03-20

PRIOR APPLICATION NUMBER: US 09/636,385

PRIOR FILING DATE: 2000-08-09

PRIOR APPLICATION NUMBER: US 09/696,347

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 08/193,627

PRIOR FILING DATE: 1994-02-07

PRIOR APPLICATION NUMBER: US 08/433,993

PRIOR FILING DATE: 1995-05-04

PRIOR APPLICATION NUMBER: US 08/434,504

PRIOR FILING DATE: 1995-05-04

PRIOR APPLICATION NUMBER: US 09/436,430

PRIOR FILING DATE: 1999-11-08

NUMBER OF SEQ ID NOS: 6586
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6585
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-877-478-6585

Query Match 97.5%; Score 15.6; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
|||||
DB 1 RGGCTAGCTACACGA 16

RESULT 8
US-09-848-754A-9645
Sequence 9645, Application US/09848754A
Publication No. US20030073207A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
FILE REFERENCE: MBH00-958-I (400/018)
CURRENT APPLICATION NUMBER: US/09/848,754A
CURRENT FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 9645
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9645
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNAzyme Motif
US-09-848-754A-9645

Query Match 97.5%; Score 15.6; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
|||||
DB 1 RGGCTAGCTACACGA 16

RESULT 9
US-09-776-474-2991
Sequence 2991, Application US/09776474
Publication No. US20030087847A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Jarvis, Thale
APPLICANT: Boober, Robert
APPLICANT: Holman, Patricia
APPLICANT: Patteay, Ali
APPLICANT: McSwigen, Jim
TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK
FILE REFERENCE: MBH00-955-A (400/008)
CURRENT APPLICATION NUMBER: US/09/776,474
CURRENT FILING DATE: 2001-02-02
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 2992
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2991
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-2991

Query Match 97.5%; Score 15.6; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
|||||
DB 1 RGGCTAGCTACACGA 16

RESULT 10
US-09-930-423-4549
Sequence 4549, Application US/09930423
Publication No. US20030092003A1
GENERAL INFORMATION:
APPLICANT: Blatt, Larry
APPLICANT: McSwigen, Jim
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
FILE REFERENCE: MBH00, 918-A 400/027
CURRENT APPLICATION NUMBER: US/09/930,423
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 4553
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4549
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-930-423-4549

Query Match 97.5%; Score 15.6; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
|||||
DB 1 RGGCTAGCTACACGA 16

RESULT 11
US-09-780-164-2602
Sequence 2602, Application US/09780164
Publication No. US20030092646A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwigen, Jim
TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
FILE REFERENCE: 400/010
CURRENT APPLICATION NUMBER: US/09/780,164
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/185,516
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 2603
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2602
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-164-2602

Query Match 97.5%; Score 15.6; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16

Db 1 RGGCTAGCTACACGA 16

RESULT 12
US-09-827-395A-2617
; Sequence 2617, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION: Pharmaceutical, Inc.
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowitra
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor C
; FILE REFERENCE: MEH80-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2617
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Definition of Artificial Sequence: Enzymatic Nucleic Acid
US-09-827-395A-2617

Query Match 97.5%; Score 15.6; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCTACACGA 16
Db 1 RGGCTAGCTACACGA 16

RESULT 13
US-10-366-191-14
; Sequence 14, Application US/10366191
; Publication No. US20030228590A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Suban, Radka
; APPLICANT: Beigelman, Leonid
; APPLICANT: Haebertli, Peter
; TITLE OF INVENTION: Antibodies Having Specificity for Nucleic Acids
; FILE REFERENCE: 02-030-A (900/047)
; CURRENT APPLICATION NUMBER: US/10/366,191
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-366-191-14

Query Match 97.5%; Score 15.6; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCTACACGA 16
Db 1 RGGCTAGCTACACGA 16

RESULT 14

US-10-435-044A-19
; Sequence 19, Application US/10435044A
; Publication No. US20030228615A1
; GENERAL INFORMATION:
; APPLICANT: Rossi, John J
; APPLICANT: Scherr, Michaela
; APPLICANT: Riggs, Arthur D
; TITLE OF INVENTION: Method For Identifying Accessible Binding Sites on RNA
; FILE REFERENCE: 1954-2851
; CURRENT APPLICATION NUMBER: US/10/435,044A
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US 09/536,393
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/127,529
; PRIOR FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: catalytic core
US-10-435-044A-19

Query Match 97.5%; Score 15.6; DB 12; Length 16;
Best Local Similarity 93.8%; Pred. No. 23;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCTACACGA 16
Db 1 AGGCTAGCTACACGA 16

RESULT 15
US-10-435-044A-20
; Sequence 20, Application US/10435044A
; Publication No. US20030228615A1
; GENERAL INFORMATION:
; APPLICANT: Rossi, John J
; APPLICANT: Scherr, Michaela
; APPLICANT: Riggs, Arthur D
; TITLE OF INVENTION: Method For Identifying Accessible Binding Sites on RNA
; FILE REFERENCE: 1954-2851
; CURRENT APPLICATION NUMBER: US/10/435,044A
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US 09/536,393
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/127,529
; PRIOR FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: catalytic core
US-10-435-044A-20

Query Match 97.5%; Score 15.6; DB 12; Length 16;
Best Local Similarity 93.8%; Pred. No. 23;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGGCTAGCTACACGA 16
Db 1 GGGCTAGCTACACGA 16

RESULT 16
US-09-745-237A-4549
; Sequence 4549, Application US/09745237A
; Publication No. US20030143708A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
FILE REFERENCE: 400/007 (MBH00-918-A)
CURRENT APPLICATION NUMBER: US/09/745,237A
CURRENT FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 4550
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 4549
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence
US-09-745-237A-4549

Query Match
Best Local Similarity 97.5%; Score 15.6; DB 13; Length 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACAACGA 16
DB 1 RGGCTAGCTACAACGA 16

RESULT 17
US-09-792-818-2304
Sequence 2304, Application US/09792818
Publication No. US20030134806A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Jarvis, Thale
APPLICANT: Von Carlowitz, Ira
APPLICANT: McSwiggen, Jim
APPLICANT: Hamblin, Paul
APPLICANT: Ellis, Jonathan
TITLE OF INVENTION: Method and Reagent for the Inhibition of Gdb-2-related with Inset
FILE REFERENCE: MBH00-801-A (400/013)
CURRENT APPLICATION NUMBER: US/09/792,818
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 2304
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 2304
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-792-818-2304

Query Match
Best Local Similarity 97.5%; Score 15.6; DB 13; Length 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACAACGA 16
DB 1 RGGCTAGCTACAACGA 16

RESULT 18
US-10-279-401-11
Sequence 11, Application US/10279401
Publication No. US20030140362A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
APPLICANT: Macejak, Dennis
APPLICANT: Lee, Patrice
TITLE OF INVENTION: In Vivo Models For Screening Inhibitors of Hepatitis B Virus
FILE REFERENCE: 400/066 (MBH01-1336-B)
CURRENT APPLICATION NUMBER: US/10/279,401

CURRENT FILING DATE: 2003-01-27
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/335,059
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: PCT/US02/09187
PRIOR FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 11
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNazyme Motif
US-10-279-401-11

Query Match
Best Local Similarity 97.5%; Score 15.6; DB 13; Length 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACAACGA 16
DB 1 RGGCTAGCTACAACGA 16

RESULT 19
US-10-201-389A-13
Sequence 13, Application US/10201389A
Publication No. US2003014892A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leonid
APPLICANT: Azharyeva, Alex
APPLICANT: Antopolosky, Maxim
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID PEPTIDE CONJUGATES
FILE REFERENCE: 600/023
CURRENT APPLICATION NUMBER: US/10/201,389A
CURRENT FILING DATE: 2002-07-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 13
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNazyme motif
US-10-201-389A-13

Query Match
Best Local Similarity 97.5%; Score 15.6; DB 13; Length 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACAACGA 16
DB 1 RGGCTAGCTACAACGA 16

RESULT 20
US-10-238-700-4666
Sequence 4666, Application US/10238700
Publication No. US20030153521A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
FILE REFERENCE: 400/057 (MBH01-1158-A)
CURRENT APPLICATION NUMBER: US/10/238,700
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: PCT/US 02/16840
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US 60/318,471

PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4666
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-238-700-4666

Query Match 97.5%; Score 15.6; DB 13; Length 16;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCTACACGA 16
Db 1 RGGCTAGCTACACGA 16

RESULT 21
US-10-277-494-445
; Sequence 445, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
; FILE REFERENCE: MBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 445
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Loop Nucleic Acid Sequence
US-10-277-494-445

Query Match 97.5%; Score 15.6; DB 13; Length 16;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCTACACGA 16
Db 1 RGGCTAGCTACACGA 16

RESULT 22
US-10-230-006-2677
; Sequence 2677, Application US/10230006
; Publication No. US20030191077A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Fosenbaugh, Kathy
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDI
; FILE REFERENCE: 400/056 (MBH01-1110)
; CURRENT APPLICATION NUMBER: US/10/230,006
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 60/315,315
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 2678
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2677
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid

US-10-230-006-2677

Query Match 97.5%; Score 15.6; DB 13; Length 16;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCTACACGA 16
Db 1 RGGCTAGCTACACGA 16

RESULT 23
US-10-306-747A-11
; Sequence 11, Application US/10306747A
; Publication No. US20030216335A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics, Inc.
; APPLICANT: Sandberg, Jennifer
; APPLICANT: Pavco, Pam
; APPLICANT: Gordon, Glad M.D.
; TITLE OF INVENTION: Method and Reagent for the Modulation of Female Reproductive Dis
; FILE REFERENCE: 01-1735-A (400/070)
; CURRENT APPLICATION NUMBER: US/10/306,747A
; CURRENT FILING DATE: 2002-11-27
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-306-747A-11

Query Match 97.5%; Score 15.6; DB 13; Length 16;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGCTAGCTACACGA 16
Db 1 RGGCTAGCTACACGA 16

RESULT 24
US-10-151-116-12
; Sequence 12, Application US/10151116
; Publication No. US20030104985A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Matulic-Adamic, Jasenka
; APPLICANT: Beigelman, Leo
; TITLE OF INVENTION: Conjugates and Compositions for Cellular Delivery
; FILE REFERENCE: MBH 01,639-B (600/020)
; CURRENT APPLICATION NUMBER: US/10/151,116
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/362,016
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 60/292,217
; PRIOR FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme motif
US-10-151-116-12

Query Match 97.5%; Score 15.6; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACAACA 16
| | | | | | | | | |
DB 1 RGCTAGCTACAACA 16

RESULT 25

US-10-163-552-1997
; Sequence 1997, Application US/10163552
; Publication No. US20030105051A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to level
; TITLE OF INVENTION: HER2
; FILE REFERENCE: MEBH01-1653-A (400/014)
; CURRENT APPLICATION NUMBER: US/10/163,552
; CURRENT FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 1997
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 1997
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Substrate Sequence
US-10-163-552-1997

Query Match 97.5%; Score 15.6; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACAACA 16
| | | | | | | | | |
DB 1 RGCTAGCTACAACA 16

RESULT 26

US-10-156-306-8013
; Sequence 8013, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MEBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 8013
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Substrate sequence
US-10-156-306-8013

Query Match 97.5%; Score 15.6; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACAACA 16
| | | | | | | | | |
DB 1 RGCTAGCTACAACA 16

RESULT 27
US-10-157-580A-170
; Sequence 170, Application US/10157580A
; Publication No. US20030124513A1
; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions
; TITLE OF INVENTION: Related to Levels of HIV
; FILE REFERENCE: MEBH01-665-A (400/051)
; CURRENT APPLICATION NUMBER: US/10/157,580A
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 170
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Motif
US-10-157-580A-170

QY 1 RGCTAGCTACAACA 16
| | | | | | | | | |
DB 1 RGCTAGCTACAACA 16

RESULT 28

US-10-201-394A-13
; Sequence 13, Application US/10201394A
; Publication No. US20030130186A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Vargese, Chandra
; APPLICANT: Adamic, Jasenka
; APPLICANT: Karpelsky, Alexander
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: CONJUGATES AND COMPOSITIONS FOR CELLULAR DELIVERY
; FILE REFERENCE: MEBH01-882-B (600/022)
; CURRENT APPLICATION NUMBER: US/10/201,394A
; CURRENT FILING DATE: 2002-07-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 13
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-201-394A-13

Query Match 97.5%; Score 15.6; DB 16; Length 16;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGCTAGCTACAACA 16
| | | | | | | | | |
DB 1 RGCTAGCTACAACA 16

RESULT 29

US-10-277-494-334
; Sequence 334, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related To Level
; TITLE OF INVENTION: Epidermal Growth Factor Receptors
; FILE REFERENCE: MEBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446

```

; SOFTWARE: Patentin version 3.0
; SEQ ID NO 334
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-334

Query Match          97.5%; Score 15.6; DB 13; Length 23;
Best Local Similarity 93.8%; Pred. No. 23;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGGCTAGCTACACGA 16
Db      4 GGGCTAGCTACACGA 19

RESULT 30
US-10-277-494-335
; Sequence 335, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
; FILE REFERENCE: MEBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 335
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-335

Query Match          97.5%; Score 15.6; DB 13; Length 23;
Best Local Similarity 93.8%; Pred. No. 23;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGGCTAGCTACACGA 16
Db      4 GGGCTAGCTACACGA 19

RESULT 31
US-10-277-494-336
; Sequence 336, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
; FILE REFERENCE: MEBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 336
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-336

Query Match          97.5%; Score 15.6; DB 13; Length 23;
Best Local Similarity 93.8%; Pred. No. 23;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGGCTAGCTACACGA 16
Db      4 GGGCTAGCTACACGA 19
```

```

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGGCTAGCTACACGA 16
Db      4 GGGCTAGCTACACGA 19

RESULT 32
US-10-277-494-337
; Sequence 337, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
; FILE REFERENCE: MEBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 337
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-337

Query Match          97.5%; Score 15.6; DB 13; Length 23;
Best Local Similarity 93.8%; Pred. No. 23;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGGCTAGCTACACGA 16
Db      4 GGGCTAGCTACACGA 19

RESULT 33
US-10-277-494-338
; Sequence 338, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
; FILE REFERENCE: MEBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 338
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-338

Query Match          97.5%; Score 15.6; DB 13; Length 23;
Best Local Similarity 93.8%; Pred. No. 23;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGGCTAGCTACACGA 16
Db      4 GGGCTAGCTACACGA 19

RESULT 34
US-10-277-494-339
; Sequence 339, Application US/10277494
; Publication No. US20030186909A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related To Level
; FILE REFERENCE: MBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 339
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-339

Query Match          97.5%; Score 15.6; DB 13; Length 23;
Best Local Similarity 93.8%; Pred. No. 23;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
    :|||||
DB 4 GGGCTAGCTACACGA 19

RESULT 35
US-10-277-494-340
; Sequence 340, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related To Level
; FILE REFERENCE: MBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 340
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-340

Query Match          97.5%; Score 15.6; DB 13; Length 23;
Best Local Similarity 93.8%; Pred. No. 23;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
    :|||||
DB 4 AGGCTAGCTACACGA 19

RESULT 36
US-10-277-494-341
; Sequence 341, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related To Level
; FILE REFERENCE: MBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 341
```

```

; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-341

Query Match          97.5%; Score 15.6; DB 13; Length 23;
Best Local Similarity 93.8%; Pred. No. 23;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
    :|||||
DB 4 AGGCTAGCTACACGA 19

RESULT 37
US-10-277-494-342
; Sequence 342, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related To Level
; FILE REFERENCE: MBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 342
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-342

Query Match          97.5%; Score 15.6; DB 13; Length 23;
Best Local Similarity 93.8%; Pred. No. 23;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGCTAGCTACACGA 16
    :|||||
DB 4 GGGCTAGCTACACGA 19

RESULT 38
US-10-277-494-343
; Sequence 343, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related To Level
; FILE REFERENCE: MBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 343
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-10-277-494-343

Query Match          97.5%; Score 15.6; DB 13; Length 23;
Best Local Similarity 93.8%; Pred. No. 23;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

OY 1 RGCTAGCTACACGA 16
 :|||||
 Db 4 GGCTAGCTACACGA 19

RESULT 39

US-10-277-494-344
 ; Sequence 344, Application US/10277494
 ; Publication No. US20030186909A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: McSwigen, Jim
 ; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
 ; TITLE OF INVENTION: Epidermal Growth Factor Receptors
 ; FILE REFERENCE: MBHB00-958-K (400/064)
 ; CURRENT APPLICATION NUMBER: US/10/277,494
 ; CURRENT FILING DATE: 2002-10-21
 ; NUMBER OF SEQ ID NOS: 446
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 344
 ; LENGTH: 23
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
 US-10-277-494-344

Query Match 97.5%; Score 15.6; DB 13; Length 23;
 Best Local Similarity 93.8%; Pred. No. 23;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16
 :|||||
 Db 4 AGCTAGCTACACGA 19

RESULT 40

US-10-277-494-345
 ; Sequence 345, Application US/10277494
 ; Publication No. US20030186909A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: McSwigen, Jim
 ; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
 ; TITLE OF INVENTION: Epidermal Growth Factor Receptors
 ; FILE REFERENCE: MBHB00-958-K (400/064)
 ; CURRENT APPLICATION NUMBER: US/10/277,494
 ; CURRENT FILING DATE: 2002-10-21
 ; NUMBER OF SEQ ID NOS: 446
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 345
 ; LENGTH: 23
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
 US-10-277-494-345

Query Match 97.5%; Score 15.6; DB 13; Length 23;
 Best Local Similarity 93.8%; Pred. No. 23;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGCTAGCTACACGA 16
 :|||||
 Db 4 GGCTAGCTACACGA 19

Search completed: January 21, 2004, 08:22:20
 Job time : 157 secs

THIS PAGE BLANK (USPTO)